

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13563	AF118082	Homo sapiens	PRO1902	83	86
13564	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	234	97
13565	Y59778	Homo sapiens	Human normal ovarian tissue derived protein 55.	66	100
13566	G01828	Homo sapiens	Human secreted protein, SEQ ID NO: 5909.	103	60
13567	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	152	96
13568	X83703	Homo sapiens	nuclear protein	1633	99
13569	G02473	Homo sapiens	Human secreted protein, SEQ ID NO: 6554.	242	45
13570	G00521	Homo sapiens	Human secreted protein, SEQ ID NO: 4602.	105	90
13571	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	110	80
13572	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	114	46
13573	X92744	Homo sapiens	hBD-1	290	83
13574	P70494	Homo sapiens	Sequence of human B-cell growth factor (BCGF).	107	68
13575	AF107406	Homo sapiens	GW128	356	100
13576	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	101	48
13577	AF220264	Homo sapiens	MOST-1	95	73
13578	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	129	68
13579	AK024455	Homo sapiens	FLJ00047 protein	81	76
13580	AF130051	Homo sapiens	PRO0898	128	64
13581	AF084256	Homo sapiens	beta glucuronidase isoform d	142	58
13582	AF118082	Homo sapiens	PRO1902	85	51
13583	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	114	52
13584	G02455	Homo sapiens	Human secreted protein, SEQ ID NO: 6536.	66	54
13585	X52164	Mus musculus	Q300 protein (AA 1-77)	109	64
13586	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	109	77
13587	AF090901	Homo sapiens	PRO0195	114	53
13588	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	95	66
13589	G03356	Homo sapiens	Human secreted protein, SEQ ID NO: 7437.	117	58
13590	AK000521	Homo sapiens	unnamed protein product	1313	100
13591	AL357374	Homo sapiens	bA353C18.2 (novel protein)	421	100
13592	AL357374	Homo sapiens	bA353C18.2 (novel protein)	421	100
13593	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	139	62
13594	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	103	56
13595	U16359	Rattus norvegicus	nitric oxide synthase	109	76
13596	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	127	88
13597	G00325	Homo sapiens	Human secreted protein, SEQ ID NO: 4406.	275	100
13598	W03642	Homo sapiens	Human cannabinoid GPR N-terminal sequence.	108	63
13599	AF116661	Homo sapiens	PRO1438	128	64

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13600	X55682	Lycopersicon esculentum	extensin (class I)	58	43
13601	X52164	Mus musculus	Q300 protein (AA 1-77)	106	45
13602	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	122	92
13603	AF149419	Oryctolagus cuniculus	eye sodium bicarbonate cotransport protein NBC2	126	75
13604	AJ005567	Mus musculus	SPR2I protein	63	40
13605	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	150	96
13606	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	121	60
13607	G02867	Homo sapiens	Human secreted protein, SEQ ID NO: 6948.	85	60
13608	G03411	Homo sapiens	Human secreted protein, SEQ ID NO: 7492.	57	35
13609	AF107406	Homo sapiens	GW128	108	42
13610	D82345	Homo sapiens	NB thymosin beta	167	100
13611	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	161	59
13612	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	125	50
13613	Y32193	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 044150.	490	80
13614	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	115	57
13615	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	58
13616	AF119900	Homo sapiens	PRO2822	95	53
13617	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	124	58
13618	S79978	Homo sapiens	prion protein, PrP {octapeptide repeats}	88	42
13619	AF220264	Homo sapiens	MOST-1	130	81
13620	U16359	Rattus norvegicus	nitric oxide synthase	95	65
13621	AL132841	Caenorhabditis elegans	Y15E3A.3	168	85
13622	K01664	Drosophila melanogaster	Bkm-like protein	118	65
13623	M86246	Homo sapiens	EHS-2	100	63
13624	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	104	46
13625	AF067205	Homo sapiens	vesicle transport related protein	198	69
13626	U39529	Echinometra mathaei	bindin	72	47
13627	S79410	Mus musculus	nuclear localization signal binding protein	102	52
13628	W80406	Homo sapiens	A secreted protein encoded by clone dh40_3.	123	54
13629	K01664	Drosophila melanogaster	Bkm-like protein	113	46
13630	AF161536	Homo sapiens	HSPC051	582	100
13631	Y27854	Homo sapiens	Human secreted protein encoded by gene No. 101.	158	87
13632	AF130089	Homo sapiens	PRO2550	105	66
13633	AF116661	Homo sapiens	PRO1438	116	53
13634	AF116715	Homo sapiens	PRO2829	101	60



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13635	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	139	63
13636	U33547	Homo sapiens	MHC class II antigen	154	79
13637	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	107	75
13638	AF090895	Homo sapiens	PRO0117	87	62
13639	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	131	69
13640	AF026689	Homo sapiens	prostate-specific transglutaminase	128	60
13641	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	128	81
13642	AC003058	Arabidopsis thaliana	unknown protein	210	67
13643	D38112	Homo sapiens	NADH dehydrogenase subunit 4L	287	76
13644	Y73483	Homo sapiens	Human secreted protein clone y118_1 protein sequence SEQ ID NO:188.	376	88
13645	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	130	85
13646	Y87212	Homo sapiens	Human secreted protein sequence SEQ ID NO:251.	423	97
13647	U50403	Homo sapiens	breast cancer suppressor element Ishmael Upper RP2	103	86
13648	G03800	Homo sapiens	Human secreted protein, SEQ ID NO: 7881.	128	55
13649	X58521	Homo sapiens	nucleoporin p62	2610	98
13650	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	141	69
13651	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	111	81
13652	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	140	60
13653	G03263	Homo sapiens	Human secreted protein, SEQ ID NO: 7344.	121	46
13654	U13066	Nicotiana glauca	arabinogalactan-protein precursor	92	33
13655	S79410	Mus musculus	nuclear localization signal binding protein	134	50
13656	Y07766	Homo sapiens	Human secreted protein fragment encoded from gene 23.	156	100
13657	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	48
13658	G01246	Homo sapiens	Human secreted protein, SEQ ID NO: 5327.	171	80
13659	AK000017	Homo sapiens	unnamed protein product	611	100
13660	U90446	Mus musculus	RNAse L inhibitor	3100	99
13661	AE000882	Methanothermobacter thermoautotrophicus	phosphoenolpyruvate synthase	88	38
13662	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	128	65
13663	K01664	Drosophila melanogaster	Bkm-like protein	97	34
13664	G04067	Homo sapiens	Human secreted protein, SEQ ID NO: 8148.	77	41
13665	Y94890	Homo sapiens	Human protein clone HP02798.	325	98
13666	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	139	65
13667	AF090930	Homo sapiens	PRO0478	119	88
13668	AF130089	Homo sapiens	PRO2550	120	77

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13669	AC006693	Caenorhabditis elegans	Hypothetical protein W02H5.e	165	85
13670	W80293	Homo sapiens	Human translocation associated protein designated Gp25L-H.	1003	95
13671	U23455	Caenorhabditis elegans	similar to D. melanogaster homeotic protein BarH2 (PIR:A41726)	113	91
13672	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	160	60
13673	AL132841	Caenorhabditis elegans	Y15E3A.3	178	75
13674	AF118086	Homo sapiens	PRO1992	85	75
13675	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	132	55
13676	AF220264	Homo sapiens	MOST-1	133	85
13677	Y19730	Homo sapiens	SEQ ID NO 448 from WO9922243.	122	51
13678	Y65416	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1577.	467	98
13679	Y16589	Homo sapiens	A protein that interacts with presenilins.	2286	99
13680	AL160371	Leishmania major	probable (hhv-6) u1102, variant a DNA, complete virion genome	104	52
13681	AF090931	Homo sapiens	PRO0483	117	67
13682	X55686	Lycopersicon esculentum	extensin (class II)	60	56
13683	AF090944	Homo sapiens	PRO0663	93	90
13684	AL096770	Homo sapiens	ba150A6.2 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein (hs6M1-21))	178	52
13685	AF116661	Homo sapiens	PRO1438	115	60
13686	U62039	Elephantulus edwardii	reverse transcriptase	86	53
13687	Y13141	Bromheadia finlaysoniana	extensin	77	36
13688	G03786	Homo sapiens	Human secreted protein, SEQ ID NO: 7867.	114	60
13689	Y36366	Homo sapiens	Fragment of human secreted protein encoded by gene 3.	103	53
13690	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	107	51
13691	AC003058	Arabidopsis thaliana	unknown protein	178	85
13692	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	94	35
13693	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	78
13694	G00416	Homo sapiens	Human secreted protein, SEQ ID NO: 4497.	98	50
13695	D63163	Rattus sp.	cyclin C	111	86
13696	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	118	95
13697	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	124	80
13698	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	129	70
13699	G03787	Homo sapiens	Human secreted protein, SEQ ID NO: 7868.	93	58
13700	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	100	73
13701	M76744	Homo sapiens	BGP	112	52

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13702	Y15155	Homo sapiens	phosphorylase kinase beta-subunit	206	100
13703	AF090901	Homo sapiens	PRO0195	100	70
13704	G02987	Homo sapiens	Human secreted protein, SEQ ID NO: 7068.	131	79
13705	R95913	Homo sapiens	Neural thread protein.	106	36
13706	M15073	Homo sapiens	MHC HLA-DR-beta-1 chain	74	77
13707	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	110	35
13708	G03789	Homo sapiens	Human secreted protein, SEQ ID NO: 7870.	150	56
13709	G02363	Homo sapiens	Human secreted protein, SEQ ID NO: 6444.	89	77
13710	X70775	Chironomus cinclus	Sp12 gene homologue	85	38
13711	X80265	Hordeum vulgare	structural protein	96	41
13712	AB007922	Homo sapiens	KIAA0453 protein	147	64
13713	G03043	Homo sapiens	Human secreted protein, SEQ ID NO: 7124.	124	60
13714	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	108	65
13715	AF116661	Homo sapiens	PRO1438	120	77
13716	AF118086	Homo sapiens	PRO1992	127	64
13717	AK024455	Homo sapiens	FLJ00047 protein	93	56
13718	AF116661	Homo sapiens	PRO1438	137	55
13719	W48352	Homo sapiens	Human breast cancer related protein BCFLT1.	93	59
13720	AF119851	Homo sapiens	PRO1722	94	58
13721	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	124	45
13722	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	117	58
13723	AF161361	Homo sapiens	HSPC098	115	50
13724	Y95829	Homo sapiens	Native human Tie receptor signal peptide.	108	100
13725	AF118086	Homo sapiens	PRO1992	166	75
13726	AF116636	Homo sapiens	PRO1488	95	70
13727	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	137	70
13728	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	149	60
13730	G00673	Homo sapiens	Human secreted protein, SEQ ID NO: 4754.	118	63
13731	U33547	Homo sapiens	MHC class II antigen	123	69
13732	R59843	Homo sapiens	ApoE4Lx2 protease.	135	88
13733	G00357	Homo sapiens	Human secreted protein, SEQ ID NO: 4438.	138	75
13734	AF026204	Caenorhabditis elegans	C30E1.1 gene product	102	51
13735	Y12950	Homo sapiens	Amino acid sequence of a human secreted peptide.	117	63
13736	G03438	Homo sapiens	Human secreted protein, SEQ ID NO: 7519.	112	87
13737	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	115	58
13738	AF130089	Homo sapiens	PRO2550	122	70
13739	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	124	74
13740	AF130051	Homo sapiens	PRO0898	85	70

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13741	AF093748	Homo sapiens	KH type splicing regulatory protein; KSRP	91	51
13742	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	150	77
13743	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	124	82
13744	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	91	48
13745	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	116	64
13746	AB001684	Chlorella vulgaris	ORF54d	70	66
13747	Y02886	Homo sapiens	Fragment of human secreted protein encoded by gene 90.	140	60
13748	AF090901	Homo sapiens	PRO0195	92	39
13749	AF090895	Homo sapiens	PRO0117	148	67
13750	AF119882	Homo sapiens	PRO2492	91	45
13751	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	60
13752	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	129	65
13753	AF161356	Homo sapiens	HSPC093	99	48
13754	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	124	70
13755	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	120	51
13756	AF130089	Homo sapiens	PRO2550	142	96
13757	AF130089	Homo sapiens	PRO2550	132	86
13758	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	163	50
13759	Y19609	Homo sapiens	SEQ ID NO 327 from WO9922243.	92	60
13760	G02832	Homo sapiens	Human secreted protein, SEQ ID NO: 6913.	154	52
13761	U62040	Elephantulus edwardii	reverse transcriptase	134	51
13762	AB001684	Chlorella vulgaris	ORF49b	100	45
13763	AF118082	Homo sapiens	PRO1902	129	50
13764	AF220264	Homo sapiens	MOST-1	129	66
13765	R59842	Homo sapiens	ApoE4L1 protease.	135	50
13766	AF220264	Homo sapiens	MOST-1	115	71
13767	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	139	73
13768	AF130089	Homo sapiens	PRO2550	97	34
13769	U80739	Homo sapiens	CAGH26	564	100
13770	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	55
13771	R10755	Homo sapiens	Non-A non-B hepatitis specific antigenic protein encoded by phageclone lambda HC2533.	102	68
13772	AE004507	Pseudomonas aeruginosa	hypothetical protein of bacteriophage Pfl	93	44
13773	AB044885	Canis familiaris	dopamine receptor D4	78	52
13774	AF026246	Homo sapiens	HERV-E envelope glycoprotein	108	53
13775	S71805	Homo sapiens	RNA-binding protein=TLS/FUS-ERG	126	100
13776	Y86248	Homo sapiens	Human secreted protein HCHPF68, SEQ ID NO:163.	156	82
13777	AB015727	Mus musculus	truncated granzyme M	86	37
13778	G02832	Homo sapiens	Human secreted protein, SEQ ID NO:	74	52

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			6913.		
13779	Y14482	Homo sapiens	Fragment of human secreted protein encoded by gene 17.	137	61
13780	M14123	Homo sapiens	neutral protease large subunit	246	55
13781	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	99	67
13782	AF132972	Homo sapiens	CGI-38 protein	902	99
13783	G02469	Homo sapiens	Human secreted protein, SEQ ID NO: 6550.	147	63
13784	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	128	68
13785	AF130051	Homo sapiens	PRO0898	138	72
13786	AP000616	Oryza sativa	similar to RING-H2 finger protein RHA1a (AF078683)	123	95
13787	Y64890	Homo sapiens	Human 5' EST related polypeptide SEQ ID NO:1051.	92	53
13788	U12206	Homo sapiens	unknown	84	42
13789	G03793	Homo sapiens	Human secreted protein, SEQ ID NO: 7874.	118	58
13790	S79410	Mus musculus	nuclear localization signal binding protein	102	50
13791	G02211	Homo sapiens	Human secreted protein, SEQ ID NO: 6292.	137	76
13792	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	104	72
13793	AB006006	Bos taurus	neurocalcin alpha	1000	100
13794	U63332	Homo sapiens	super cysteine rich protein; SCRP	183	95
13795	W34499	Homo sapiens	Obesity receptor C protein.	120	85
13796	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	127	67
13797	U41038	Caenorhabditis elegans	Similar to cadherin-type repeat	182	83
13798	Y02671	Homo sapiens	Human secreted protein encoded by gene 22 clone HMSJW18.	112	71
13799	U63332	Homo sapiens	super cysteine rich protein; SCRP	91	84
13800	G02902	Homo sapiens	Human secreted protein, SEQ ID NO: 6983.	105	67
13801	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	154	72
13802	AF119900	Homo sapiens	PRO2822	131	50
13803	AK024435	Homo sapiens	FLJ00025 protein	117	95
13804	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	142	53
13805	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	109	48
13806	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	98	66
13807	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	98	66
13808	AL359782	Trypanosoma brucei	possible (hhv-6) u1102, variant a dna, complete virion genome.	150	54
13809	M37679	Mus musculus	Ig heavy chain precursor	70	100
13810	AL451015	Neurospora crassa	putative protein	96	55
13811	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	88	77
13812	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	128	71

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13813	AF130089	Homo sapiens	PRO2550	93	75
13814	K01664	Drosophila melanogaster	Bkm-like protein	119	60
13815	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	64
13816	AJ011435	Blackstonia imperfoliata	maturase	93	48
13817	S58722	Homo sapiens	X-linked retinopathy protein {C-terminal, clone XEH.8c}	130	76
13818	AF119851	Homo sapiens	PRO1722	141	50
13819	G00985	Homo sapiens	Human secreted protein, SEQ ID NO: 5066.	74	60
13820	G02485	Homo sapiens	Human secreted protein, SEQ ID NO: 6566.	76	72
13821	Y02749	Homo sapiens	Human secreted protein encoded by gene 100 clone HNFIU96.	135	50
13822	K01664	Drosophila melanogaster	Bkm-like protein	95	52
13823	L10908	Mus musculus	Gcap1 gene product	103	50
13824	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	146	62
13825	G00376	Homo sapiens	Human secreted protein, SEQ ID NO: 4457.	125	83
13826	L10908	Mus musculus	Gcap1 gene product	96	43
13827	G02971	Homo sapiens	Human secreted protein, SEQ ID NO: 7052.	102	64
13828	G02532	Homo sapiens	Human secreted protein, SEQ ID NO: 6613.	135	53
13829	Y27868	Homo sapiens	Human secreted protein encoded by gene No. 107.	142	70
13831	AP000060	Aeropyrum pernix	101aa long hypothetical protein	79	50
13832	AF119900	Homo sapiens	PRO2822	94	46
13833	Y19767	Homo sapiens	SEQ ID NO 485 from WO9922243.	145	40
13834	AF218028	Homo sapiens	unknown	117	57
13835	L10908	Mus musculus	Gcap1 gene product	79	45
13836	Z26876	Homo sapiens	ribosomal protein	129	93
13837	Y36495	Homo sapiens	Fragment of human secreted protein encoded by gene 27.	124	76
13838	AF044311	Homo sapiens	gamma-synuclein	603	99
13839	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	100	82
13840	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	154	46
13841	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	122	64
13842	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	92	62
13843	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	93	60
13844	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	130	63
13845	G00427	Homo sapiens	Human secreted protein, SEQ ID NO: 4508.	145	79
13846	G03790	Homo sapiens	Human secreted protein, SEQ ID NO: 7871.	102	50
13847	G03469	Homo sapiens	Human secreted protein, SEQ ID NO: 7550.	101	68

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13848	G03240	Homo sapiens	Human secreted protein, SEQ ID NO: 7321.	107	43
13849	U05313	Trypanosoma brucei	CR3	98	40
13850	U28971	Caenorhabditis elegans	similar to RD tandem repeat region of RD protein (nuclear rna-binding protein)	100	65
13851	AF159055	Homo sapiens	leucine zipper-like protein	103	55
13852	R59842	Homo sapiens	ApoE4L1 protease.	99	71
13853	Y01158	Homo sapiens	Secreted protein encoded by gene 18 clone HCACJ81.	142	65
13854	G03714	Homo sapiens	Human secreted protein, SEQ ID NO: 7795.	119	79
13855	R59842	Homo sapiens	ApoE4L1 protease.	93	69
13856	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	114	76
13857	W48353	Homo sapiens	Human breast cancer related protein BCFLT2.	94	57
13858	U63332	Homo sapiens	super cysteine rich protein; SCRP	105	58
13859	AF289022	Homo sapiens	formiminotransferase cyclodeaminase form C	467	100
13860	AF078844	Homo sapiens	hqp0376 protein	488	100
13861	AB032436	Homo sapiens	brain-specific Na-dependent inorganic phosphate cotransporter	2968	100
13862	G02514	Homo sapiens	Human secreted protein, SEQ ID NO: 6595.	91	72
13863	AF130079	Homo sapiens	PRO2852	131	63
13864	Z29701_cd1	Homo sapiens	29-MAY-1998 Wild-type human c-Src tyrosine kinase cDNA.	2380	100
13865	L77967	Ovis aries	small proline-rich protein with paired repeat	80	33
13866	AL050318	Homo sapiens	dJ977B1.5 (myosin regulatory light chain 2, smooth muscle isoform)	904	100
13867	U37690	Homo sapiens	RNA polymerase II subunit	358	100
13868	X13923	Homo sapiens	cytochrome c oxidase subunit VIb (AA 1-86)	491	100
13869	L13848	Homo sapiens	RNA helicase A	6669	99
13870	G03172	Homo sapiens	Human secreted protein, SEQ ID NO: 7253.	133	46
13871	K02064	Bos taurus	cytochrome c oxidase subunit IV precursor EC 1.9.3.1	96	72
13872	D31763	Homo sapiens	ha0946 protein is Kruppel-related.	4606	96
13873	Z14014	Nicotiana tabacum	Pistil extensin like protein, partial CDS only	83	43
13874	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	117	70
13875	Z52203_cd1	Homo sapiens	17-SEP-1998 Human PRO217 protein encoding cDNA, UNQ191.	2135	99
13876	G00397	Homo sapiens	Human secreted protein, SEQ ID NO: 4478.	106	64
13877	G03807	Homo sapiens	Human secreted protein, SEQ ID NO: 7888.	143	50
13878	G00689	Homo sapiens	Human secreted protein, SEQ ID NO: 4770.	104	60
13879	L25404	Brassica napus	cyclin	124	42
13880	AL390114	Leishmania major	extremely cysteine/valine rich protein	139	59
13881	AC003113	Arabidopsis thaliana	F24O1.6	70	64

SEQ ID NO:	Accession No.	Species	Description	Smith-Waterman Score	% Identity
13882	AB000098	Rattus norvegicus	MIPP65	905	50
13883	Z95114	Homo sapiens	bK212A2.1 (TNF-inducible protein CG12-1 (similar to apolipoprotein L))	1639	100
13884	AF132984	Homo sapiens	Nuclear pore complex interacting protein NPIP	551	82
13885	AF121862	Homo sapiens	Sorting nexin 13	1453	99
13886	G02493	Homo sapiens	Human secreted protein, SEQ ID NO: 6574.	83	69
13887	K01664	Drosophila melanogaster	Bkm-like protein	109	77
13888	AF217197	Homo sapiens	FBP interacting repressor	2725	99
13889	D38112	Homo sapiens	NADH dehydrogenase subunit 6	187	94
13890	AF118086	Homo sapiens	PRO1992	85	62
13891	M58664	Homo sapiens	Signal transducer CD24	371	97
13892	AK023443	Homo sapiens	Unnamed protein product	125	45
13893	AB040972	Homo sapiens	KIAA1539 protein	2271	99
13894	U03750	Escherichia coli	DeaD	95	48
13895	G02538	Homo sapiens	Human secreted protein, SEQ ID NO: 6619.	73	53
13896	AF078851	Homo sapiens	Secretogranin III	2384	99
13897	U62039	Elephantulus edwardii	Reverse transcriptase	109	48
13898	X07816	Human herpesvirus 4	Epitope Cl3 (57 AA)	55	53
13899	AF116661	Homo sapiens	PRO1438	146	48
13900	G00354	Homo sapiens	Human secreted protein, SEQ ID NO: 4435.	77	60
13901	Y28643	Homo sapiens	Human serine protease inhibitor from cDNA clone HETDK50.	2191	100



TABLE 3

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1	13902	A	1	114	434	AIFKCVGEMFRIAMVNVCFVSSGSLLI* PLTY/GVYDEWTHFAYMTIDLLEIPITG SHPVVLNALFCLEAP\WISPNTGSPAYP VYPKSLIAHDFAVEATMPYIRLSST
2	13903	A	2	124	466	KSNIPNLGDCGWESLFNR\QSWRSSLAV \NDTYSSKKSNAETFTFHADLCTLSDKD RPITITQTALAEVLKHKPKATYEQLIAVL DEF/ANFLKKWWKAYDKENLFCCEG*KL CAASN
3	13904	A	4	1	427	EGFLELLRTRNHSNSQLQLTTGIGLFLN EGLKLVDKFLEDV*K*YHSETFTVNFSD TE*AMKHINDYVEKGTQGKIVDLVKELD RDTVFDLANYIFFFKGWDRPFEVNDTEE EDFHVDQVSTVNEPIMKLLS\MLNIHPC FKL
4	13905	A	5	1	464	KIKSFYASKDTIKRMRVTDWKKIFAY*I SDKELIFTLRTLKT**K*GKQPNLKNQ EI*VPISPQDIQIAHK\HLEGWSTSLVS ELAPCEAPV/RHPLTGLTIAGLQGFGEA GRLVRGRWGC*W/VHPF*KYI/WQFLSK LHISLPYDPTTPLLGTCSR
5	13906	A	6	308	3	HFVTHSKHDLATAHLGIY/PREMKT*VH TKTCT*IFTVALSVIARAWNQPGRPLCS EWL\KYMVHTME*HSAIKRLNYRYKNNC VNLFLGITLSEKSTQONVI
6	13907	A	7	587	2	FLTRETGDPTGRSSSHANTQSRFFDDP PG\PLNNLGNTHGCGRRAGRCPGTGPDG P\AGCGGPRCWPSGHLAATGD*GPSCGR LGANRGEAGPAGFTACSPLSGCRTPYTH HFPASRMSCHLNCASPRTYRSQGNRGCE RVAQGSQGAGGERGAKSQVPVPAPARNK DPAKCRKPRNRRPGNSGPVVRAYRRQR
7	13908	A	8	1	474	RILNEEHGKYEGLHE*EVKWHLYIKSPA FTDLHLCYQKDMNGISTASSPAVGTVG MDMDEDDDFSKWNFYSPHSYPDK*LTI FKTESRVRESDEVTQIKVNWDEEVISGL LTSKDNVLKATGVLYDYAYK\YLCEHT RSTLKEESLKLERNLQNH
8	13909	A	9	3	539	SQCSPIFSPACSLTALTEETEALRVHPR LCLSPNLAPSSGPPRPPELAPCPPSSQA GLRTCHSWVKGLHQLPVASGMKSTFCN KTYTCTPYPPP/PPLCPNHSPNALTLPS VTHAVPFE/L*SPSAPPSSTA*ILGSPS \CGASPCNHPSHPGICPTPPGLWPVCP CAPRAWQRDGTROT
9	13910	A	10	2	453	RL*LGLEYALLVWGTPKV*H*GGFPIYY YIVLLLSYALHQVTEYSMYVSIMAFNAK VSDPLIVGTYMTLLNTVSNLIGNWPSTV SLWLVNPLTVKECV*TSYQNCCTPDAAE LCKKLGSCVTALDGYVESIICVSI AF V/W*VFLVHKFK
10	13911	A	11	20	475	KMGVDFLLMSDPNRFLLFPKNFLREKTIS PPKTF*PLKIWVKGWVLNFLGFPFGFKI FFPVFKFFFFFFFF/RDRVSLYHPGWSA VSQSELTAALTSPGSGDQVILPSQPPK* ENHLNLGGRGCSEFRLPRAEFLDLRSFS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IIVIFP
11	13912	A	12	392	63	HIRADPGLEPRPSARTGLGPGLGCCTMN KLGDAGSATQSLGGSQSLWSRREQEL EQARWEAQ*QVETLGRVAREKEALAKEH AGLAVQLAA\AEHEGRTVSEETHLQ
12	13913	A	13	18	338	APHPQYLLQMPMLLPRTGPGQFSLFSS RHGGHLE/GKEHETSVTLGCGEPPPTP PRDPDPGP*ARRAPCPRRPT*AHPRALS RAAPQEPRALAGPRARHPICPGSL
13	13914	A	14	2	371	TTKQ*KDNPIQTGAKDLKRHFCKEDMQM ASNHT\KRSLTSLVSREMHIKTTRMAGI KKSDDNNKH*GRGEIRT/LLRCWWDCKV VQLLWKTWQFL*GLYQYIPHPVISRL GISLILYIALRTF
14	13915	A	15	443	1	SRTFLDMDKSMRGFKAS*NRQTLLLGA NAAGD\KLKAMLTNHSNRKILQNVKVC TLPMLYKWNNAWMTAYLFTTQCTEYFK PTVETHCSEKKISF\KILLTIYNAPGHL RALMQIYKEIHVVFPVNIPISILQPIVQ NVISTFKS
15	13916	A	16	375	38	HQQNGFLKKTDPDLLCLQETHFR/CKDT KRLKVRRY/QPNSNQKRAR/VPILIEDK IDFKTKKIFMMIKDLTIINI*ASNTRVP KSMQKLAGLKEEMDNSVIMVGFSYPV SIRK
16	13917	A	17	448	189	NRDRVSLCCPGWS*TPGLKRSFHLGLPK CWDYRRDIY*LL\FARHTQMISTHS*QT TNTCSYPAF*KSRP*EPGYNTTHTPHSS DML
17	13918	A	18	1	426	GMSHHARSLIINQLFKKCSLTLFVL/REM QIKSLASSSSSSSRNSVSGQGFETVGT HCGQKCKLVQPF\WKAVW*YLLKLVFI LFLIYNRNAHLEDTCENVDRALFVIVKN WKLKYPGKWKRIKLWYSHSVESSTAV LPKV
18	13919	A	19	2	423	YFETFPQLLRRLGYQGTFFFF\KPWSSC LGIEYNSGPDSCA*FFLQNIQLVNSAN IRLMAMTLKTNQVAIAQFLECKESDQOF CIGVTHVKARTGWA*F*SAQGCDDLQNL QNVTO/GAKIPLVV*GDFNAEPTQEA*K HF
19	13920	A	20	10	443	LKVDSGDSEVRYVFILQHITLLMCSAYM NQLLNI FVRPSLLAVALHMTPGFTKEDV YSCFRFLRDVFADEFIFLPGNTL*DFEE SCYLLCKSEAIQVTTKDILFTEKGNLTVL *FLVGLFKPF/VESYHIICKSLLEK*A PFIEEP
20	13921	A	21	11	426	VLVETNNLRMGQVTM*PELPDM/SPDAW TLDSPSPQKIGHAQQ\KYSIIKWKWYTE DWAQACLEDTSKYEQVTQIPMAPNDATL /PSS/AHLAFTAS*GAPSDS*LRNTLGL ICDGT\KPSSTN*KQTVIALQSHAGLN MKEC
21	13922	A	22	1147	1768	QLGMSHGYSSKSMPPQKLMCFLNHHLQK GHECLPKVLNSNPPPIIKYLALQDMLL SQYSPSRQEVFSLSQPCGHPHNWTAS RECLNLLNGMTQKLILYQEAATNGRVS SSYPVEPKKLNSPEETAFTQTPKSSQMPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PSVPPPLVKTSLFSSKLSTPDVVSPPFGTP FGSSVMNRMAGIFDVNTCYGS*AT*HSE W\LLNLSLLYHVWLCGVFLLT*TWVSWI LFKIYATKAHVFPVQPPFAEGS*VPSKS VK*QSSP\LIKYLALQDMLLSQVSPSR RQEVFSLSQPGCHPHNWTASRECLNLL NGMTQKLLLYQEAAATNGRVSSSYVPEP KKLNSPEETAFOQTPKSSQMPRPSVPPLV KTSLSFSSKLSTPDVVSPPFGTPFGSSVMN RMAGIFDVNTCYGSPQSPQLIRRGPRWL TSAS
22	13923	A	23	421	3	KIIFRAFKG*KSPSPMPGFK*KDRLILL LGTNADNDFKRKPM/LLYHSKNPRALKN YIKSIQPLYE*KKA*MTAHLKVVWTEY FKPIVGYC*KI/SFKILLNDDAPG/H PKALIEMYREINIFMSANTLFILQPMK GVI
23	13924	A	24	226	2	THERTHSKI IHVITIKITHPLNPSILRP QTTA*IKWRDLGSLQPLP/PG/LKRFSY LILPSSWDYRCPPLRPAFNCIF
24	13925	A	25	2	611	FFFFLLGLLHQIPDVSP*TKYTTLLPL MILMISGIKEVIY/DHK*HGRQNS/VR NTKLL*QDSWDTFKWKEVNVGDTVKASN GELLPADTVPMC\YIATSNPDRETN/VK TRQALPETASV
25	13926	A	26	1	443	ATQWRPSLVPASAENVKARSFAAGIHA LGGTNINDAMLMVQLLDSINQDELVT* GSVLLIILLTDGEPTAWETNLMISQNNV REAVRGYSLFCLGLGFDVCYAFLEKLA LDNGGLARRIHEDSDSALHMQDFY\QEV AHPLVTAV
26	13927	A	27	2	359	KAQSKQWLPRGGSGPVK/ARVDEESAKV IVRVYWEAQGILLIDFLKGQRRTIYAYS ENILRKPEL**RNAWGSFSRVLHHDRA AHFSHQ/TRAIG/REF**KTIRHPHY/S PNLNPLDAFCF
27	13928	A	28	2	427	WRKTVKGHFTDQCRKHKAM/LGN*IHFL EYHIHKHSIQYSGIQATQEKFGGLKTSY CSKD*YITVLDLTLKISNKDVSN*HENP ISMYKN/IPTVIYGSVKIKDRKLKA*I* CP/HRNKKF*YFDYFYVLLNTMTFLKLW RIITEI
28	13929	A	29	47	412	HCDVLLASSRYTCILPYSRDRDDGPQDQL KMSVDFRSRRTGS/WFPQNSWGHMGVCG WGGAGRTLDLIHLRIPMRGLRSGGFLLCR RKLVSSESYG*EPSPL*K*KGGWGSEPS/ LTTVPSQL
29	13930	A	30	336	419	RLECSGMISAYCNLSLPGLSDPNSASR
30	13931	A	32	1	408	KIALKLRSNYSKISGY/MANIQLIIFL YTSNEQIEFEIKNTIPTFLAPPKIK*LG TNLTKC\VOELYEKIYKSVMKNIKELNK WRSSYGKGSKIKIKINK*MDIACSWL RRLKIVKISVLHNLIRFNIPIEIP
31	13932	A	33	412	2	QGHLSLQKFL/LPFFVQLCPAPRGGVYRG RQDSLSCGGLHPF*ASGLLCLPTQASAM VGTPPPASLLLCSSILDCCASNERGSGV VEPPEPGTGHNLLVCRLLRPLEKRSIRW KSAVGVARFSRCRPSWLPLARKKNSP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
32	13933	A	35	304	33	KVWGEKVWYQKMTQIVQWDRTESPQID N*SLTKEIQWRKDSL FNKW*GNNWTAPF SS/RSLNLNKDLTAVTRIKSKWVTDLNV KHKTIKLL
33	13934	A	36	2	424	SKTYSIGHFTYEGKGTITSLWGKVNVED AVGETLGRLLVEYPTWQRFDFSGKLSS ASAIMGNPFVKAHGLKGLTSLGDALQHL DDLKG\TFAQLTELHCDKLHVDPENFFL LG*VLVTVLALHF/SRRFTP/ELQAS/W PKM
34	13935	A	37	2	433	NKRLPGPGF*KRPNPPGEGGPARYFNPL GGPNREIPLGPEV*THFGPQMRPPVFLK ILKISGAFWGPVGPPTWGG*EGLNPRG PGYN*P/R/PPAPPPWG*SQAPFPKPAP PP/TGIKPNP
35	13936	A	38	3	425	GAAQLLPVSLPSAQRAIDLQILTPWEN WTSIASLQHKTTIGRSWLITGPISATSS TPTSCTVASP\TRGHV*RSASWKYDVLQ HSSHMWVHTAVYLGEAFHQVHATGSSCH HRVLSCCPITGRSGRDAL*QLLPL/HAL TEA
36	13937	A	39	2	463	LNEVRDIKLSSDHWPSKTNFLHSPGFL SRFEPQPASVA/PRP*SQQSLPGKAST SLWPPNPVFPVTSSLSALPGLFLWLP SIPPLPGSPFFSPE*PEVPLFPGPPTYHN PSPPD/PTVLEAHPDQAPLP\PGVPTAE QRPTPAP*AHRRPS/LPLPP
37	13938	A	40	223	408	RNTV*NIGTDKDFMT*TPQAIATKAQID KWNLEPMSFC/TYRETIIGVTDRYTRD KIFESGR
38	13939	A	41	3	427	NLKMKSRTSKENIGEHIYDFDIGRFVNT *SKPERKRLSFKTSVQEKTP*L*GKHK* MKLEP\LPYPKINSKWKDNVRSKAIKL LEENRSESSIWQRL/SIMPKAQAIKEK VDNLDFFKIKNCVSKDTIKKALDRPSE EKI
39	13940	A	42	30	448	FEMREITVAFHSILIRYHGLINLRKFQ* MDRRYSKEVQDLLETMKLFARIVGPL*H DKFIESHALEFELLREIKRLQEYRTAGI TNFCSARTYDHLKKTR*EERLKRMTLSE VLQYIQDSNACQQLRRETY\IESGPNP
40	13941	A	43	1	928	LRQRMPPQGLQPCPWPPRYP/PDSPLGC PGGLA\PPNSPSWPKLASLAGSGSSAP PGVWGLVATGA*PLQRPSAPPPCPR/LC PGREPCMCP
41	13942	A	44	2	409	SKSPDPTQQPLRGSLTHSAPGPSLSQP LAQLTPPAFGPSTSSLFNLQKSSLSARH PQRKRGGPSEPTPGSRPQDATVHPACQ IFPHYTP\VWHILGPQRHTP*SVD/HPG LDKRLLPETPGPCYSNSQPVWLCLTP
42	13943	A	45	3	136	LPMTLFTLELE*ATLRFIWNHITIQIAKA ILTNQK\NKARGITNIC
43	13944	A	46	365	2	AWGSLRAPRSAPVPEPGTPPVMGNALARR QFSPCLDGLSCPSFLRG*NSPPHPGSPG LPKHA*APAAVSPWVDPDRTVQPPPPAP PST\D*PHCSPPCTPWCPRRLGSAPVMP GCPTASYPRR
44	13945	A	47	1	456	AELSELYEESDDLQMDVMPGEGDLPKW\

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EEATGTRAAIPWVPPATGAQQLEEEGPM EE\EEAQPMMAPEGKRSLANGPNAGEQP GQSPGRRTSRAEDEA\EEFDDWEDDYD F\PREEPVKGARLRFLPPS*KTPPSFWE NRNTPLWGGLKIFY
45	13946	A	48	116	442	PQNMGMERKPGPPKGLSWASGDLEDNLG VMSVGFLSSPDDAVIWRGPRKTGLIKQ FLRNGTGEKVDYFMGDTQLGTSDEHLSS VATWAKAHLGEPGAFTTFQRVSLRE
46	13947	A	49	434	3	FTVPGPLLTVIPFIFISKVPFKFSLPQIF NFTPFQFPQIRV*TIIPISLRFPRKKP LFFFF*NKVPLCSPYWNISARSWVPAAS VFQV\KESFYLNLLSVPPQVPLNVFLTF FFFFFLGRDR/SLPLLRMVWNSWAQAI LPLWL
47	13948	A	50	1	482	EKPYQCSDFGKAFNMKTQ\LVVHQGVHT GNPNPYQCRECGKAFGRKEQLTAHLIAHA R*KPYGCSECGKAFSSKSYLVIHRRHTH GERPYECSSCDRAFCKGSQLIIHQITHS TENHYECNECENTYPRKASLKIHKIDL GKKPF/ECNEWGKALLK
48	13949	A	51	1	470	REFLWQEGHRAFATVDEAGEEVLQILD YADVYEELLAIPVANGTKTDKDLAGGD YTATIEAFICASGRAIQGGTSHLLGQNF SAMSEIVLEDPEIPGENQFAYANSWGLT TRTTWVMTIGHGDNMGL/LLTTPRVA*VQ /MVIIPGGIPKAFLKRQKT
49	13950	A	52	26	448	SPGTEREYRIGQQSVTVTSVDDNSY RIRGKSATVCERGTPIK*GQPIRLTHVN TGRNLHSHHFTSPLYGN/QVAL*GDIVI IL*RRKQRLKGFTTEGIKLRFEKVSFAFG DEGEDYLDWTVLCNGPYWVRDGEVRF NT
50	13951	A	53	3	495	AMEVKAFETHIRGFTLNDAAANSRLIIT QVRRHYLKEAATTLKTVLDHQHTPSRLA VTRVIQALAMKGDV\DN1*VFHKLNLGL EDSIGLSKMDFINNIALAQI*NSNLDAS V*HIENMLTS*NNVIEPQYFGSAYLFRQ VLEEQLPTVEKISIMAERLAKPLQ
51	13952	A	55	1	428	QERGTTKEMEDRMTLEETK\EQILKLEE KL*ALQEEKHQFLQLKKVLHEEEERRRR KEQSDLTTLTSAAYQQLTVHTGTHLLS VQSPGGHNRPGTLMADRAKQMYGPQV LTTRRYVGIAAFAAGTPEHQGFQGRPGG VYG
52	13953	A	56	2	453	EDGDLDAFSSDEGLTMAMSYLKDDIFRI YITETQECRRYHRPPCAQEAPCNMVHPI VICYGCYGPVGVTRYTCSVCPDYDLSSS CKGKGLHRGHTKLAFFSPFGHLSEGFSS SRWLRNVKHGLLRWS*WEMGPPGNWSPR TSCA/GEARLGP
53	13954	A	57	3	435	ELNTSIFRSRPIEGLNLTVLTNDNSNL VI\NRIGIV\PSVTEKEYTDPSSDGTYA WKIFSHTITKAQILKFLSYDYAVNNP WLAYPHYKSPEKCPISILHDLRYLNLGL *CAASAMVMIAIVTYNVALLAYHRWNL TYMID
54	13955	A	59	409	1	LCCEHRGKTVCVPRGKFTTLNASINKER

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SKISVLSFRLMKLKKEYVK*K*\EKEKINNRRIRIEKINKAKS/WFL*HNKIE*TIRMINHQKRENIQITDFRNERTELPDSTD IKKAIRKY*K*FYFNI FYNPEEMNKF
55	13956	A	60	1	393	GNVSSCGDHPCEG*LCP\PDKVM*GI*VPEEACTQCIGEDGVHHQFLESWVPDHQPCHICTSLNGRKDNCTTQTCTPGKASTCGLCELARLRQNADQCCPENECVCDPESCDLPPVPN*ERGLQSTLTNP
56	13957	A	61	250	1	REDCKRVLYKDKVSLCCAGPCSA*SC KAASTFQ\VKHFSLSQSSWVYRHAPGLANFFHFLQRQVLTTPPGLVLNSWVHAI
57	13958	A	62	365	3	IKKKLIWRLFTFPKPSWGKKTKGIFPF*GPKKIPGIKFPQGIKKAFAKGNR*TLGKGN*KKKKKKKECGPGDIPCS*IG/RNIVKILII PKAIYSFNTIHKIPKTFPTEIETTLIKFL*NH
58	13959	A	63	245	558	FLPTQVISYVKRALAEGAQI*CGEGVDKLSLPARNQAGYFMLPTEITDIKDESCMTEEIFGPMTCDFVPDSEEDVIERANNVKYGLAATVW/SSNVARV
59	13960	A	64	106	532	ERACQSGTSGQGGVPRRAIGAPR/E/DAFTGAVYIYHGDAGGIVPQYSMHPFA*SLYPSGQ/SVAARGNLSGDSFNCHN*GLQG LLLASSV*RPVMLLNDPIIYTTKN/ISGPKCHE
60	13961	A	65	2	548	VQKYPQQRSCVPPVAEWA VPPQSSRLKYRQLFNSHDKTMSGHLTGFPQARTILMQSSLPQAQLASIWNLSDIDQDGKLTAEFFILAMHLIDVAMSGQPLPPVLPPEYIPPSF/RRVRSCSGISVISSTSDQRLPEEPVFRDEQQQLEKKLPGTFEDKKRENS*RGNLBLEKRRQALLEQQRQG
61	13962	A	66	72	952	SSRTYTTSPLLLKKEVTRKIRKYFILNNN*NTTYHNLWDLTKVVFSGKLLF*RSR*EYRKDKISDLCFYIQMLE/QRQVIKPKVSTRKEINKSRTQ*SGKETMERPKLEDKFLVNINNINNP**LNL*RKKEGHHCIFYRH*KDNKGYTYANNFNILDQMDKFFERYVTKMD\QBQIVSLNIP IADKSNA*LNNFSSSSSSSSSSSS
62	13963	A	67	139	422	VNGNEPEPL*KGISRHEHRRQPHNGFRPKNKGGAQNQ*ASLGMKTPEAPAHSDKPRRQHAAYSS*AMPFLGICISFSQCNL/CPPKLV
63	13964	A	68	274	1	NLKNKAVITKTA*H*QKNTDQWNRIKNPEIN\HPFYGQLIFDKDAKNTM/WKR/DSNFK*CWEN*ILTCKKMQLHP/SLTTNTKLNSQWIKDL
64	13965	A	69	22	419	KTIIGEDGT/PLSEMAKSQRQIFSKDLVKLDSTINQVDIIDIYKLHHP\KWTVYTF FSSH*GTFISKIDHILLDKTYPNNL*RTGIMQHMLSDIKVFKLEISTRKVTEKS*HTMSLCNKTLEHPSGNEDASAYLK
65	13966	A	70	57	423	KDKNSQVTSEEEQEGKIKENLNSWRDTR/CH/WIGR\NIVRLSFLPKLFI FNTVPIKIRTQFFMKLNKPVLFKFIY*TKRTRIAKSLKKK/RQEGKISPTNRRTYEAYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TLESTIGASMPSLDLG
66	13967	A	71	394	1	KHFRCLQEDCRILLWFFSETGSPCAV SPRIECSSKIIVHSLKLLGSSDPRASLS *VAGTIGVHHHTQP*GI/CNI*GSGRRR SEKQWIEKNVSSEAKRRRTF*NE*SV* KGDYNKDQGLRLGTVAHAYN
67	13968	A	72	485	1707	SALGLSQPRPPGASDAAPDSTPAGV*TA SSSAPAGEKDANQMEWARRDPGPHLHQA PAPH*SHLVRDKRAQERLRKTSRGPPHS HRSGPVDLSPRSSHSDSTPVHGPYFRS APDPRGSAPAFRGPIATRGR/RPRAPRA TASHVPLSSSSWKEPEEATAPRF*ASAC MKWRLEAGCPGHRGVWPGPPSRRLFWA TATGEKSTPSPFTGVWRFGVEACT*AGS PTAHIQHSQRTWQPVPPCTNGSRSPWTS SYPKNQSKVGTVPKRGWACQPIPETAVR QATISQ*ARKGAARPHQARQVEHSTQ/ QRPSGDSGKFDQSLCEASTLLQPERPE VQKICKFRV/GERRRTASPNSAVPEKR TRTQTMVGTAFIGCSGKWRVYSVRR/R SSPRIPPPGVGSS\PLKTPPPP
68	13969	A	73	1	462	QDHRSSSHSNKRPSLASSLSENFQRA AKPLQVNWKKLYSTPLLAIPTCMGFGV HQDKYRFLVLPSSLGRSLQSALDVSPKHV LTKRSVLKVACRLNLNALKSSLKMSWVYG RVT*KYLL*F/YRTTNRGLL*SMGFAFR YLPBGDNPAHLERGN
69	13970	A	74	307	436	LP*VGCTEGIPEQDMVRGKHKLRLQEK TRLIGPNCPGVINPGECKIGIMPGLHIK KGRIGIASRSGTLTYEAVHQTQVGLGQ SLCVGIGGDPFNGTEFIDCLEIFVND TEGIILLIGENGA/NAEDNAAECL
70	13971	A	75	1	435	EISDSKAQLAAMALIIDTWERMNCFS* NHEPLRTHCALAASKLLKKPD/QAE\RE HLCTSL\WSGTNTDKNGEELHGGKRVME RLKKALIIAHQGMPSLQVRVFIETLNR YIIFYEKENDAVTIQVLNQLIQKILEDL PNLESWK
71	13972	A	76	58	366	EFPDLVKDMNLHIQEAQCIPNKINLNL MNRHRII/RLNNTTTKKRILKAAKQK*N I/T/IRGSSICMMMDFSSEITEDRRKWH SI*KILK/EKTQNCPLPRVFCPVKI
72	13973	A	77	1	445	YHETGCFLMGAIVDITLTFNTYVHFQK MKGFSLLADPQEFWVDNSTSMSAPMLSG MGTFQHWSDIH\DNLSVTHVPFTDSACL LLIQPHYAFDLKVEGLTFHQNLSLNMW KLSSRTIHLTMPQLALQGSYDL*DLLDQ A*LSDILT
73	13974	A	78	53	444	ERGGYGAGPVAWQFLVPSTAPMLQSPPL GFAIDHTPPVPAPAN*APCPLPYAA*RT TGPHHIAHLDTTFGTGDTPHPSSPASPP STPWLPAFPCPLPTWD/RPPCLQPLLS SLPTPRLPFLCFLLLAPYAP
74	13975	A	79	1	353	HIRTELDDYGLTVVITYSDT*EAYNYIY IMVT*NVYKPOLWNI FDRATMHSQDVRH HLLCIRLMLKNPKHHAV*/VLNGHYAFV SR/SFKHALVQYVQAFRTHPDEPLYSFC IGLTFIHM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
75	13976	A	80	1	350	LYFYALLFLSSG/CVAYVATRDNCCILD ERFGSYCPTTCGIAYFLSTYHIKVDKDL QTLEDILHQVEDKTS*FKQLIKAIQLTY NPDDSLKPNMIDAATLKSMMKL**IMTY EASILT
76	13977	A	81	76	386	PAYPQVRGPASTPASCIRPTNARVLSTT PRGKSVAEAHSVSPSAHRGVTSVIKLWS AKRLH*YGA\KVRPNS\GCTP
77	13978	A	82	1	360	ESILQEDITVLNVGAPNNRASKYMRQ/M LVELQRQIDESIIICEDFNLTISEMDST RPKISKDIVGLNGTIN*LDIIDIYRLL* PTTAEKTFSSSRGAFT*MDHILCYETH LYKFKLHE
78	13979	A	83	39	344	WGILEGGEYIWHVGGGKSLRASGGLWSQ PPRQPDSDRLVLPVCHLLPHWIGPTD LGHKRQW/MGPGAVAHVCNPSTLGG*GE WIT*GREFETSLANMVKPC
79	13980	A	84	1	427	QQAHLAGHHRIHTGEKP*KCEACDKVYR GKSSL/MK/HRRIHTGEKAYKCEECHKV YSR/N/SQTVKDRRIHTGEKP*KCKS\C DKAFGHDSHLAQHARIHTGEKPYQCNGC GKAFSRQSTLVYRQAIHGVGKLY*GNDC HKVFSNAT
80	13981	A	85	88	307	TWTQRRAKLVRRIGWALLPFPSPSGSKP PP*TPPALPPCVP/PQSSPWTTPQPAP DSREVSKDWTQMRSEKEN
81	13982	A	86	5	375	NSLLNTHSRGPGASHCTFWLHERASSRD LTGAESYGICRLRLRLISLIVFSKSIHG LACISILFLFLFLFLFFVKTSWLCCPG WPQAPELQSSLLSLSSWNYYR*PPHQ LIF\DFFCRN
82	13983	A	87	2	342	VIKNEDHYIMIKCLI*QEDQTILNLHSF NKTNINIKPHMTNLQKAVDKITITV*T CGTSLSLIAVCRLKLVKL/VEDLSNIN KLDLM/DNIYKTLHLNIRDYTFKHTWN IYKN
83	13984	A	88	1	338	CNEPRSHCTPAWRQSKTPSKKKKQKKK LTTS/CIKASMKS RVQG*LR/CWAQVMG **GGVLWLFVK/REFFTLSINLSKEGHS RRVPCLGCLKKKKKKKKKKKKKKKKKK KKFF
84	13985	A	89	931	2	VASPNALPE*LLPVSGHThDLERVGVAR LQQPHHTELTA CRAMESRDTCPGVTLH P*PPSFPSSSSPSPGGPRTRLTHQGAGL EGSQGPLQSQNPAA/PLGACRGGWEWP QGP GSGS*GG*LMLREIRE/WQEAQVL PTPG*PS*ESGRPLSSASGPTPPGSP/ SP*PGTQGLCGCHPSGLCATAAGPDGS GPTPTPH\PVQPSCRDSGPGQRLSPTPS LTSWPNTRPSPPTGPGGPGGRATW/PG S/PSPQRESPPQLPCCTPGSFAGHPCP AP\AAPSSVACPLP/PDGFPRAPASSGI TTAPSPGPDF
85	13986	A	90	66	464	LWVYSSFPRLPLHSGAESPEGDILWPG TLFLSPSPSPLS\CHSHLSPTCRRPRES PRFSLCWRPHPPSKPPG*VKRDCCPSP DPVRLSVSENPSAGPR/VFLRPP
86	13987	A	91	197	2	NAEIIAPQKVGPFFIKIWINFFFPFF



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFF*DRVLLCHPGWSAVVQS*LTVASNF*F\K*SSCLT
87	13988	A	92	317	2	SRTPDFR*STRGLPKCWDYRCEPPCPA TSSF**HLSLC*QGNL/VVGPPDSIRM AG\TRKTKWEGCHFLFLRRSL/NSVA QAGVQWRDLCPLQSLTPRFKRLS
88	13989	A	93	1163	0	FAFGFEM*YCSVAQAS\WQYDLTLLQP PLPGVQSDSPASSLPNKLGLQGTSHHAW LNFL
89	13990	A	94	3	363	VLWPCRPAAGPSLGLNFPLYSWRLQTFA AIRPGSTGRRLCLPNWVTRNSLPFH*L VC/CSSRHNTYLQECTGHREPTYQLNIH DIKLLFLRFAMEQSFADTGGGGRESNI HLIPYIIHT
90	13991	A	95	17	353	PEPRYVGFISGGKVDIKKTWKTQGRLER TVYYTGMFYFINCH\VLKNTDSSWGTS* *IQQHAGKRDNNYQLL\KLQG\QFSEAY TKCYSNPDSHTDVRKVYQDCPLLAFLND TS
91	13992	A	96	3	355	ANYPRDLCKVTDEGGYTKQOIFNADQTA LYWKKMP\SRITLMEREKSVSGVQASKD RLTLLLGGSVAGDVK/LKPMLIYHSENP RIC*SYSLPVLCKWN/NKTWMTAHLFTT WFTECLNPL
92	13993	A	97	367	2	SLHRARRGKGVGVRMGERLPSFQSWRLR L/RRRKLRRWGQGRGN*Q*QKPDGGA RASQTDGGGERRRGVQTGSQAERDTSRE TYSPRGIQREIVRVSKGKGTGRQWQSQR QIQREKRVGR
93	13994	A	98	115	359	LNFFFFYLLNFMLLFHRYALKVSYPKSS LDRKLELLWNKYWVNTLSSSSLLTVS/ DYTCKECI*ILSKLHSRLISETLFHRK
94	13995	A	99	1	490	CVDPRVRTIFKKDKVGLPLNLNCIYYK ATVT*TVWYHKD/RTDQWDRIKSLIN PCIYGLIFFNYYFFSQ*QDSSMEGNS LFNKWC/CRPLTLYTRIGSKWIKYLM*E LKLYRLSLHDPEFGNGFLBITSEVEITK EEIGKLD\LAKLKTFC
95	13996	A	100	195	3	SRCCQRHLVQWNRTEKPE/YGRLLFNK GVKTN*WGKNNLFNKWYWDN*ISTCKRM NLVPYLSPYT
96	13997	A	101	1	371	FSLIKISMMLLMKMER*NLQFIWN/HRR LQIAKARLNKKNKTETGLPDFKIYYKA VVWYWHKKRHIDHWNRLSNSINRHICS QLILTKVPGANTKDHPNEWSWEN\VCT KMKPDP/YLSSYTK
97	13998	A	102	6	370	KKGTIPNYF*RE*TDRSKPN*NYATKEN YI/PIS*NKKIL*KLANKIQHIKKKPD NSLFYKIQFGSILETFITINQISKPEK NHIIISTDAENA\FDKIQH
98	13999	A	103	298	24	KCWTSTYLLLFRRDEVSLCCPGCAQTPR LK*SFCLSFPCWDYRREPLVPLDQ/L FLESNRSVSVLKKNP*WFSNSSGSKSG NHDAFCGIS
99	14000	A	104	2	352	GTIADFTQCCQAADKAACLLPKLDEL*\n QNGRLRS AKHRLK CASLQKSGKRTFRAW T*AGLIHRFP IAEFAEVS NLPTELTTVH TECCHGD LLECADHRADLA KSICENHDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ISSKL
100	14001	A	105	139	361	KHTEAF*MPCAKYY\LFGLNQICALPE KTPVSDRKTCCCTESLVNRRPCFSALEV DETYVPKELNAETFTFHAK
101	14002	A	106	3	350	ELEMIMLSEEVMLKAKIRQKLGLL/QPV S*VVNAKEKFLKEIKSATPVNTQMI\KN SLIAD/MEVWIDDQTSHEVPLSQSLIQ S/K/ALTLFSSMKAERGEAREEKELEGS RGWFTTRFKER
102	14003	A	107	225	1	QGIMMDTVEYVVGKGPVRCWWCKLVAL L*KTTWKLLRKLKI*\YDPAVPLLDIHP KEIKSIYQRDSCISMFTA
103	14004	A	108	390	2	LGYSQVVRAPLEEAFCRFDLKLKLAGRTT TLFKADROGHLSLQRFLLTFDSLCP/AP RGGVYRGRQASLSCSGLHPVGASWPRCL PTQASAMAGAPAAASLPCLSLISDCCAS NE*GSVSVGPSEPPTGHN
104	14005	A	109	304	33	KVWGEKVWYQKMTQIVQWDRTESPQID N*SLTKEIQWRKDSL FNKW*GNNWTAPF SS/RSNLNLKDLTAVTKIKSKWVTDLNV KHKTIKLL
105	14006	A	110	135	1	KQAILWPGAVAHA/WSCNPSTLGGPGGQ IT*GOEFKSLTNMVKP
106	14007	A	111	140	338	IMSIIYYGSICYCYWLID*LILRWTL ALVAQAGVQWRELGSLLQPLP/PCLSLSS SWDYRPP
107	14008	A	112	26	361	RSFFWVFFFEKKSLLGIPGGKKGPPLN* LEPLAPGPKGFSGLNPLEGNWGPGPC RGDFGFF*KKTPFPF\GPGGVKTPNPGE TF/EPKPPKGVGFPGETPGPGPGENLYQ WK
108	14009	A	113	11	330	ASIWLHIFLFLSYFLEKGPVYAQAGLN LLGSTGPLSASRAAGTTGALHCTQL*TY LLLPHKGKAVFF\QETLLLRSTHFPFLK HVYTPTYELLLVWDRDSLSPR
109	14010	A	114	350	2	GCCPCLLFPGSPTVFGSLYSIRLVAFVR AVPPVWKA VPG*PPVKM*FFHLFIYLF KQ/VSLWHPGWS*LAQSQVSRFFPRSLP SNWDYRGAPPRLTLFFFFFKQSQGIEM VLAL
110	14011	A	115	3	341	RMVSIS*PRDPPAFASQRAGITGVSHRA RPVYSFLLLSNVPMVDPQDIYPLVDG YLSLPLVCCV*V*VLLCYPTWPPGLKRS SCLSLPSSWDYRHEPLKPA/SCCVLLSS G
111	14012	A	116	1	384	PSYPGDLTEIMDEGGYPNQOIFSIDDTT FYWKMKPRTFLTTEKSIS/GF*ASKNK LTFLEENAVAGDFKLKPVFTYHALRNPR TLKKYATSTLPVLCKWNNKA*VT/AHVF TTWFTEYFKLSVETCCSE
112	14013	A	117	43	347	CAAGFGLL*TPPRT*TRKPRRNGTYKPI SLMNINAKILKK/ILANRIQHQHKT\L LQSDQVGFI
113	14014	A	118	351	23	FNK*CWHNWIFTCKGMNLEPYFTPTNTKI NAIKAIQLLEENKEVNLC*LGLGNCF/S RLPKAQMAKETIDKLDKIKLKALCSK\N TIKKVKKSEELEKIFANHIGTSIQNI
114	14015	A	119	123	340	AADSSTHSLTKPAYLEKQNFQFFQMEYC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LIPLAEGFWENLA*MQBPPTGFKQSSCL SLPSTWD*R/HWSPRLAN
115	14016	A	120	1	371	PSYP*DLTEIMDEGGYPNQQIFSIHDTT FYWKMPSTTFLTTEKSI/GF*ASKNK LTFLL*ANVAGDFKLKPVFTYHALRNPR TLTKYATSTLPVLCWNNKA*VT/AHVF TTWLTEYFKLSVET
116	14017	A	121	82	367	YSKRSNTIVAGD/FTPLSALDSSSRHRI NKKTSNCTIDPMDVIGIYTVFHTVSTHEY TFSSANGPFSKTDHLLGYKTSKTF*T KLK*HQ/CIFSDHN
117	14018	A	122	27	253	MKTENILGENIGEVFGVGKDSLDMSPKA *TIKEKNDKLFKIKVNFYSKHTI*KI KNQATVWQ/KLLTVHKSDR
118	14019	A	123	3	305	GTRQGCPLSPL*FNTVLEILVR*ISQNK *INKT/SLTADP/MVLHIENPKGSIK*V LELINEFSQVAGYKINM/QKTVAFLYTN N*LSKKEIKKTIQFIASKRT
119	14020	A	124	1	327	QVIFCLGLPKCWDYRHEP/RMPGLRGAD FFSLI*ILWEHMF*VMCILPHPCGDFWA MLNF*EREGMFF/CLKRWKSHNVSA/G PQTPRFKRFSRLTLLSSWDHRHAPPHLA K
120	14021	A	125	74	334	IFEFGLVKVITCLSVSSHEVGKLCPPFF FFKNGV*FCCPGLQGYNGS*L\TLELLK QSSCLSL*CTQDHRCLPPCLANFNILNS SIH
121	14022	A	126	381	60	TVSQVLAHTCSPSYLKAKAGGSLEPGSC YPGCSEL*SCHCTPAWIT\SQTPSL*KI H*KKIIVKRAIVECVVYVYTYIWLIL KFSDSIPFAQIWFHEEPYWNQC
122	14023	A	127	323	2	RGFLGLSDEVSGQQLFSILSEIENQFKN NLEGCGGSCL/SIPKCWDYRCQPSRLAY A*LIFVFLVE\TKNTGFRHVQAGLELL TSSDLP\ALASQNAWLTGISHHAEPY
123	14024	A	128	2	354	ENCQINLRPFHLRKPKEEYTKPTASRR K*IVNIRIERNGIEQK\TIEKINELKSW LFENINKIDSHSGKWMVGEE*CVFVCVC VRERQSDRERETRLIKI*NERGDITADL TEIK*LLILQKLNNY
124	14025	A	129	74	327	GELAMLPRILNS*\PCNPPA\SASLVT GTTDTPLYPAHYYY\IIIIIIIEMEFH S\VAQAAMQWCDLGSLEPL\PPGFRRFS CLSL
125	14026	A	130	83	382	YEFHASDGGSRLLSQHFRPRWKDYLSL EVEGQPGQHSETPSLSLSLSF/CFLEME SCSIAQAGVVQWPYLGSLQPLPRFRRF *CLSLPKCWNYGHEPQL
126	14027	A	131	749	2	RQSLALSPRLECSSTTSAHNNFLQGS DSPASASRVAGITGVHCHAKLIFVFLVE TRF\THVGQ\AGLELLTSSDLPALASQS SGITGMSHHVQARCVIF/CGPTFKNQDM KY*NKKEKNQSTFLEHLQNNQENRHAH TLRHHTAS/LKSSEFLFAIRTSFLIS*K RSGTTGMF*YN/WTIGNGVEDRFVLGPP FGLGVQWYHSLLPQSPGLKQSSLSL PSS*DYRHVPTPSFLKFLRRWGLAILLR L

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
127	14028	A	132	371	1	KKNLNLNLTL*VKINTNWIMDLTIKYKI IT*KKQEKVGNLEQGKEPSDLTPKV*SI KGNTDK*DV*KPFSL*KPM*GNRQATD *KKMSAKHVSNNKYP\LSRIYKFNDKAKN KPIRKWAKQMN
128	14029	A	133	2	318	NHKIILKDAKAFDKM*HPFTMKILNK* GIEQYAT/DIIKAMCDRPTADIILNGEK LKAFPLRSGRRL\FH*IW*VLARTVR PRKRNGKSQEWLMLIPSTLGG
129	14030	A	134	3	362	WSELLGSSDEPPALASQAGIIDMKHYAQ PGTDF/STSVYFTLPTQIRL*ALKRKFL L/EFK*IFASI*QFAKSCMSRNFLPAQ PYHHWHFPNEETEAAQGNFSLWAC/LRE DWIPTD
130	14031	A	135	12	398	KCSTSIIVIREIQVKTREIYHYTPTKMAK IKKPDNAK/WSGCGATKTLIHCW*NN\ SLEIWLFLMKFNICLPDPEIVPLDLYL REMKTYIHENTYTKVSIAPLKF\QPKSP STGESINCSIIIPRMECII
131	14032	A	136	309	1	QSEAPSQKNTKKQKTKVGLTS*FQTYH NATVIKTVWH/W/YIGDIDQWNSIQSP EINFHIHGK/LISNKAATNEWGKNSLF NK*HKDNRIFTCKRMKVDSQPHI
132	14033	A	137	2	251	QCGKAFAASVLRMHGRTHPEDKPYECK Q*GKAFRSASHL*MHGRTHNQEK/P/HE CKECGKPFSAQNLRIO*RTQAHIRMHS G
133	14034	A	138	396	3	LELLTS*SACLGPKCWDYRREPPHPAK MIL*SKSS\LPFLCSKCLNTIALLLLL CSLVPLLLTLPLKEFYAAH*SPDSLKYFV LQKLSKLEMLVLHETVQRKEQLTYSLYK PIFGFLVGYSFPLFCSYKTS
134	14035	A	139	3	384	LDFIKMKNCCSSKELCGYKPK* T/MEK MFAKHISNK*FIFRI*K*LSKLTKKK*A KDLNRYSLKEDIQMAKCM/KKCSI*LV IREKQTKNTMRY*NGLS*RS/GQTK** QGWGWTGPLIHCWWEYPMI
135	14036	A	140	63	388	FMVLFY*LER/CLTLAQTKVQWCDHSS LQPQTPGLKH/PPASAGVATTTIMPG* FLFFF*KRGPCWVAHARTT/WLNLGSF
136	14037	A	141	370	3	GPGHFPALFFKGPGLGPWPPIIPALLE G*GGGFPGP/RGSGPPGQPCFFLKQNF PGFV\GAPVVPFGPGLRGRTALNPEAE GSINLKGPPGLQPGGKTKLFFQKKKKKY QHFQKTQLILCF
137	14038	A	142	363	2	REKATEENFATS*DWMFMKEGSHPHSI KVLGETPSADVETVVSCEPDLAKIMDED GYTKQIFNVGET\PSRTLITRKEKSVPG FKASKLQRI*LLLGVNAAGDFKLQSVL MDYSENHAE
138	14039	A	143	99	375	KNKNQNTSEPLVRYTLLSPLLLPFIINS FFFFFFSF/CFF*KKSFEKPVAFQGGN LS*LNPRPKGSKEFSCLSLQSTWITGGP PPHWADDFD
139	14040	A	144	39	399	LQIINYIWIWLYIYFWLVSKIYKELL QINNKETNKGQKT*IDVSSNNMYMNG* *LHEKIHDIVIR*MRIKTTVYHVMSTR MVIKETENKYW*GYGE\KILIYCWEN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FEK/SVWPFL
140	14041	A	145	358	3	REHTAEDKYEASRSWFFRFKEK\SPLRN IIVQGEAATNGEVAVSY/PEDLAKNID EGGYTQQIF\NADETF*YWKMLFRFTFIA REKS\RLPSRDRLTLLGANAAGDFKLK PMFIYHSDSC
141	14042	A	146	3	376	AVMCMYKINVVFVPTNTSILQPID*GVI LTFRSY*LINT\FCNTIGAIGSDSSDGS GQSKLKTFWKGFTTPKS\IKNTCDLWEE VKISTLMGVWKNVIPALIDLFERLKTLL EEVTAYMVNIGRRL
142	14043	A	147	374	161	EFHRVSDQGLDLLTS*STCLSLPKCWDY SKWQRRI*TQ/DLCSDED*SSIKPIQLC QELMS*MAEMAHGQP
143	14044	A	148	373	2	FFFFFFFFCDLLFPKQPRSHASFSLPSV VPFPEMPSSSLTLFYLFPYNLLR*YL/N SVTQAGVQWHDHGSGLQPRP\SLSSWDH WCTTPCPAN*IFFL*RVGLAMLPRLLLN SWAQAILPLWSPK
144	14045	A	149	3	282	ILKRIIHPDQVFFIPAMQGWFNi*K*IN TV\NHIIRIKGK\NRMIIISLDTVKAFGK IQPPFMI\*KLGIKGNFLNLIKGTYPNP QLAGHSGLCCL
145	14046	A	150	3	360	DII*ESKFQGHHTTGVOGKLOYGIIIFI I*EVFFAGFFWAFYHSSLAPMPELGGH \YPPTGIFPLKRLEVP/LLNTSVLFASG VSVTSAHHSLLIEGNRKQIILALSITITL GIYFTLLQI
146	14047	A	151	349	3	KKSSGSHLETKSNRLPGSPQGPWCKEIR KGS LAWQEKSWPFYKPFLLVEVGGGRVIR GSRMTRHGHLIRSSKTLIKHHVPK*TVQ FNFCLFIFLEMESRS\VAQAGVQWCNIG SLQP
147	14048	A	152	500	0	MPSRLECSGA/ISDAQCNLQNSGAPSEP SSALSNPCG*DYRDTLPLPGYFLKFFVK TRSRVTPAGL*LLASS/IPPTSA/FSK HWDYRHE
148	14049	A	153	373	2	QAGFTLLTSSDPPASAS\QSAGITGMNH RTWPGNF*PQKSCDSFVTKLMCTCHKNH IYAQSLVT*LGHSYIFF*DSLQPSPPRF KQFSCHSLPSSWDHRHTPPCPARTQLHF GYEYFSRHFLRRR
149	14050	A	154	332	3	THKFQRLTSKSKKLKRKLIFHQGAQKSN SLNPDIKKNLKRQRNME*EKIFTDHL SRIYRELLKLKAK/INLIKMGKGYFEG DT*MADKHIKRCISISPIREMQUIKTIR
150	14051	A	155	337	21	LGLLPFFQRCPAKRGGI*RGSLAAVALL NCGELHPV*ASWWLCL\PVRGKLPTEAS VMGDAPPPTKLECPRTSDCCDGSKNFE SVDLSLLGSVGVGSVDLDPVAP
151	14052	A	156	21	491	HPGSRGCSEPRSGHCTPAWGTVKTPAS TKTKQNKKKK*RTVCLTPWHTLL/RVWC DGGDYSSLL
152	14053	A	157	3	394	REDLLSPGFQGCCCL*LCHCIPAWVT/S ETLSQKKKK
153	14054	A	158	36	354	LSAAFTSQLLGRLRQENGVN\CSEPRLH HCTPAWATE*DSVSKKKKGKPFWI PNPL SSLSPAFISGQGPWESHLKNPGRALQGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GFQPLICPRPGRTHMSLKSPWRP
154	14055	A	159	78	340	VVFHKAQRGILLAEALYPSGSAGHSIEPK TITLFFLGKLVLLCCPGWSAVA*S*STV ASN\FGPK*LLCLSPSSSDSRYPHMANFK
155	14056	A	160	2	362	HLSPLSIPQNRHCHHGPFVSCWAHLPD GVVAGQRGSSLP/M*GRPGRGAPSPRR GGWPGGGLTPHLPSSGRGWPGRGTP\PS Q*GRPGRGAPSPPGRGWPGGGLTPPPP SQTGRLAGRR
156	14057	A	161	293	2	PHLAIRPPTTVDKSALYWKMKPSRTYKV RQKSMPPGFKSSKDRLITLFLGAK\AAANF KLKPMILID\HSKNTKALKNYAKSILPVL CKWR\HKA*MSPHLF
157	14058	A	162	2	136	LIVPILIAMAFRLRLTERKILGYIQLRTG PNVWTPPTGATYRLLS/P*QP**LFTKE P\LEPVTCTITLYITDPTLALTIALVL* TPLPIPNPVGNLNLGLLILATCSLAVY SIL*SNRNGIPKTYRTKNSRLYTTTHRP QRLDAAYWCYVQTPIA
158	14059	A	163	1	464	RQGL/DSVTQAGVQGRNLSS\LQPL/PP GLK*SSRFVSNSWDYRCAPPHLANFEN LEFVQRG\FTMLPKL*TRS\GPGD
159	14060	A	164	1	353	FNYSSSLGNKSETPPQKKKKKKGRGPG ENPGTPTFGAKGGGNPGIKILKTTGPK GGNPFCKKKPK*PHRGRP/HGNPVYRG GPGKKNFWPPGGGSGK*KSPIKPPPGG KKGDF
160	14061	A	165	45	389	FFVCTFCRERSLLCCRSWSGTPGLK*PS CLSLPKFSDYRHKWPCSARNFLPACLP CLPPLSPSFFPS/SPSSSPRQGVTVIQ VRVQWRDYGSLQP*PPKTKRSFTLAPQD LGPQ
161	14062	A	166	330	2	WDYRCAPPHPVLYLKM/STFNIFFL*RG VTMLSRVSSDPPISASQVARIIDVSHW AQL*RSV/CYVFETGSSSLTQAGVQRYN HGSVQPOHSRLS*SSHPSLWNYRPPPC
162	14063	A	167	2	396	YSNVLLGIYPKELKTLVHWMFICV*NTC IWMFITALFLA\ES*CSSVGE*IGKTWY IPTMKYYVSMKRNAISSHEKTWTRLKCI LPSESRCDRLQTV
163	14064	A	168	486	2	LIFGKIYKINNSSKTDNKRKGTQIDILG MKTGDIMTY\QOTSKEYYAHEFNNLEEM DQLFKKKHRR/RIHQYEKHHLTGPMNTIN EFEFINVKTPKNQSPGWDDFIGKFYQMF EEFLSENKTGELIL*S*YYSLTNSPYEA SITY*PKPDRQ*KKQSCGPISFM
164	14065	A	169	200	3	GRVDLPPTQESRPPGPPSPDPGVQAPRP SIVRNCGILTRGSPGD\PSPLSS*AQL CGSPPPPSFS
165	14066	A	170	2	327	PGGIGCGELR*HHCTPTCATERDSV/WN KIIHYIIMLASPNEILPLLNICLEIL* AGPLTAICISMFMATL\FTIAQMGKQPK CPSTNEWIRKMWYIHIMEYYLHFKMK
166	14067	A	171	2	343	PGWSQTPDFR*STCLGLPKCWDYRR/AA TVPGLFLFLTALC
167	14068	A	172	367	3	FIRDVQFISALRYLLTPERMA/MIKSK NNRYRCGCGK/RG/TLLHCW*KCKLVQP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						L*SVWRFLKELPLNSVIPLLGITYPK/D KEVIYEKDSCLVFIQVFAIA/RNIHP TYCPINE*IKKMWYIY
168	14069	A	173	102	345	YQLQNI PRWVYSKLQNL SFAFVLL*RDR VFLCHLGWSSLL/QLKRSFHLYLASSWD YRQVTPRPAN*ILFRD/RGLALLPR
169	14070	A	174	22	401	STRGLPECWYRCESSCPATYLPF*HS IPFLSQLKVQVHHRRYFHLFPPELSNLPL LSKNVS*TY*KSFLS/WPSLRVLFPCFVL FCFVTGFHVSQARVQWGNHGSLOQPQPPS LK*SIHLSLPSS*DCR
170	14071	A	175	2	388	SDLQLRAGRRTALFKAVRQGHLLTLQRFL LSF\V*LCPAPRGGAYRGRQASLSCGGL HPGRAYRLSCLPKQAWAMVGAPTPASLS SCSLISDCCASNHRDSVGVGPFEPFCAGC NLTEHRFLSPSGAVVSC
171	14072	A	176	334	1	KLLELIN*FNKVAVYKINTONQLHCYTL IRTTQKGS�KTILLTIAPKRIKYLGI/Q /LTKEVKDLHSES YTLLEIK*KDINK*K DIPCS*MGMVFFGVCLFVYFCFEMAFRS
172	14073	A	177	339	2	KNSPYNFPKGNKPNGL*SLKSRI/CWG STFAHIGELFFFKMGKKFPAI/RPFFFF EDRVLLCRPGCSGVVRSWLIAAST/CLG WDYRCTPPCLANFL*ROGLTMLPRLLSN SGLQ
173	14074	A	178	3	303	DLRRAACLILPKCWDRHVPVPPADNSG FLHLIII*VCLPPLLCHQLVFIFFIETG FCHVAVAGLKLGLGSSSPLTLA/FSKCWD YR
174	14075	A	179	342	1	INRLNIFTMAIFSTLIYRFNTIPIKIPA GFVEMDKLILKLWVKFAHGIGKTTLKK NRVPN SKAYYNATVSKT\YWNEDRNINQ WN*IDNLKINPCVCGQLIFNKDAKTNEE R
175	14076	A	180	2	323	STSYPTGSHAPL*PQNVVDAETNS*HI NNVNRLRLKIIKLEENTKNC HDLGAT DYY/SVTPKA*ATTTKIDKLELIKIKNF CTSKDI*KVQRQLIGENSCKSF
176	14077	A	181	326	3	RKRKKRRREREPPKDEERKRLYGKDIK KRRKDTM/DWEKILQKGVRRQMC I*KI* RGVQTQELKANPIRKGNNLNKVHORI*M ANKHKMRCPKS*VIREI*IPTIMRYH
177	14078	A	182	5	326	TKTIEKAAN*IRRSRRKKIKFKPEIKNR KTTTKINESKSCFYKKTNKTDKLLVKLI RKKKTKKIITKDEKNHTI\*DCTEVKGM TECYEQVYANKFDNS\BKMDNFLE
178	14079	A	183	3	378	TVLCSTFVWGLDFFG*HTTIYS*VFCYK WNCVHNFLFRFFSAYI*YLLIFVY*S*I MHLCLICY*LLL/CSIFFWIFMYLFS FWL/CFLYFYFYLCPFIFF/CIFICLL FVYLFLLFIFFFIFF
179	14080	A	184	365	3	MLKLCIMKSISVQAGVQWHNFGSMQGGP PW/LHHFPASASLVGTGTWARHQGRVIF /IFFFFLMRRSL/DSVDQAGAQWHDPSG LQPLLPQFK*FA/CPCWDDRRAPQCPAN FVFLA\RHGFTILAR
180	14081	A	185	51	293	PYVNQEASVLTNSFYQAS/I*KKSNYRP ISLMNIDAKILNKTOQIKLNKVND SRQT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GEDQIPKYCTVSDGRMMRDYFPLFSS
181	14082	A	186	326	3	TKICQWILNLGKKREFGFKKKKIKCPN KRHRLANGIKK*DPTTGCLQDICFRSKD AQRLQIKGWKKIFQKTGI*/GVAULTS DNIEFKIKTVTRDRVANYIKGSIHQ
182	14083	A	187	17	330	KDNEM*IKRTMRCYYTSFTMAKINLKIN NIKC*QG*GTTGT/L/LYC*WKHKIVQP FSKTV*QFLMRSNKYLRYPAILLLGIY SN*VKI/C*KTYMRMFIVFLITKDWKQP NYSS
183	14084	A	188	124	357	SLWGGDLEGGGEKKERGENPGGPKKPGK KKKKGGNLGARG/VFKKRGPRQKEKPGK KGEKGGP*GAGI*GGGGNGVKKK
184	14085	A	189	333	124	RLRQENRLNF/GSRGCREPFSRHCTPGW ATE*DSVSKTNKKMYKSIARDCHAENS IVSFLSKRGCVFLF
185	14086	A	190	1	327	KSWLIGDNIPSSQSLLIQKGVNPSFKSM KADRGKEAABEKSEASRWFMRKERSH LHN/IK*VQGAASYPELASSIDEGGY TKQ*IFNEDY/MWKKM*FRSFLTREKL
186	14087	A	191	53	400	VNILGPFHLFFTFVQNALSPNIYTHML TSLGPLHMSLQGTGFPKPSYLFQPSPH SVPVGF/IPGMQR*FSIHKSUNVIYHVI RMNDISHMIISKDT*KAFDKIQHIGSLF PALSL
187	14088	A	192	65	321	RARTEIYLIHTLLGVYAGETKTGPYDC M*MFPTAPTILVKTWI*PKSLSIGERIN KL/WILICTYMEYSAIKSVLTHLTWV NPH
188	14089	A	193	127	241	IIKNDSTRICNLTEKLPLRKINS/WPGA VAHACNPSTLGG*GGESRITYNESRNKG EQTQNNK
189	14090	A	194	1	337	DLPASASQSAGIIG*ESIRN*NKLVKKT LKCSQKDPKEDLNK/WKDIVCSWLGRLS LTKVSIPLKLIYKFAKIPTKLYY*KKN RPGAVAQAYNSSTLGGRGQI
190	14091	A	195	2	333	NFNSLFFFVEIEKLILKFI LNCK\VAR ILQRKNKVGRLTLPNFNNDYKATVIKTA WH*HKDTHMDQRNRTESTKINTYKGAKT I*WRKNSLFNK*CWDK/WITTCRKRKVD P
191	14092	A	196	299	2	PHPQRDVVQSPSPSICRIFSPSSIPGIQ SWFNIQKSINVFYHIVLNTQHRSSSSS SSSSSSSSSY*LMIKF/LNKLGIENF LILIKAIHGKPTVNH
192	14093	A	197	2	199	LALSPKLECTGAIYCSLELLGSNDPP TLASKVF/GITGMSH*AQPQVFLLLYY FIFFFSSSVL
193	14094	A	198	226	2	KKFFFFNPNLKNFPLGRVFF/CSFG*KF FAPLGFLLVSFLRQKVPHLSPGKTFFF FFFFGDRVWTCPCWSAVA
194	14095	A	199	338	93	PQHNGSCL*SQLFERLRAEDPLNLRVQG CNEL*LYLCTPSWVNPVSEKKSIOEKNA NLDFREY/RDKRRENWTCV*NSIERSSE
195	14096	A	200	1	361	PRSHLSQLRVRLSQ/IKKNQKTIGKGF AIG/MGKKF*GKTLKVPFTRGVNQWKE LKLKSFLLPRKKKTEITL*TLGKHFRKWE KFFATYPSTRE*ISKICRDLNHFTGKKI



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TIPIFQRAKGL
196	14097	A	201	2	358	ENKTTMRYH*IPIRMAEN*VLAVGTL/L QPWWEYKRV*PLWKTNLAVTLLNINLP CNPTILLVGIYPRERKTYVYTVACTQMF LTVLFTVAPNWKQSQGPSTGE*KNK*WH IHIMGHYS
197	14098	A	202	110	357	IWVFIWCHFLLPEKTSFFPGFPQCLDIS *KTLFVHVSVLFFFKDRVLLCHPGWSAVA Q**FTAASD/FOESSCFLPGSWDYKRM
198	14099	A	203	2	374	ILKLHAFMAETPGACKTPCDLRQVFIF IFIYLF/MRLSLTLVAQAGVQWRNLGSL QPPPPGFKRF*GRCLFYPKDGLVCPLGA GS*TGQIGKGIRTLSPDLCLSDGFCGSK PKS/ASASQGHVG
199	14100	A	204	375	3	LSSILIRGSFNLSTLITQEHL*LLPS W\PLAII*FISPLAETNRTFPDHTEGES ELVSGFNI EYAAGPFAILFIAEYTNIII INTLTITIFLGTTYDALSHELYTTYFVT KTIPLTSPALMNS
200	14101	A	205	393	3	SARLGLPKCWDYRR/ASTVPGL\SLMLL LKSYVS KMKKCE*LVKPLKAKL*DSCKE L*VCNNLIMPSTYDQENDRVDSSTLWLC VLLLLLLLLLLLLFWRQSFALVARAGMRW RDLSSL*PLPPGFRQFSCI
201	14102	A	206	2	377	FRAVLQGRWSLQKFLLEFVQLCPAPKGG VYM*RQRS/SLSCGGLRPVRASWLLCLP TQASAMVNAPPPARLLPERSISDCYTSS EQGSVSMGPAEPGVGYDLLVCCLLRPLE KHSIWVRVSCFSRY
202	14103	A	207	327	1	ILTGNFKQIRMLIYHSVNPRALKNYAKS TLPVNYKWNKA*MTAHLFIAWPTGCFK PTVEPYCSKKK\IPFKVLLIDNAPGH PRALMKMPEEISIVFMPANPASIL
203	14104	A	208	310	2	FCWWAPGMGFPLGEWGLILGPGSPFFLK EGFPGVGQPGPKRWGLKG*PPGAHWKG F/IFFFADRVSLCHPCWSAVAQSQLTAN PASQVQAILLPQPPDYRIR
204	14105	A	209	374	3	GVRDP/LEEVVCPF*DLKLVARRT/SLF FKAVRQGHLSLQRFLLPFVWLCAPARGG VCRGTQASLSCSGLHPVRASWPLCLPTQ ASAMVGAPSPASLPPCSSISDCCASNER GSVGMGHSETDVG
205	14106	A	210	3	196	LENLKF/LDKFLETYNLTRLNQEETEIL NRPMTSSKI*SVIKNLARAMAHAYNPST LGGKGRRRIA
206	14107	A	211	34	339	IIKSKRINYMSCELYFNINIDNFFFFET VFRSVI\KLKCYGAFMVHCTNLNPGSTN LSTSASQVSGAINRGYPGQF/IGLEK*F LVKTGFCHVA*AGLEPLGSG
207	14108	A	212	200	312	HYGQFHVLFCSLF*MESHSVT/QAG/VQ WP/SLALQTPPPGFKQFSCFCLVSSWDY
208	14109	A	213	300	124	NHIFFYFQIHRVCVCVCVCVCCLVCV YRYIYCVSPW/RN**SL*KECLSLVLLT PTC
209	14110	A	214	1	357	QVDHTSDRKANLNMF*KIKVIQTMFSDY NGVKSENNRRKTGKLTNIQKLNST/L*I SNETNEKPQEIRKYFEVNINENTTYQDL WDEVSIQAHPNSTLEAEAGRLLEPRS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LRSAWTTTE
210	14111	A	215	360	1	LTITETCYSE\KKTFFKILLFIDNLAGHP RALMEM*KEMNVFMPAKTTSIMLPLI\S SFNSYYLRTRIHRFTFVVVAQSWLQCPTT AISDIOIGPVAMGLLLIPSAFVLCWLSI QQVSKLKH
211	14112	A	216	3	347	SSRSRADGLFFYQCK*QTLYW*HLWYKT QKEKKKTQMKEKKQRINKAR\GDKLPEC EAVCGKPKNPANPVQRILVGHLDAGKSF PWQAKMGSHHNLTTGATLINEQWLLTTG KNLL
212	14113	A	217	75	347	PPIFKRTARGKVTPGWEYPAKG/CGGTF LGNRGLFPNPGFSGPFPKKQVWEGALCA PG*KVCTLKF*FI\SLAIPNGSKNFFT LFEGPSPIL
213	14114	A	218	3	397	GGQGYSGTGHHGGIWHKMEH*R*PLPPK KKKKKKKKKKKKKKKKKKGGPPKKKPR GGQNLKGGGKEKPPQKGVKKKTLSGRI IKKDGREKHTRGELWKKTFIW/EGEKIG EKPPKKI*DHEGKKKVLRGKG
214	14115	A	219	3	401	DSWATLHGNIKM*SAAVL*ALGLV\FGF TVSGPTGIVLSNS*LDIELHDTYYVVAH FHYVLSIGAVFAIIGGLIH*IPLFSGYT LDQTYAKIHFTIIFIGVNLTFPQHFLD LSGMPRRYSYDPDAYTT*NIL
215	14116	A	220	162	3	KPAQRNL*SNPEKEDINILKRNQS/WPG TVAHACNPSTLGGQKQIIRSGV*EQP
216	14117	A	221	374	2	WCDRERERERATERERERERERQTRDQ TDRRREEA/EGWAAWAIN*GRAPGTSLE AALECSPPRPQPAPPEQGFPPRTTAR GQPRPPKLLQPEAPSQTRPHGYPWPLRV LPQSGPEVRPRE
217	14118	A	222	3	264	DHMRPKVRGCSEL*SCHCTPAWAT\SES LSQKKKKKKKKKKKIGEKI*GAFFKVAP PFFFFKKKMNLSKSPVGIAGVAKNTRWIL KHRG
218	14119	A	223	2	410	ATSPIIEELIT*HDAHALINILLM*FLGL HALFVALTTTLTNTNI*HAEETQT*TI LPAILVLIRLPSLR\ILYISDEVNDPS ITIESMGHQWY*TYEY\TDYSGLILNCY ILPPLFLEPGDLRLLDGDDQVALPI
219	14120	A	224	399	3	GVGKPGFPWAKKWALPPYSGYYPK*VON LILKVLLLLLKKNPGENSLEATGTWGLP PKARAPKLKPNW/DSPKRKNPGAFKKKK KRQPTWEKIFANHASDKRLTSRIYKEL QQ*KSKQPIFLIPIVHLNHFKG
220	14121	A	225	360	71	NRTTWVPFKTPPLLHINTKKK*HTGNK KHKTKRAKKRKKTKNAKK/EKEKNHPQ RPQKRK/EEQKPKRGKKRGKKKPKFK EYSYL*K\YIHTNLQ
221	14122	A	226	3	386	PSTHVSINLAMGIPL*ADAVIIGFHSKI KDALAHFLPQGTPTPLIPILAIETISL LIQPIALSVRLTANTAGHLLMHLIGST TLTVSTINLSSTLIIFTILILLTIL*IA VALIQAY/VCPLLVGAY
222	14123	A	227	3	372	YSLDSPSLTRFFTFHFMPLPFISAALAAL HLLFLHETGSNNPLGITSHSDKSTFHPY YTIRDALGLLLFLLSLMTLTLFSPDLLG

[illegible]

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LEL
237	14138	A	242	3	339	RKDSRKREKRNKEKRKGRKEGRKKPIRM TVHFSSKTMVAK/ARRQ*NPVFRMLEE* KN\FPPRILYSEIIFFGSESQIKKFSGD GNPKGSFPPELFFLRIPMEVFNLKEAYLR KS
238	14139	A	243	216	3	NSTGTQTQSQKFMLSLVKKLISFIYL*D GVLLFAQDGVKWRDLGSLQPPPP/GPTL FKQFSCLSLPSS*GSRI
239	14140	A	244	408	2	VLTS*SNIAST\WYGLYQ/TQLR/KILA YSSI/THIG/WNNPVLQYHNITILNLT TYIILTLNA/FLVLNFNSSIGTILLSRT *NEIT*LPSLIPSTLLSLGGLPPLTGFL PKWAIIEEFTKINSLIIPITIIATITLLN LY
240	14141	A	245	3	243	IIMLKAGQMTVFPNEDVWMAYKHTDRYS TSLVMNEM\QIKTTMGVHYAPITVAKLL N/SNTRYWP*RG/CSRVHCWRKCR
241	14142	A	246	2	337	FLIMDLQKYINPKIKEPQGETNHKTVSF MNINAKILNKILVIQI**FPKKNVSKF G/FIP*/SQGCFNINQCYSLDERRKYMI ISKNIEKAFNKIQHSSFMIKTKNRKKLP EL
242	14143	A	247	347	1	HYTPIRMTKIQNTDNIKCW*GCGNP/GT LLHCW*ECKMVQAL/WL*TVWQLFTKLN LLLPYNPITFFGIYPNEGRTHVHTKTCT LIFIIAALFIIARTQKQ/PRCSSVDEWI NKLWYIQ
243	14144	A	248	319	2	KKIILFIICTERVFLCCPGWSQTPRLKQ SSSLGLPKC*DYRRESS\PGLNVIL*CL KFHLRVAMLFYVFEV*\IVIFFFLRQSL /DSVTRAGVQWYNLSSQLPDPGFK
244	14145	A	249	329	3	KFPFFHTGEAKNYAVFVINKRIKKQHI HIIYNYGGHQAECKEIEAHVHCWWEYK MMQ/SL*KTAW*FLKK*TMELPYDPVIL LLRIYSKELKAGTRTDVCTSMCSFEL
245	14146	A	250	316	3	KTHKTIMGTNHPNEKIDST*LKNLNIR AITIKLL\KNNRVSLHDLRIGHGLDMT PRAQAAKKKIKR*IDEFIETKNFCAKSD NIKRV/NRQHKE*DTMFANHIS
246	14147	A	251	152	364	QLTLSNHINNQIKYK*TRHS\NHHHHHH HHHHHHHQ*KRLPE*SYKSKSQEHYTY GMDITGPKNLRTIPL
247	14148	A	252	230	1	PCWICEFIVSSNFCWFVLETGSCYVAHA RVQWCDNRSL*PQTPGLKRYSCLSFRSG WD*RH/VP IANF*TLPRGGVL
248	14149	A	253	3	345	DVGLAGLELLTSGDPPALASQIAGITGV SHHSWPLLEFFFFF/CFFEGGFFFFLP V*SQGGDLGSREPWPYGFKGISLRFPN EGKIGPQPLAPDMFCFFDKTWLSTVVP GFH
249	14150	A	254	194	1	GRVDTKWANTHERFSKCS/TTVD*WIFK SWYLCTMEYYSTINKKEILSFVTWMHL EDIMLSEVS
250	14151	A	255	327	3	VKTAEFVNKQKNSTKLWNSQAQIDKKK IVNQINDLRQTEIWMGDRI MNLESRIQM QCDWNTSDFCVTPQ\YNETEH*WKKVKR HLEGREENLTL*IVKLKEQDFEASQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
251	14152	A	256	314	3	KNFPSLINFLRQSFANQGQGVQRVDLG SPQPLDSRVSDRIRLCFKTKKKRFS* QTILKLSKV/E/MTERVLKTAREKHLVT YK/GKPIRLTMDFSAETLQARRE
252	14153	A	257	2	308	RWWW\EEEEVEVDCGGEV*FFFFCFFF FFFCFYVFFFLFFFCFFFIFFFLFF LFLFIFFFFFVFFIFFFFDCFFFFFF FFFFFFFFFFFFFFFFVFF
253	14154	A	258	52	186	CFGKLGWDDCLRSGVQGCSET*ACHCTP AWAT\NETLSLKKRRRG
254	14155	A	259	1	269	LKRSSHLSLPRSWNYRCMPPCANF*TF FVETGSHHIAQAHLKL\PPASA/FPKCW DYRHESLCPALDSPFTNINSATIITILQ GKCWHYC
255	14156	A	260	387	3	PLLQVAKINPKRILDNLVPKTIKCLQE NTGENCWDFGSGKDFLDMTPKMQSTK*Q ISKLIKIYNFSSKTQ/SFCTTDHENFLE DIVKRIKIQSHKLEKRFVNHIPDKRLIS RIYQELFRTOHEKPHTIK
256	14157	A	261	62	72	LRIIKFSEESMLKAEMG*KLGLFHQAVN KCNSLTVNEVVNAKKRFLKMKMSATPVK THMIRK\DMKVLEVWIDQISHNISLSQ SLIQRKVLILFSSMKPARGEEAV**KNY
257	14158	A	262	2	193	GGRGCSELSCHCIPAWVTRAKLSLKKK KKKNSKF/RELGNKGQFMGP*LRKGFTC YKKRSPLIF
258	14159	A	263	3	330	QLKKKYEEELYANKLGNPDEMDFLETC ILQKLTQHKN*KFFRDSRRKSKMNRPI NRLIQ*PKELPKRKTLPDGTGELYHK HFFFLTKPLHKFF/AKIEEPPFNS
259	14160	A	264	326	43	TQETEAGESL\DPGGRGCN*LGSCFCTP AWATGMKLPFKKKKKKITSLELRLSY TCSSSQNFLYLNDTIIHPVAQAKNLGD LDSSPTDPIQ
260	14161	A	265	311	1	FPPFP/SFPLERKEFKGRKKRGGTRKG FPPFFFPFSSPLGFP/SPQRA*FLLE FREFLKFFFPFYLPPKPLGKFFFFFFF FWDGVSLCRPGWSAVARSRLTV
261	14162	A	266	5	323	DSTKAQKNVTVSIEPGEVGTLIHC/WVQ PL*KTVWWFLK/DVK/LELRYPDAIAHL GI/YPKKNKT*TCTQVNITALFIMTKM* K*PKD/PINNEWVT/KLWYMHTMEY*ST IN
262	14163	A	267	3	293	GSLQPLAPRFK*FSCLSL/SAGEWHEP WRRSLQRSCHCTPSSSLGYRAGLHLKNN NNNNKSEVSRICITIGIFLLFIY/CIYET ESHVST*AGVHWLDF
263	14164	A	268	3	332	HLSIINLVNQLNSPLKAYTLFVWI*KK KWPNY\CCLQEIHFAKNTYKLVKELK KKFQANEKEKHADKTGFKSKTVK\KNG HYIMIKRSVQKENIYIMFLIADPDIC
264	14165	A	269	3	326	KVLERHDVLKLTQ/DKICNLNM/PYTRK MESIVNNLPKKTPGLHSFTGEFYQTFK NEMILTSYNFSQKFEAEIILNSFYEASI LL\IPKLDKDIIRKEN*R/PNAKILNKI L
265	14166	A	270	1	318	PYPAKLSSLSKGEIGTF\LDKQMLKEFV TTRPALQEILKGALNVL*/LERKDHQ

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						QMCKH
266	14167	A	271	1	318	LKLLTSGNLPASASQTAGITGINHRAQP HLSFSL*LNWET/CVPG
267	14168	A	272	108	322	DSHVI FLLCGNLT V FVCLFLRWGL/DSI THPGVQWHHNSL*P*TPGLK*SYHL SSIWNYYRRTPRLIAFFL
268	14169	A	273	341	3	GFFFFPFFFRQGFPLLAQVK/VPWGNFR SLQPLPPGVKQFSCNLNPKN/WGFSLKG FFKKGCHFPF*Y*IFNKGKKPKDIKPSI FTNPPFFFFETESCSVVQAGVQ*HDLGS TRP
269	14170	A	274	41	328	FWLLTPGQETERERESETERESEREREA GEAERGRETGDIDSLIYSKLYSKIHLK ILEYI\ATYFKRLFYNWEL*T*AK/TRI IEKPSVRHQCCQRS
270	14171	A	275	3	322	EAQELL\DPGSGGCSELRSHHCTSAWAT KAKLRFKKKKKKKCPGRYLGNIVLQ*FN LIAKCDKYHIVKLIF/CFSSAYTASIQK LIQVSRVTTHRKNKKTQYVYILD
271	14172	A	276	175	313	STLISYFRDRVLLCYPGWSAVGQSQFTA A*NFV\VK*SSSLSS\PSSW
272	14173	A	277	254	3	RPRRQFGIEGSFLNQIKNIYKKSTANVI LYVDRNLNAFSLISGTRQGCPLSRLPFNI VL*LPVNIIRQ/EKVI*GMQIVKEELNL SL
273	14174	A	278	186	1	PETMQARRQ*SEIFKVLKEKN/LQHRIL YPEKLSFQSEREIKTF\QRLKKFITSRP ALQRMKE
274	14175	A	279	288	3	GRLRGKKGFNPEGENSKFEFFKPLPSGLG AKTQPVFKKKKKKKTRNPIKK/WAKDP NRYLTKEAI*MASRHMKRCSTSCVIREL *IKTTMRDYVLI
275	14176	A	280	3	329	LKSSRLSLLCSWDHRFALPMLSGLVW NSCPQ/CDPSASASLSGITGMSHTWL *WLF/C*ETGSHPVQTQGMQWYDPSPLH PTKKGVYLT/RRFWRLGSPSAW
276	14177	A	281	233	3	IITKDKEEHFIMIKRSTHQGITITNIC VPYNRGSK*MK*KLTKLMGENR*/HSII IAGDFNTTFSIMDRAIRKSAKNG
277	14178	A	282	32	309	LPDITPRDHLSPGTMDFIQETGCSKCWR GCGTPVCC*WECKL/VIVQSLSRVWRF LKCLKIGQVRWLMPVISALWDVEVGGSP EARSSRPAPW
278	14179	A	283	1	302	CKRNNKAWMTVHLFTAWLSEYFTPTVET YCS*KTIPTIL/LLDDNAPGQPGVLVE MHKDMNVAFRPANTASILQPMNQGGIST FNSYYLRNTFPKAIVAIE
279	14180	A	284	155	1	PRRFFFFFF*DRVLLCHPG*STAT*SC LTKSASQV\RQFSCLEPPSSWDY
280	14181	A	285	131	15	DRSNPGRFLWTSNSSLYERPREIRPSSQ APPPVNDPI*T
281	14182	A	286	1	359	FFFFFFSVFWCFSTFFFKKGGAPGGG GPPPPKKTPLFSPQKNFFLQKKPPGKG FKGPGLPENFGPG/RNGGPKPGDPHP PDFTPPRWLFKPPF*KRGEFFPPPGFP KNLFLKKVP
282	14183	A	287	52	419	LEERAGTSWPKKENKKQHFCMKKKKKKK KKKKKKKKKKKKFFKKAQIFSF*GGV

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						NL/H/SGPGPVLKTTGGGRHSPPPPSP PSSLFFPSSSLPFLSLPLSPFLSS PPLLSS/CPPLFSS
283	14184	A	288	236	325	LNIRTPGSWLXAVAHACNPSTLGGRRR IT
284	14185	A	289	218	409	KVKGKADLIRSANGS*N/VKGVLCCHQY LEKSFCLETFHSCPLQVLHWPDLGLLQ PMPPGIARF
285	14186	A	290	3	426	HEETGSPRLECSGMITAHCSLDLPLK* SSHLSLGS/RHVPPCLAHFLY
286	14187	A	291	382	1	ANFYVTLVQ\QGFTMLRSWRPA*PCDPP TWASQSAGITGVSHHAWPKMSTITLGVY SFGSEVFSIFKFYFLETGSSFLPQAGA **CNHSSLYP*TPGLKQSFHLSLSTSV YRYLPPCPLCPVLV
287	14188	A	292	3	309	HEVPYFTLNQOLEMIKLSKGGVLKAKMG \ISQIVNAKEKFLKEIKSVIPVNTRMK QNSLIA\ETQEVSLVWIEDQTSNIPLS *YLIQSKFLTFLNSPKADM
288	14189	A	293	2	415	ARDQYKKSTKK*AKDLYRHFKNEAI/HM ASNYK/KRCSIS*VIRKIEIKSSMTSCY THLQN/ALKLSDNFKC*QKCTAMGIIL SWWECNLVQSLWTW\QNLLMLNTHKPY* SAI/PTSGLYPTMYRNIEQASLRMFWA WRGG
289	14190	A	294	335	108	IPTPK*PLSSPPIHTPYTTIPKP/RPPP P*HPPHIHPPPPPLTP\PLPHTLPTPT PTNLPHIPPLYSIPSSPKIS
290	14191	A	295	266	2	GFPKKVFSFPIGPPKLGFPNSVFS/LFT FFNPGCLCKFFQFFPFAFLPLGFSFPF FFFFFFFF*DRAVLCHPGWSAVVRSWLT ATLV
291	14192	A	296	347	1	DSLQP*TRGLN*FFHLSFLTRWEYRCAP QCPANFC/VFL*RWGFAMLPKLVSSDLP ALASQSAGITGVSHCAWLVLFLSLYFI HFSKASETPWAQNSQTPSEYPATYNFK IYSC
292	14193	A	297	284	2	CRQGFVLCRLVSNSCDQVLCVRLCV*VL GLQACAT*LGAEVGSIEFSCFHKGRCCL CRHRSS/HSMFSAWC*PHTHTHTHTHT THTPSMQLV
293	14194	A	298	1	96	GTRLCIGAITTLFAAVCALTKQDLTKIV DFST*SQLGLILVTIGINQPHLSFLHIC THALFKAILSMCYITIIHILNNDQDSQT IRRLNTHMHNSTSLTIDSL*LGK FLN/GYY*QKDLTKIVDFST
294	14195	A	299	3	134	HEGRD*PGNHGDTLSLLKIQKLAGSGGV CL\KLRKLMCENHLNP
295	14196	A	300	2	333	GVGREGGSREGGEEESGNGGIRERRSG KREEEGKEYRDEVDRKEREGEGRERER GRGWEEQKGAS*C/EEGRVK
296	14197	A	301	354	1	TENELLSRIYKNFYQIN/RYQKNSIKK *RK*QAI/TTETIQTVNKHKKCSISLI IRELQTKTR*ILYT*LVEKKLKTNGIYC WECCRELGSC
297	14198	A	302	1	282	GTRGMVAGAYNLGLPSSWDYR/*CLPPC LANFFVSLVERGFTRLTLVLLS*LYDS PASRSETAGIPLIHTSCIVYWSLRNNAD

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						TAILCKAQAV
298	14199	A	303	361	3	LPKWWDYRHEPLCLATFFFF*AFPPVPL CMYVPPN/RVVAFFFSLSF*ICCTFTL YIFPQLMDG*AVSSFLFLQPVGVKFKK FFLSFFK\KRRSLGMLPRLILNSWAQVI HPPWPRPRA
299	14200	A	304	2	352	ARMVSVS*PCDPPA*ASQSAEITGMSHH AQPIIIS*TIAYVSFSLSSLT*ISSVR SFTKMSQLLYFYFVSL/PSFW
300	14201	A	305	334	1	KNSFFFFFKRSLGLLAQI*/VQWGFKT LQPLPPGVKQISRLNLLKKWDY*RGPSG LGKFW/IFL*KQGFPQLFQVVLNFFFF/ CFFETESRSVAQAGVQWHDLCSLQAPP SSC
301	14202	A	306	270	2	DWCAGGGDGVPRRQVIFVILVETGFWR VGQAGFQLLASSYLPALA/FPKCLDFRH *PPHSALKALFFF*DGVSLLLPRLCNG ASSPRA
302	14203	A	307	306	2	HIFQCVVCVCVCCVVCVVCVVCVVCV KLVISQT*LSPLCSGP*A/CTFFSVCVC VCVCCVVCV\CVCVCVCVKVSDLTNLS TLCSGP*A*HFFSVCVCSC
303	14204	A	308	117	332	SPPVILRCSLSLSVQLNGKTRFLK*LK MEL*PHSAIPLLGIIYKGGKFLYQKDT/ CHSIFITALFIIAK
304	14205	A	309	1	351	GTRKTNN*KWAKDLSRHFSKEDIRNGQ* V*/HMKRCSASLIIRIM*ISITV\RYNL TCIIM
305	14206	A	310	1	352	PSPPNSPSPPLSRPPQPPYPPPPPRP PRSP*YTPAPPYW/PSPIITPS/PS DPPEPRSSRP
306	14207	A	311	1	405	FKPSP*PLTGALLGLMTSGLAM*FHLH SIT\LLILC\LLTNT\LTIIYQ*WRDVTR ERTYQGHHTPPDQGLRYGIILFITSEV FFFAGYF*AFYHSSLAPTQGLGHWPPT GMTPLNPLEVLLNTSVILAS*VSI
307	14208	A	312	3	176	HEILGSNF/CGETQVSIHCPG*S*TREL KQSSHLNLPKCWHLRA*TTVGLTTIFH LGKPKHKRVR
308	14209	A	313	298	327	SLTSLPRL*KIKK*KKK*NKCWQCKEI GAFTHCWGCKMVQPLWKS\W*LPKKVK *KLSYDPAIPLV
309	14210	A	314	344	3	HSTSLVIREM*IKTRMTYPFTTTKMAII *KNRS*\WLGCGKTGSLIHSW*KC*MVQ SLWNTFGQFFIKLI*ELTIPLDLYLRE MKTYDHTKTCI*MFIVALFIIAQNVKMS LV
310	14211	A	315	18	321	WALFVVCLEKKEFGQPRLACFFFWDRV SLCLPGWRAVMGSWVT/VRPKLLAFN*S SHLSLPSSWDYRLIPCSAKDSICEKNR VSTVDGADKKVRRGKEGD
311	14212	A	316	289	52	ETSCDVPSKGIHFGRNTHIMPEKWK GMR*YFH\KEDK*MAHIHVRC*TSLVI MKMQIKSSTPYHFIPRLTKPLKSANTK CW*TCIWAIIYLSMMKILSHALCPFFWH DVCISLLEVKNFAFTHITRRFS
312	14213	A	317	57	324	YCVTFFFFGKQSFVLSRLNLCMPFWVN CSLSLLSTWNYGLVPGTQPPF\EFVLQR



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						GFHYVAQVGLKLLTSGDLLP*GSKGAGF TGLTHC
313	14214	A	318	65	341	QWLLKSRSCYFFFL*DRSWAVAQA*VQWR/NPPPPGFKQF/SCVSLSSWDYRCLP PHLADFWIFSRDQPDQHSSTSLKKKK KREIPNLPGLG
314	14215	A	319	2	182	ARGDYRHMPPT\H*LETGSCFVIQAGL ELLDSSHPPALTSQCWDCTCEPQSWAP CVSI
315	14216	A	320	345	3	MPPRQAHF\VFFIEMGFHHVARAGLELL GSINPPTSASQSSWDHR*SQSAWITGVS HHAQLGTITSYHILLFLKKGRAHAC*SQ HDPTTCLHVNLCSSLLAISRPPTTNL PRA
316	14217	A	321	122	466	QSFSTYC*KNWVTI/CFLKSIDSYLVPY TKIDSKWIIDLNVPKPTIKLLGNGMGEN LCHLMLSKDSSDVTQKA*SIEKQINKFN SHGGTRLRSQPLKRAEVRVRLSPGGRS YSDL
317	14218	A	322	3	345	HEDAVSAPCNLHLPSSNCPASASRVAE MTVPA\PCPANFFFFFLEREFGCCPG /CK*K*VFQKKPKGKKKGRIEGKKGVWG PKLKERERKKRKKERRKRGKERKEVRTE MNGG
318	14219	A	323	206	446	GNLHQCPYKWTHLAKYMCEKQDSTC*IL KECYQKPLLEKSHLIAQVENDEKPADW/ PLLRGEYVEWND
319	14220	A	324	62	327	VERLLRDLRENFCRNPDGSEAPWCFTLR PGMRAAFQYQIRRCTDDVRPQGEAQAWG LQSRAGSLEPEGRGEVSA*W/SARTRHR
320	14221	A	325	441	1	RKKK*ILQGL/EFRLEHVVASPHRDHRV WPRQEGKLFSEGKNKATRMVLYPEE/S SKKLGSRS*GSE/CTSVFRITLSVGYVA YTGA PVSI SERPSAATYHRMNK*HQHR RHLLGFSEQEPVQGEPLQSSSQGPKEP QPSPSNPAPRA
321	14222	A	326	2	358	ARARTLRIMVNLNYAKSTLPVLCKGKNK VVVTALHFTASFAEYFKPAVETVCLEKT FFKILQLIGDAPCHPRPLMDMHKEVNVF VPAKTSIQQPM\ISPFKSY*EITFQA GCCGSCL
322	14223	A	327	1	430	ARENMPGHLHRCITIEQDWRIHMLIPKLN TQMIKIV*YWKDRYVDTE/YNNIESTE VNLICGELIFRSAKIIQWVGKRIVLN KWCWDD/WNL/SCKSM*MDSYLTLC\K ITPWIINPTGRAKTMRLLP/EKTGVSFCD FG
323	14224	A	328	146	374	KCLMLTKPYNIMRLT*PYEIR*/CGDTF P*SYA*TGTAVRTWGLTPVIPALWEAE AGGSRGQEMETILANTEKPR
324	14225	A	329	2	322	ARASRTFIVRKTQCLASKDKLTIVRG*C SCDFQLKSMIDYSENPRALK/NMLYKR NNKAWMTLGLFTAWSTE\KPTVETYSQ *\KITLKIWL
325	14226	A	330	350	47	EMGFLHAGQAGLELLTSGDPPASAFQSA GTTGVSRRARPAN*KKKF/CLKT/RVFL CCPGWS*TPGLK*SSCFGLSSHWNYRHE PPRPAQFLIDFYLRHYRES

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326	14227	A	331	753	458	FFFVE*GV\HVAQAGLKLTSRDLP TSAS*VAET'TSTHHA*LHLENFEKYFCKE QILLCCPGWSRTPALKRYSHLCLPNSWD YRHEHCNEPEEISLI
327	14228	A	332	256	3	TLVLMQSCSLSSWDYRHKPP/*LSNI FNLPMGLSGHNPIINGISVSILDRVVVL FLFC/LCFETGSHSVAQAGVQWHDHGS LHSC
328	14229	A	333	25	358	TPDLR*STCLSLPKCWDYKHVPPHPANI FI*QKLFILSDGQYANVLTWFEFGTFHT *A*RPNHHSYKLRKDQTIIFIYLF/LR WSL/NSVAQAGVQ/WHNLGSLQSLPPEF K
329	14230	A	334	3	329	HEDVVSFPWPGWSQTPDLR*SACLG LPKCWDYRREPPLALNAFLT*NIFNL*W/C LSGSNPIIRSICIRFLGKGG*LLFIFIF VWFLTQSLTHSVTQAAMQWHDGSLQ
330	14231	A	335	26	330	SQILGRPRQENHLNTGEGCSL/CKIIL VCFWLGHLLPVWFR/LYLF/CVVSILG FNFCFSLVL/CWFLLCFFCAFMCLFY* WVICHFLFFFLFYFFVMFLFF
331	14232	A	336	3	348	DEVFKS/YH*HPMLKC*GDYSLLFHGES DLDTTQILTHPSTTAMFYVHYCQSP*IL YGTIDT*PPVIHRNPIHIRTYPCLQAS TAINLQLSHMNCNSKATPHSLGYHQTY PLTV
332	14233	A	337	2	329	ARAARAARVTGIAWAYHLIGKLEPFFF MALLFLR*GL/NSVTLARVHWYHNGSM* A*PPGLRCMSLCPA/NFLYFLVE/IGFA TLPRQLQATCLGSSDLPTSTSGSAEITGV S
333	14234	A	338	60	354	NGKECKLIYLSIYLSIYLSIYLSIYHL C*YL/SCLSI*LSN*LAVYYLSVCLSVS VCL/VASCL*ISIYLSIHLSFYSIDRIL AHCVPPTCSLPHATH
334	14235	A	339	1	351	RDADVMLQILVIFQALALGVQTEGMAG VTHHDRVLVNWRFPQCL/HRV*SNGT\ P*VGTSASERPGLKQSSHPSLPSSWDYR CEPPCPVNF/CFV
335	14236	A	340	190	358	FGSWLVFFF/CFLETDSRFAP*AEMQGP NFG*LNPPPPGLRGFFGLSLPGTGDYGP V
336	14237	A	341	306	119	LRWENHLSLGN*GCSEP*FRHCTPTWTT E*DSVSKQKQKQNNLELKKPGSS\CVVF LPETLFT
337	14238	A	342	1	122	GTRGCGEPRSRHCTLA\W*QSKTPSKKK KKKKKKKTGPFFF
338	14239	A	343	92	316	VCWDIPHRKSRTICILFYPLVIFLFETK ICSSF*KGCM/WLGAVAHACNPSTLG QSGWIT*GHE/FKTSIA
339	14240	A	344	83	329	ATAPAPCYFLILCICMVCVCMHTSVCT /CVILCMCMGLCHIL*TCVA/CTCLGMR FLLPAHIIICVKRFLCMCGSGNSGSLCL
340	14241	A	345	127	357	YGVLSRGRVLPCWPG*SRTSGF/SSPEA NSWPPCLANILYLVEGTGFCHVAQGLEL LDSSHPTASASQSAEITSMN/HRA
341	14242	A	346	312	1	LMNLNRSVGALLTRGVKCHKAFRSTISL LIGALK**QSKSDLGISLSKVVDLND

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						IYRSLLRQSEEDTS\KWKDIPCS*TGTP NIVKMSILTKAIYRFNASC
342	14243	A	347	350	243	FHHVGQDGLNLLTL*ST/PCLGLPKCWD YRCEPPRLAY
343	14244	A	348	165	338	HTLDPASHEGPTFLFSL/PVEQCLK*LT LKVATIVLFCFCF*DRVTLCHPGWSAVM QSQ
344	14245	A	349	328	2	SVCPHGSINLSPAETTGACH/RRLA*NI DSRV*AKTFKGK*TNCYNNNNNNNNNN NNNKPFLLRLAGDRHPDQLCPPRRCH FNGATPAGPPSCLRRSHSSAVCSC
345	14246	A	350	3	338	HEIEELTFHDRALIGNILICSLVLYAL FLTTLTKLTNTNIIHAKRIDTVRTILPA IILILIA\LPSLRILYITDEGNDPSLTI KSIGHQWY*TYEYTDYGGLIFNSYILPP
346	14247	A	351	124	382	NTFKS*NSNKTKNART*AKDTKQHFTG EDIQIANKHKRCLIPLGKR\SLNQEIS PRVRINKIRPGMVAHTCNPNTLGGWGRQ IT
347	14248	A	352	3	368	RDRASLFCPGWS*HPELK*SSCLGLPKC WDYRR/AATAPGLLCL
348	14249	A	353	390	161	FSRDRISPRWSGWSP/DLRLSP/CLSLP KCWDYR/R*ATMPGTFFHFNLNQDARN QIITCPNLTKYIYMTSSFILVHS
349	14250	A	354	123	345	LAPQHFASLRLARP/PAGPPCDRPLAPP RPS*FSPAPLPPGADRSVPLSPSVPP*S LPPPAGAPPR/PPPRDPSRR
350	14251	A	355	37	393	TKHFVSTCYVPEFIAGTNQRKRNRISVL ANVKDKQIILLRVRTAITEGYRNYHVL LVFVCFSPPKQGL/DSAFQAGVWHNH NSL*P*TPGLKLSSHLDLQSSWDYRRVP /RMSSYF
351	14252	A	356	2	335	ARETSKDRLTLLGANAGGDF\KLPVL LYHSENPRPLKNYAWST/LPVL*KWNKA *MT\HVFTEWLAELYFKPTVQTYCLEN\K FSILLINNPLSHPRALMDRFKETIGVLM PA
352	14253	A	357	199	377	VGSSCFLKVCQ/C*AVCVVCVCVCVCV CVCLRCV/CVCL/CV\CVGFFFFLVLCG CGCVCVC
353	14254	A	358	1	335	GTRTTCMYHVPPRSANF*LVLERWGLPM LPRLVANSPPQTILLQPTVLPNPRT SALY/YRPLLDLSPTSLSPRISSPLTS SLSIPAPPRSHLAPPPRPPPHPIRPS A
354	14255	A	359	3	369	KPSP*PLTGALSALLMTSGLA\M*FGFH SITLLILGLLTNTLTIIYQ*WRDVTREST YQGHHTPPVQKGLRYGIIILFITSEVFFF AGFF*AFYHSSLAPTPQL*GHLPLIVII LLNSL*FPTLY
355	14256	A	361	337	121	LWSQLLGRRLRQEDCLSPRSQGNKP*CH CTPAWVTE*DSVSKKGKVVIHNNKSSL KKK\NSCNMQQFGGT
356	14257	A	362	256	375	EKKTTVQYPHTYGINV*KNLPAKKTGPG DGFIDKLYNTFRGEITTSPHILFH*FKE VAVLLNSFSK\AASITLTPKPNKDIMRK ENYSPISSYIWNQCSFFLEQIFPLSFKL NCPGLIIPH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
357	14258	A	363	170	1	SQLLRRRLRSQGACHHAWLIFVFSVDTGS HHIGQAGLKLLS\*AIHPPCPPKILARA
358	14259	A	364	330	3	RIMSASASQSAVISDMSHDVRLLDI*HE P*FYQALYSFRQ*ITSSPSYR*SYLLSY KWQDEARC/AFVTAWQAEAGGMLEPSRL VLDS*PRDLPTSASQAGITDMSHHSC
359	14260	A	365	1	341	SQYGLDFHDLSDLPMTASQSAGISGVSH RAWPASG*FYVSREVICSYRL*GYTBSL LVLESGSSSVTQAGAOWHNHSILYPHTH GLK*SSCLSIITR/WDYRHESP
360	14261	A	366	2	338	ARMVSIS*PRDLPTMASQSAGITGVSHR AWPATGKFYVSRGVICFII*KDTHLEF/ CFLETGSSSVTQAGAOWHNHSL*PQTP GLK*SSCLSIKPC/WDYRHESP
361	14262	A	367	2	337	ARAGILKH*QRCKKSIR\PLWNNVGYI LKLNIIGITHDPAIPFLVLYPSEMTHAY *KTSMRMCITTLFIMAIN*KFKCS*SEE E/IGKFWYFT*LLYSNENEHLQLHTTW IN
362	14263	A	368	59	348	SAFGIQENEMPAGRGSSHL*SQHFGPR RVDHLRSGVPD*LGDR/GETPSKKKKK
363	14264	A	369	350	3	GWSQIPDLRWSTHLSLPKC*DYRRGPHA QL*TLMYKYLFEHLLSVLLGICPEVEWC /DHMAILCLISLGTIVLSSKALHHYTF PVTCKCSNFSISLSTLVTFHCFINACYF PLFSRA
364	14265	A	370	908	30	ECSGTILAHCKLPLPGSCHSPASAS*VA GTTGVCHRARLIFLYFLVETGFHRLNL LTS*ST/SASASQSAEITSVGHHAQL/C LELELK*STCLNLPKCWDYPA*ATVPSQ FGSVFLRIF*PMFISNIGQLFSCAFVW P*HQGNAGLIE*VRKYFLFLKFLKEFA\ RTGINFR*MSGRTDW*NHPVVGISLLKG F*LVI*CSY*L*VYPYFLLF*EVSLLSP RLECNVHSESAGITGGSHHAQLVYPYF FFVCDSVLVGVFVLEICHFIWLFNLLVY LCLWYYLIITLIIVKSK
365	14266	A	371	164	1	SCRQVESYGIKRICISLASSWNYRHAP PRPANF\*FPAEMG\FLHVDQASLDSC
366	14267	A	372	3	383	MVSTPAEDAVNIVDMTTFN/D*EYSLNLV DKAVAGLERIDSNFEISSTVGKMLPNSI ICYKEIFHERKNQLMQQKSLLPYFNKLP QSIQHSAITTLISRLSTIWQS/PPPTK /RFQLTEGSDD
367	14268	A	373	1	349	TLLGNDHIYNNVIVTAHAFVVIWVPIPI IIGGSGN*LIPLIIGAPVMAFARINKLR LRLPTS\ILL\LAYAILEAGARTG*T V*PALTRNY*NPEAYGHLSMFSHLTG VSSISR
368	14269	A	374	443	2	SSGSRSECRFLPLLFNVVLEILAGAIRQ /EKE/IKGIHIGKVKSIVIKLTVINKFI KVA*YKIN\QKSVVCLYTNNQLEKKFK IPFKIASKRIKYLEINH*GKDYNNENLK TLLKEMKENKWINIPCSWIRLNNVNIS ILSKVYKF
369	14270	A	375	3	201	LWIKKLDIPIIPS*LFFNTELDKILK LIWKFRGPR/ITQNSFEKPIVGGLILSD FKTTYKATVLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
370	14271	A	376	11	324	DKFLEHPDLLVLQAVAGKGSPLHCLSTL PTSLFI*DRVLLCSPAWSAVAQWFTAT ASWAQ*SSNHSPSD*R/PHTTTGHFFCR DKVL/TMLPRLVSNSTQAI
371	14272	A	377	85	364	YQHNSYFCFISQYVYRLFFFF*TFKKK GEWF*RLNFQGGNMG/SMEP*PP*IRQF FCLNPLN/SPDYRGPPRGANF*IFLKKK GEQVFPPLSKIP
372	14273	A	378	1	382	GTSGTSTYSTIFAGTLITALSSH*FFT*V GLEINMLAFIPVLHQYT/P*YTHAAIM HFLTDSGA/SVLLIEILLYSNSLGE*S SIIELQLISIFLSMMLVIPNKGAAYS IHALCLDRPQLLHILLI
373	14274	A	379	24	323	IPGLKRSSRLGLLKWDYR*DNFQHMCL KNFNNWAAYYFVCKICCAVDPHGCSIKV SFFLSF/CFFFTKSRTVPQAEVQGGDLG *LEPLPPGLMPFSGLSL
374	14275	A	380	2	317	AGWFQTPDLR*SPCLSLPKC*DFRG*PP CQKLFLCPKIF*TRLK/CYLNLT*QSL PLMHFKKNVIYFILYKAALFFFLLRRSL /HSVAQAGVQWHDLG/S/LQTPSPGFK
375	14276	A	381	1	323	VKRQPTWEKIFA/TLYPSGGLITRIY KGLKQLEGKN/KSNLILKWAKEDIQTA NRYMKRCSTSLIIREI\MQIKTTTRYHL TPVKMAFIKR*/GNNEC*GYSEKRTL
376	14277	A	382	2	248	TQPLILRCLPPRSIYRFNSIPIKIQVNF F/*EKEKSLKFIQNLKGP*ITKILRK KKVDGKTFPDFTMYKATVIKTVSWYQ
377	14278	A	383	178	1	HNPPLAISFCFFPFFFLRQGL/NSFAQ AIVKWDHDLQ*PLGLKRFSLSLLS SWDH
378	14279	A	384	312	26	FLRGVFFFFFLRRSL/DSVAQAGVQWPS FGSLQAPPPGFMPFSCFSLL/SFFFFFL VE/MGFTMLARKVSI*PFGPPASASMP VEITGMSHCLANMFF
379	14280	A	385	1	849	FFFFKQTKFIKLSKYKNIKK/SAFLY ISNYLKMFKKIPST*L*FEVNLTKKLK HLTFYSKEHYTN*VTHKWNITHS*GTI FNS*IFVLHKMICRYNATSIKIPVTYFI DIF/EKAYLKFIIWYHKTP*IAKAIKTKE GI/LPDFEIHKTIVTKTVWHLNKNRDI GQWSRRKREQKYISVFTAN*F*IQVTFF FKGNNSIFNK*CLNFMSTCR\KKK*DP HLTPYVKINSK*ISHLNVRPKTLKLL\H QKIE*KPHNIGLGSKFEDLT*ISQDTKG RTSQSDHF
380	14281	A	386	3	318	LREMQLALESLSNRTEQVEETSELKDK AFE*TQLNKDK\KKRI*KNE*RLQEVWD CVK*PDLRIIGVPPEEGKSKYLENMFFEE IIEQNFPGLARDLDIQIQVAQR
381	14282	A	387	1	382	FTPTRTAVVKK/SNDWCWRGCGSIGTLR HCSWECKMAQLLW*TV/WTFPRKIRQPS DVCCDMVIGLPYDPAVLLLGICPREMKT YVHTADMSVITSVSLVII\ADSENNLNV PSADEWINEMWYIHTVDY
382	14283	A	388	1	341	HKLENLENIVKFL*TH/TLPRLNQEKIQ TLNRSITSSKISLIKNTPTRKBBKK\N PGPKGFPREFFPRA\KKQGVPTLGNPFQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KFRERGSLLNYFYKPGFLFRIPKLGKNPRGKKK
383	14284	A	389	168	1	KKFFFFSFFF*GDRVLLCHPGWNAVMQTRLTAAS\TPGLKQSSHTLPSTAGYTG
384	14285	A	390	337	1	TGITPLNPLEV\PLINTSVLLASGVST*AHHSVIESIGNLIIQALLITILLGLYFTLVQASE*FESPFTISDGIYGST*LVATGFHGLRVIIGSTFLTICSIRQLIFHFT
385	14286	A	391	1	235	LNFSYESSMYFALFTTIV\WVFLNF*KFFMN*YHLCYVL*YFLLV\FVCLLTWFMVFCFFFFFFFFFFFFFFFFCFFFS
386	14287	A	392	1	258	SCDRLFANHLSENKELVSRKIYIF*KSQDSTIRKQTDKK*AQELNRRFSTKDLQMG NKHMKRCSTPLAI/REMQUIKTMLRXHCIPIG
387	14288	A	393	2	317	LAYCNLCPLGSSDPPTSSSRVAGNYRG\HHDSVF*RAEDINMHEIQFISFLFLNRDEVSLCCTGWS*TPGLKRASCLDLPKCWN YRHEPLCLAFFFNCSWFQCCI
388	14289	A	394	91	408	LGAEFDVRAYLTSGRLTGPGVPFLTGFYSKDHII\ETANISYTNA*ALSITLIATSLTSAYSTRILLTLTGQPRFPTLTNINE DNPTLLNP IKRLAAGSLFAGFL
389	14290	A	395	3	165	RNKKLKNNRHWRC*EGTLIHCCWCKLVQPLWKAVW*VLR*/LKTELPDPAIP
390	14291	A	396	661	1	LCPLSSFYRKCALLGFVFCFLVFQIRVSLCCPRWLQTPGLKGSSHLSPISWDYRHLPPRLAIGAVFLIFVLMRTCLR*FADPISLSFE*QQRN*LHILISLL*MVDICLTQFTKWIPL*PKNS**LKRQCKLPKITE/LPKNRIQIYPTD*MSSIPHLSLFYLVCLFVCLF*MESECFVT/TMAAVQWHDLS/LQPLPPGFKRFSCLSLRSWDYRRSPC
391	14292	A	397	320	1	PDSKQQIFNVDETVC/WKKMPSTRFLAREEKSMPGLKASKDRILLVQANPAGGFKLPVLT/YH/SENPRAIKNYAKS\TVL*KWNSKVWMTGHLFTALNVLSPPRAL
392	14293	A	398	1	158	CIGPMWENRLILGGRGCSEL*SCHCTPAWAT\SKTLSQKEKKK*NMRKVMIQC
393	14294	A	399	264	1	LINEFSQVAGYKINKQKSLVFLYTKY\YSKLSEK*IKKAIPFTIPAKKKEIKYLGINLTKDVKDLYNENYKILKKIEDT\XKWA DTPC
394	14295	A	400	3	343	HEQKRQSKVREVRELSQGLNMDRKRWSQDLNPGCRTVALSPYHHTRLALNCPGRQWFVGVNFF*RKKIFFFKFWDRVLLCHLGWSAVVPSWLTAALISW\VK*SFRGLLS SW
395	14296	A	401	1	345	GTRKNTDNTKCR*VCEETGYFIHCWWGYKMVYPLGKLVVHFLKKVSIHLPGTSALLSLMIEKLTFT/CHTKTCTQM/FHVVLFPVKKWKQPKCLPVGELLNKLWYLSIHTIYSAI
396	14297	A	402	102	355	DRVIRLANFCIFGRDRVSPCCPSWARTPGLKRSTSLSPKCDHT*ATAPG/LRAILLYFWDYRCLSPDLVNEFACEHFSVELVAF
397	14298	A	403	156	3	NNKNGFP*SMLFQPSNGLVSI*NI\PLK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						*QKWFSFFFEERVSLFHPGWSAVV*SWL TACSLDLPAQVILPPLSLPNSSC
398	14299	A	404	1	364	GTRSEVIYKLLQTPWVI*HMRTRLLQ ACGAR*MMIL\MIILGLVTCRLTIYQ* WRDVTRESTYQGHHTPPVQKGLRYGIML /FITS*VVFLSCVI\WVFF
399	14300	A	405	3	365	HEQTSNIPLSQSPI*SKILMLNSMKA ERGEEAAEEKLEASRGWFMRFKKRSHVH S\KVQGEAANADVEATASYPEDLVRTID EDGDTNKQIF\NVNKTAFCWKNMPSRTS TAREEKQCLE
400	14301	A	406	3	356	HERSDQLYAN/KLDNLDKRSKFL\EGYK LQKLTQKEIQNTNRPTTRI/EISKKKKK KKKKKKKNFSPGGFTGEIPPTFKGQPKK IFKKFFKNLGGEKTLPI*IYGAG/IKLL PKIKK/DPSKKK
401	14302	A	407	116	362	YKSLTPQKLYNHSYIKKNHNKQNNRNH STTTTQKPPPPGFKRYSCLSFPLS*DY RCTPSCPVNLF/CVFLVETGFHHVG
402	14303	A	408	3	360	HEVRLWDFAFERNEGGGENEEKVDWLNLY RMWFHLIF*ABCYSICRLHAYYSCILGP VLLLLFVLIILLFCCL/SFFDYF/VFMF FIFYSFLLLSLFFSLFL/CFIFLYF FIF/CFFLYFFFF
403	14304	A	409	388	1	ALLKFPFPKVLKKPP*GSFFP*GF*LLS /LIFPPYFGRETLLLLF*NKVPLCPPDW SSMARSRVAGSVFPVK\ESLSLSLSV PPQVQVNGFLTFFFFFSW*ROGLPLLP RMVWNSWAQAILPLWPHAS
404	14305	A	410	1	386	VFNAEESAY/YWEIMPQRKFIR/EEKQA P*FRQERIS*YCANAVFTIRTTHICKP ANPQALKKKKKKQTLVFWLYTKKS*T MRTLFLDWFCQCFVPKVRKYLASKTLPL KVLLILDNAPGHLKPHFN
405	14306	A	411	2	417	AHHIFTARIDVDALAYFTYVTTIIDIPT GDEPFS*LATLR*INMK*SGAVL*ALRL IFLFTVRGLTGIALPDL*LDIVLHDTYY VGAHFHYGLSVGAVFAILGGFID*WPLF \SCYTLDROPYAKIHFTTIFIG/VDLAFF P
406	14307	A	412	295	397	WQWPGTVAHACNPTLGS*GGRV/TLRS GVRDQP
407	14308	A	413	437	3	PGFGLIGNLIPASGNRKS KSCVCVCV CVSVCFKSCT*SLCEHLFTCLCPQICVR LQLMV/CPQNCVCWCPEGLFLDESVCV RLCVCAMAVWMGGSGSG*VCGCGC\MC ICVGPLLDSELCLVC/LLGQSKDCGL RCRLPAWCV
408	14309	A	414	2	392	HLQFIFFWILKIFHYL/FLWFWFYLTSM ALFYLQ*QKRNCMYEVENRGLFF/SCGE GVSGSPASSSSSPSCSSSTRGGGAVGGG GLGFVCFLLFWGFVFLFCWFLVCVG WVVCVWVVFLLGV/CCWCFFF
409	14310	A	415	376	1	GFOASKDRL/LLLG/ATAAGDLKLPML IYNSKNPRVLKNFAKCTLPVLYRLYR*K NYAWMTAHLKSWFTEDVKSTIQ*KISF EMLLIINNVPGHPRTPMEMYKELNFF\M PANTSIP*PMDQGIVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
410	14311	A	416	409	2	FFPIKKKKFAGALVFFFRRKIFFFFPK GEGKRGVLVSLNLLPLC*KDFFSPPPPG EGVLWPPPPGPIFFFFFLKKGFCLFCQG GFYNPSLYLIPLSPFKIWG*TRGFT/LP PEALFFYFFFF*DRVSLCHPGWNA
411	14312	A	417	425	3	RELLAFWQNFKLRPQGFFFP/GFGGEK KR*SLPKTPPKGGPPGP/SPNGRLPSGG QLPPPRGG/SPQGPPPLPKGPQGWGPPF P*RSPPCPPHRIGVPPQVSSSPTPLGVFP RGPLNPGNLGGTKKKKKISSKAARDLEL VTRG
412	14313	A	418	1	346	LLPDRNLNTTFD\PAGGGDLILYRHLF *IFGHPEGYMLMLPGFGIILHIVTYYS KKEPFGYIGMV*AMISIGFLGFIV*AHH IFTV*IDVYTRAYFTSATIIAIPITGVK VES
413	14314	A	419	2	382	LESTNHTDIGTLYLLFGA*AGVLGAALS LLIRAELGQPGNLLGNDDHYNVIGTAHA FVINFFIVPIII\GGSCN*LLPLIIGA PDMAIARINNISFRLLPPSLLLLLASAI VEV*SRTG*IIYSSL
414	14315	A	420	261	378	KKNFFFF*KLNFF*KFFLIFFPPKKKIF FKKKKKFFFYKIFF/I*KNIFFSPQKNI *PFLFFFI*YPPFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFTLN SLYFSGRVGGRV
415	14316	A	421	124	428	KPAATHACATIFMCLDQEAIIISN*H*AT TQTTEVSL\SFKLDYFSIIFIPVALFVT WSIIIEFSL*YINSDPNINQFFKYLLIFL ITILILVTANNLFQLFIG
416	14317	A	422	8	355	PVFSYNHSTLLTFSLSLSSFFFFFAPGK KGEKNGKPGPFRRGGFFPKIKKPPPPP/ GGPKKPPGPGFPQKPHFPFGGWPWSKT LFGRGGKPNFGGPQKPLV*NPPSQGP/ HGPGSGG
417	14318	A	423	356	3	KPLGIDLTKVKKLSKKNYKTLMKKIED DSN*KDNSCL*IR/MTILPKAIYRNTI SVNIPMRFLPDADAW
418	14319	A	424	2	338	PSVRLGGHWPRSGITPLNPVE/VGLLNT IRLLASGVSITGAHRLIECNRHQIIQA LLITILLGLY\LTLLQAS*YFQAPFTIS DGIYG*TFFGSTGFQGLHVIIGSTFLTI CF
419	14320	A	425	55	342	GPFTPWSLC*GDLQR*P/RAVKFLLKKK KKKKKGNPIRN*RDISS*FLKNLETA NFWTFFSYFKSKKLIQSDHPLKNVKKI LQNDKRYLKLDWG
420	14321	A	426	2	367	DRRRFCTYHKDIGALYLLGA*AGVVCT AVSLLIRAELGQPGN\LLGNHDHYNVIV SAHAFVIMFF\MEYPIINGGFGN*LVPL ISGAPDMECSGINNISFWLLPPVLLLL ASAIVEAGSRT
421	14322	A	427	359	74	ICADYTRKPPYMGAPIEFSCATCVL*LT STQRECVCVCVCVCVCVSM*VALIPD SN/CIPLSAYVCVCVCVCVCVCSI* VALLDSNSYH
422	14323	A	428	52	361	NYPQLSEI***VS*LHY/LFSFLFFYFF *LVSRFVARLECSGAWH\IIAHCSLDLL



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GSS/DSSPASASLVAGTTGMCHQNQIIF LFKKVVFVGRVQWLTSPVATWE
423	14324	A	429	105	361	SRLFFFFFCKTNFGFVKGVK/WAFF GLMEPPAFRVK*FSGLTHPRTWYRNP HCPVNLEF*VKTGFNLVDKAGPKLLT*K DFP
424	14325	A	430	1	379	HAYHIVKPS*PLTGALSALLMTCCGLAM **RLHSITLLILCLLTNTL\SIYQ*WRD VSRETYQGHHTPPVQKGL*YWIVLPIT SEGVFAGIF*AFYHSSLAPTPQLGHW PTTGITPLNALEGPL
425	14326	A	431	1	390	KKVKKWKNLIFMIGRLNNVNMVSLHKVI YKFRALCLR/TFHFHRKKKNTWA*KHK KALIPKTLKNGKSGGITLSDYKM*YK TTITTTIRFWWK/DINKYNKITTHEIY FHIYQMYFFKIAKTFQGIK
426	14327	A	432	1	392	TRTRGRTQWD*T*LRPI/WTKKKKKKKK GKKRKKKKGVFFFFYFFLGF*FFLWVFF FFFLGFFFFFWFFFWFFFWGIF FFFLLIYNFFCKF*FFFFFGFPNFF FFWFFFLDFFFYFFFPV
427	14328	A	433	382	1	RGGKFNQKQKRVSPPPKKGFFPPAA PKNIKGGKK*TPPKGGVS\PPPKKR KSPPHKK/IGNFFPPRGKGGPPKNPKK PGPFFFFKNPPPPFFFWFFFLFFFA HKDGLLAREQTQAEVKT
428	14329	A	434	375	1	KYSQLIFDKTAKAIK*SKDCLLKEWFN KWTSTHKSLLD/SPFTKINSK*ITGLNL KCRIITLLENNIEENLRLGFGNDFLT LPEAQSKTELISY/DFIQTNFCSANATV K*MKRQATEWEKIF
429	14330	A	435	1	459	PTRPPTRPSTRTLGFTMLAKLGSNARPY /DYPSYSASHSAGITCVKHCARAVIHDF NGVHRPLLIW*EFLVEISFIDFFLETN PGFITKGELQCHNLGSLQVSPGLTLFS CLSLQKSGFYG/HLAKYLVKF/CFGIFS KRGF*GGYPGGAQSPPP
430	14331	A	436	14	382	MARNTSQDIRIDPNNKCLWLVKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKRKNYFHV\LNKAVNNGSTITS TNVMSPGLHIRLIIILSLMIYKKSTTE* VEKQTCYIILM
431	14332	A	437	3	192	TPGLK*SPCLGLPKCWYRR/AAVPG *DILAIFFHHILSECLFLVFIHCFNA NLFLRWSS
432	14333	A	438	1	364	DRIALGTVDLPGRPTRP\AHPIILKVS LADRDAL*NLWQIPIVAS*YIPLGF/WS KAMPCSDIYSSFEEKKKTFFDRGQGP TPEIQVLGAEGVKPFEPGRGSKPSWRIM AKPKFYKRFKL
433	14334	A	439	336	2	GMIPEMKNAGP/SG/PRKPGFFLG*KG KVKAWLNFKPPFRAFVPPKKILLPLGFS GILGPGPKGNLSRPGPPQAFPLGFCQV LGP/SGPGVGFPKPGQIGWSNPNCLTLQ KNK
434	14335	A	440	1	333	HKLENLENIVKFL*TH/TLPRLNQEKIQ TLNRSITSSKIKSLVKNTPTRKEK/SKK PLVPKGFTIEFSQLCKLRVPVFMKPFQ

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						KYGERGLFLNGFYEPGLTLIPKFGKNP G
435	14336	A	441	320	1	WGINNWLSP*EKKGRPFLL\SHPKINSK WIKDLNVKGI*KPLEGQIG*YLMIFGV EKGLFKGGPKYTLTKRKY*NRELLFIKR YFSLTEKSPAIECHIKKLAKKK
436	14337	A	442	8	391	ERILRHDQVGITPGM/QGWVRI*ESVDE I/QHV/NQLPKITHTTTSVSVGKARDKF NIYS*FKLGKTEKERNFLHWIKSICTSP AASILLEGKESPF\PFSGTRKD/CLL* P/LGSGMVLEALGTAERRTRKEK
437	14338	A	443	363	2	HHVGQACLELLTSGDPSNLASQSARITG MSYRAQLSIVTFSAFLVV*KLSHARGL ML*QSIII/HVLHFHQVKAFHVS/PEN SQPLHNVEPEDWIF*EHQRKTVPPIH TARKLQDLEPCLV
438	14339	A	444	1	900	DSSAGIT/GICHHAQII/LFVVFVETGF HHVGQAGLELLTSGDPPASASHTG DYRHEPPLLASLSFLNKLCTWPERRR KPIFSLPKLDPNKRKFSFPP*LF/IGS* TLIWSLFCFRNVCTQLADPTKSIAYQSS LMKPFQKSI CFGSEKFPDKVYLFSSDR KAKEQVLVVVVVEY*I*DMSACFQ*ALG FCYCLSIWN/YELPEKFEVLACSLPSR NNDLILSLKKKSQNSFFVCVFFFKTKS NFVPQAEGQGPLFG*LKLPLPGFRNISC LNLPGSC\QTGAVPPPPVNFGLKKNR VSP
439	14340	A	445	3	346	QIGKVKKLNK*VPHEPSKNKL\FLEASS LILCENNNEPFLSRIVTDENWILYDNH* QPAQLLD*EAPKPNLHQKKKKKKGLAP FWGAFSRGNPFYFFNPPQKLHF*KFSSQ KRG
440	14341	A	446	2	246	FKCGKTRALMHCWEGKMLRQL\RKVWQ LLAMLNMELEPREPAAPLLSISPRERK/ STAKTCA*MCIATVCI TVKKWKHRLG
441	14342	A	447	38	393	VILHRQGLSL/VTQAEVQWYDYNLSL*P* TPGLKQSSCLSFLKSYCHG*LFVVVVVF KWM\GFTMLPGLILNSWPQ/CNPPAVDA QIAGIRGFHS/VGQAGVQWHDLSLQPL PPGFKQFSHLS
442	14343	A	448	54	540	RIPFEHASGFLQSSHQKPHCLLHPLSGQ VSSDGQ\FRKFGISRLGNSGIYKAAPPL HDCKFRRQSEDPSCPNERYLLYREWAHP RSIY*KQPLDLIMKYGEKIGIYFAWL GYYTQMLLLAAVVGACFLYGYLNQDNCT WSIEVCHPDIGMI IMSAQRDRL
443	14344	A	449	2	310	FFFLRQSL/DSVAWAGVQWRDLGSLQPP PPGFK*FSCLSLPSSWNYRHAPRANF FLYF**RQGVMTLTMVLIS*PRDLSS ASQSAGITGVSHHAWAKISL
444	14345	A	450	2	466	KQKIFSVDETA FYWKKMPSKTFHS*REG TASKLHTAG*ILLGPNAAGDLKLKPVFG DDSGNLRALKNYAESPLPVLYKWNKAW MTAHLFTAWFTEYFKPSLRS\FRKISWK I*LFMDNGPHHPRALMEMCKE/NAV FMPANTTSILQPMDKGVILI
445	14346	A	451	670	212	SSSSP*GS*YQNRNTNTPSPKKKQTKK\ KNNHYKSIFFTD AEILSNILANAIQSSI

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						KRFIRHEQLGFILVVLGVWNIQTPTNAT CYTNRLKKNHMTILINAEVLYKIQPSV I*KLFPLRGAF
446	14347	A	452	407	219	PLISLRWENHLGPGVQGCSEP*LCLCTP AWMTE*YPIPSQNKTKKQ\HTRKQNQH KNKCVKN
447	14348	A	453	2	395	WFLWFRERSHLH/RVQNEAASADVEAAA SYPEDLAKI IDAG\AKQIVSVEETAFFHW KKVPSRTFITREKTTTSALKG/RC*LSLV DNAAGHF*VEA\MLIYHSDNPRTL\KN/ YAESTLPVLYKWNNAWMTACLFTS
448	14349	A	454	424	38	BETEPL/HRPISAEVELVTKNLPT/KH KSPRPDGFIAEFYKMQKE*LVPILLKLC QKIKEEGLLENSFYEASISLIQ\NSGRD TV/RKENFRPIFPMNIFAKILNKILANC IQQHINKLIHHYQVLFSSLSHR
449	14350	A	455	2	309	PRVRSQTPGHRSTCLGLPKCWDYRHEP LHPATASFLVAAPGM/FADPP/CNMHL NE*MNE*MNGDDASEILSFEMRSHSVTQ TGGQWCSHSSPQPQPPGPPK
450	14351	A	456	3	441	DAWGLVLDREPRFFIFFFFFFLGNNGYF RGPGRPGGEGPPMETSVPVKILRGP GQGGGKARKPHPLGGPRGNHKTGG*KR AYPTGENPVLTEKPKFTGPGGNGPETPV IGKAGAGKPLNPG\MGGSRNPKWAHCP* TGGKKKGK
451	14352	A	457	1	234	PTRPNHLGLGDRGCREPRSSHCTPAWAT ERDWVSKKKTG/EKF*KGRTK*MS*VE QGGSGGKGLFTLAISNSLPFF
452	14353	A	458	42	470	KRIPQLKKSPLPLKNPPGEWVGKINFPF PRERPKNFF*KKTKLTPPKQKFLRKKS PFKKPHFLYSKATKKQKRGKKKRAPPP KKKKKKENPKIVIFRTEITVASPVLWSA VKPIIHIFFPREKKPHA\KPPPP
453	14354	A	459	2	393	DRPIEQWNKRERPRINLYIDQMIFSKG TTAFE/WK*NLCNKYVWNAWIC\NRRKN PYLTSSRKINLR*IIDIKVK/PKAIKLP EQNIRCSL*VLGVGRDFLENMNYTRKK\ IGKLDFIKISQLGMVADTSNPI
454	14355	A	460	338	33	GDEKIEKSFPPFISSLCFVP/AYL*QQI RLLIPTNRSLFFIY/CLFLEMGSFHV QTGVQWCHHSTLQPRPLGLKQSSHLSLL SSWDYRHLPLVVLKWTEACAV
455	14356	A	461	77	435	AKEVEASLSTLARPISLQQQQQQQNEK KNKN*PRIAKAI\LS*KGEITLP/ELQL CYRAMITKTAWY*HKNRHIDQWNRREN ETNPHTYSELIFDKGPKSI\SLFNK*CW EYWIFICTR
456	14357	A	462	157	3	NGRVDLKIQLARCGGACLSQL/ROEN HLNPGEKGCSSES*LHHCTPD*VTQKQ
457	14358	A	463	363	3	PSVAQAGVQWCHHSSSLQPQPPRLR/HPP ASA/SQ*LGLQGQATALYIHKYILFPCN VLISFIFFFFLEMRSHSV/SQARVQWH DGSPQPPPELKRFSWEAELAVSRDRAT ALQPRRQ
458	14359	A	464	3	396	LKETAEKVKKIIFKKQLRL*MKKIINR YLKEN/LNQLLEIKGTLRELQNAVESFN NRL*QIEEGISKLEDKAF*WTESGKIRK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						INK*TK*TDYIKEPNLRITDVPGGEEKA KSLKNLFEVIEENFPGLAR
459	14360	A	465	399	1	PPGVLLNGPPFFFFFLILGPGWVFGQPL KTPLVFFPNFYHIFPFKISRIF/LPTR FPFQVPLPCP*PFSSPWGLKVVFILLSF FFFL*DRVSLCHPGWNAVM*SQLTAASN TW\VK*SSHLSSLSS*DYRCVLS
460	14361	A	466	279	1	TTNIFNPRRVGSTDAGPLNMKEKEKENV KRRQATGWEKIVAKDTSKGLLSKIYEE LLKLNKNEKTNK*/ILCLKWSKGFNRYFA KEYIQMANK
461	14362	A	467	2	436	RGELPQLDKYLKKTATILNGEEL/E/A CPLRSRTRQGCSLSPL*KKFFPPKSHI ESLLFFNIILEVLVSARQENEIKIVEI GKEEMKMYLFTDGNHLCKNSERIRN/YS KVAGYKVN*V*T*ITFLYTSREQVEFEIK KTLSMNRRF
462	14363	A	468	2	420	RTTALF*AVRQGRSLQRLLSFC\CLC PAARGEAYIG\QASMSRCGLQAVQASC LLCLPKQAWAMAGAPPSASLLPCSLISD RCASSQPDVGVGPSEAGVGYNLVVRGL LSRSEKR\NIRLGVTRFSRCV/LSPLSL TRR
463	14364	A	469	1	416	PSP*PLTGALSALLKTCGLAM*FHFHSI TLGILCLLTNTLTIIYQ*WRDVTRESTYQ GHHT\QAVQKG\LYGIIIFITSEGSFF AGLV*AFYDSRLPPTLQLRGHWPSTGIT PLN\HLQVAVLGEPVLLAS*VSTIT*ADH
464	14365	A	470	211	398	IFFFFPKMGGLSIIICWRRKRHPQK* STCLGLPKWWEYRCEPP/VPGQKKNFRP *KTKESPPLVSGGASSASNIKL*TALPP FLEKKKFKKGFKDPPFPLFFTQNPQQG NFFFGKI*YCPPIFFFLRRSFTLVAQA GVQWHDLSLQPPPTGFKRF
465	14366	A	471	62	424	TLMHCCWWKMKMVHLWKTVLNLLIKIN/ RTLNHT*PCNPAIPLGVSLREMITYVH KKPCP*MFIVALFMVTKNSKHLKCSLTC KWINKLSLYTMKYLATKRKELLNHNR SCRNYSSDMS
466	14367	A	472	427	20	LGLRLPFVEQENKPYPLAFSPPEPP MSLYKNSPIYPGKGFLLPSPKNNKIPPLN FLKMSNLF*/FALLGNKDFHLLLLGGP IGIMGDNMATTSMFYSRVPIFF/CFFE TGSHSVAQAGVQWCNLSLLQSLPRLK
467	14368	A	473	424	98	NWYLYYYYYYHLLF*RQGL/DSAAQAGV QWHHHCSSLQPRRHLKQILPPQLL\TSW NYRHKPRLSPYVAQAGL*LLGSSDLDP SVSQSAGIIGNEPLHLASL*FLFAP?
468	14369	A	474	415	75	NHFLKFFPQTQANGPGGKNNFFLKTRF CFFPPGKRPPWAYYSKSLQPPNSGGQOI\S APTP*IKGAPKGGPPTRVKFFFFFLF/L RWSLSVAQAGVQWHDLSLQAPPPGFM PFS
469	14370	A	475	3	413	PVQKGLRYGI\ILCITSEV\LFAGFF* AFYHSSLAPTPQLGHWPPSTITPLDPL EGPLLTISVLLASGVSI*AHHS LIEN\ NRDQIIQALLITILGLYLTLQA*EYF ESPFTISDGMYGSSFFVATGFHGLHVI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
470	14371	A	476	1	440	ITLTDRELSYY*ANRL*LAYTITFIV* IPLYGLHL*L\PKAHVEAPIAGSIVLAA VLLKLGFGVIRLTLILNPLTKHIAYPL LVLSL*GIITSSICLRHKDLKSLIAYS SISHIALVVTAILIQTP*SFTGAVILII AHGLTSS
471	14372	A	477	2	397	LFVYNHIDVGALYLLFGA*TGVLGTGLS LLIRAEGLHPGNLLGNDHIYNVIVTAHA FVILFIEIPIIIGGFG\N*LVPLIIGA TDMAPRINNISL*LLPPYLLLLASAI AEDGAGTGGTDYPPLTGNYS
472	14373	A	478	442	44	SSSSPFTPPRGKFFFKTPRKKFFS/SP GNKGFFSPLSP*KFFFFFFNFFFFGGFF PNFPPPKKNFFFKNSPGFFFFPPLKKKI FFFFPPLNFAPPKVFFKSPPPFFFFFFF FFFFFFFFFLRGHPWGREGI
473	14374	A	479	1	439	PTRSPTRPLVLDREPRPFFFFFFFKGPP SVPPAGGGGANLG*GNPPL/GVKKFFG PKPPKIGE*RPWPPPPGQPECSFFLKKN GLPHGGQGR*N\PPPRP
474	14375	A	480	420	0	YSPSPPK/YRAPGKKFF*KKPRKEKF* KKKILGFFPLSPLKFFFPKAFKFFGG VGPNCPPPKRFFSKNSPGGFIKPLKG KNFFFPAPVKFGPPRGFFKGPPSFFFFF
475	14376	A	481	371	2	NKI*NKFSKLNKSSSSSSSSSSSSSS SSSSSSSSSPSVNK*IKCSTSLTIS SSSSSSSSSPT*IAIKNIDSPKCWQGC RETGLTV\LVQPLWWQFLKLMSQII*D SANMILSMHARG
476	14377	A	482	3	335	HASGKDRHTDQRNRIKNPETDT*ITYTF *QKC/RLI*WRKDSLWNKWC*SNWA\SP MKKIKLDSLSSSSSSSSSSSSSSSV*NV KLLGNNVGGNLQYRGLRVHTVDVKAQHI
477	14378	A	483	1	418	GVR*FSPLNPPSRWGPKHGPPNL\LNFF FFFFVFLVETRFHPVGQAGLELLGSRAP PASA/FPK
478	14379	A	484	1	356	FCANAVRSMIKTVLIDKATK/RAWKGN YKYHLPVFNCKTGRT\DSGNPLNWFYQC FVPEIRKYLARVGLPFNVFLILDNAPGH PEPHEFNTEGFRVVFLTPDMPLIQPLEQ GVLRLTLTA*YQCFVPEIRKYLARVGLPF NVFLILDNAPGHPEPHEFNTEGFRVVFL TPDMPLIQPLEQGVLRLTLTA
479	14380	A	485	166	406	FIFWGSVSSSAEGGWSSVSSSLPRVTVR PDETVDVTIHLLE*CRPGAVAHACNPS TLGGRGGRI/TLRSGVQDQPSQHG
480	14381	A	486	107	429	FWVTQTFGFFWLNPPGGLELWPPPCPG NFGGNFKKKGGFPLWPGGVQTPGPRGIT PPGPPRGK*RGGP/SPGPGFLGKPKG GGP
481	14382	A	487	399	2	GSPAPGLPKGWGFRGPPGPGKFVFFKL PKGGFPGAEIFLGEFFQGRKKGLGPIFP PVFLKTEGGTSL/NSFFKGRVFLVFKP KAGPKKKKKKNTNYKPIYLNNTDTKFFNN MLANRI*QCIKEVMQYDRTRG
482	14383	A	488	419	2	PPPPPPPREKKGGLYFNPKIFLGKSFP RNPKDPS*KPRVGIFFEFGPKPPKKKF* FGPWGKPPGDG*RKNPFK\PPFFFFFFF

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						*DGVLLCRPGWIAMAQSRPGLQEWNSIS KKRSGPCVLGSISSKEVPDAWADAWADAW
483	14384	A	489	629	0	SSSSR*SLCKCFKN*GEKIRNPTEKWA KVMRLFTKRCINI*KDVRSTSLMVRET *ITTLRYHFSPIRLSKT*KLNRITLYG* DCGETGIFHCWWECKMF*VL*RE/VWQ YLIKLL/LHIPVDTA
484	14385	A	490	2	351	KNRPMDPGM*GY*VNDEGDTTYQQGNE ELRS/WCWDNRLAKVKLDLYFPPHITI EINSKWI*DLNKKNPPIHVLEENMN/I* F*HVGIGKHYLTI*LKI*NP*K*IWLH ENKMYCL
485	14386	A	491	42	507	NLAK*IQ**IQTIMHHDQVSFIPGIQGW LNILKSINIIYTNRL*DKTHITISIDA EKAFDKI*YLFMKGK\KPLSQLGIEGN/ YLIKLIKGIH
486	14387	A	492	18	417	REGKKSRVHHFNKQGRVMSTKH*KTQL /SHSNAHSNKAQISKSQPHGLHDFKKK KKKKKKKKKKKKRGEKKKKKKRGGKKK KKKRGGGPP*KGVREALFCFFWRKKFFF VGGGGGKTPLGCLQADTPLWGA
487	14388	A	493	413	82	FFSSPPPLPFFFFPHLFPFPPNFFFFFS PPPPFF/PPP*KTKEPPPPPLFPFPPPP LFFFSPPPPPPFFFSPPPPPPPPPPPP FFFFFFFFFFFFFFFFFFFFFFFFFWL
488	14389	A	494	1	413	PTRPPTRPPTRPPTRPVLDREHSPSNLP KKKKKKKKKKKKKKKKKKKKKKKKPG GAKKKG/EKKKKKFF*KKGEKKKPPGKF GKKKKIWGGEKRAKTPQKKKTP*GKKKI LKGEKKKKNPKPRGGKKFFSGEKKKKK
489	14390	A	495	274	1	IYRIDCAYMKKVERSISILSFHRLKLE N/QLNPK*/RRREIKIGAEINETENRK *IEKINETKSYF\WKISKPLAKLIKEKT QITNTRNRAY
490	14391	A	496	336	1	VFQYTYNKLVSIFYCFFL*RWGLTVLL RLVSNSSG\PSD\LPSSAS*VAGTTDAHR HTQLCFTTSLDLEPYFHLGSIFFSL* FFFLNTESHSSVVQGV*WHNLGSLQPLP
491	14392	A	497	445	382	PRVLIFFFLTTPRGPPPPPPPNKVFPPPP PPQNFFPPPPPPPSWGGFAPK/PPPPPK SFFPPKPPPVFFSPPPKKKKFSPPPPPH FAPPEVFF*PPPEQ
492	14393	A	498	430	2	SPPPKPTRM*\KVKFGR*KKGGGGGGGS PPLSPPLWGSKPVP*VPKGR/PLPG*A GKPPFFLKFPFPRPGGGPRCPPLFGGL GQKNGFTPEVVLL*PKFSPFPSSLVDR RIYCLLMLEYKSVMMILLFASCLNLYT FPIV
493	14394	A	499	363	3	KKLVTPARVLGDIIPRNRFLQMPQOREN FLCQVWMTKPPPTTIFVKTKTKGYLISL KRFCPAKKKT/IKILVNRVNRQPPPEWEK IFANYASDKGLISSLYKDLQVYKRKN PITK*VKGM
494	14395	A	500	145	435	VFMCINSSFLFIPWYEYTTVWPVTCRR T*MFIAALFVIARNWN*SRCPSTGNW/L KLWYITME
495	14396	A	501	162	1	FYNYTIFIFYLFIFIFLRRNL/DSVVHT GV*WRHLGSLQPLPKKFPFRLSLP

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496	14397	A	502	343	2	TKKFRWGPKEPPLKEPPGV/SPDFPII/NFGNPGVPVPGKDFKFPNFPKKKKWGGRAPPVVPTTPGG*MGFRFP*PPAFGVPRGGDGSPPPGAPKEGPLSKKKKKENEKEKERKEKSARL
497	14398	A	503	23	405	KGRNYLWEKKKKNMLVRGKIGGGPPPRI PKF*KVIFKTPPGPPFFFGPPLNFFFF KTDAPLFF*NHPPKSKIWALAPPKKKIF LNPKKPPPPPPPHFFKKNFPRAFFKNF \AFSPRGASPSPPP
498	14399	A	504	418	247	PPKWGF\FPKPPRGFFPPPKGKKFFFP PPG*FGPPQGFF*RPPLLEFFFFFFFFFF
499	14400	A	505	26	426	GCTGLLHS*MYAKVVCCTDHPIT*VLSP AFISRISYSPTHQLILFF*IFFLFLVE TESCHIAQAGLK/LPASSSLPVWASQSA
500	14401	A	506	337	2	IPNLKESA/CPNLPKGWGF*PPPPSQ ISLIFKYPKFLKFEI*KKKPPLKKGLEW WV*RKKAPVGF*G\EMALGEKFFFFFFF FFFFFFFFPRRSFAFVAQAGVQWRDLG S
501	14402	A	507	454	2	TSKTGQPGRRGSPFPI*WAAGQKRSSPP RRGSRAEALLTSQTGWPGRDTPHFPDDG RPRGAPLFPDGAAGQRRSSLPRRG/VP GRGAP\QSQMGCQLGRGAPHFPDGVAGQ RCFPPFRWGSQVEALPTSQMGQPDRCGP HIPDGVAAGQRR
502	14403	A	508	390	13	RIPPPKSRWKKGKGF*VS*NPRPQI*KN FLPPPP*K/YGDPRGPPPPPIKFLPLKK KGAPPICPGCFEIPAPRESPPLAPPKS* NSRGNPPPPFFKKKNPLFWGGKTKKLK IFFFFEAGSCYVA
503	14404	A	509	2	282	WQFLTCLNLLPYEPVIMLCIYPNESKT* IYTKTYA*ILLAALFIMAKTWKQGVLLK V\TDKVWHIMTEY
504	14405	A	510	400	250	LLSVTQAGVQWHDHSLLPQTPLRK\HP PTSAS*VAGTIGAYHHAWIIFFF\IFY CRDAVLLYWLGWFPKGLLKCDWYCEP/ RMSGLFVFWSDLGFRSEVS*ILSSWDYR CVPPCLDNFFF
505	14406	A	511	99	242	VTKEKEGHFIRIK*LIHQEDTTTINIGV PNNRTLKCMKQKLTCLKKEI
506	14407	A	512	139	374	SLWGKRTFFFFGADPHFVPQAGGA\WGN HG*LQPTPVGLKKSSLLTFPISWYVRLG TPPPANFKIFCKNGVKPCCPACF
507	14408	A	513	23	401	STCLRLPKCDYRRESEPLALCMLFL*M KGKYVYMGFFI\LFFFLFLHKKI*LLQEN FVYVCLKKNKTKLKA*TKKQKKNETG*N ILVDLNLVLS*KKWKCLLWGFILFYF/NF LRQSL/NSVAQAGVQW
508	14409	A	514	7	386	FFVFSTHITLLFLFLFFFLFPPPPGFF LAGKKNTPAPPEKPPPP\PPKKRGPP FFFFGPPQKKPPNSPRGGRGPPPPRPPR KMEKGPPPPPREI PPPPPFF*PKTPPP PPGGGGGKKTTPPKR
509	14410	A	515	370	2	FVFFQVVLPE*NSFLFSPF*KGLC*RD LAFKRFFPWPNNKKLWPSLF*GFLKNS*K FNFSLKSLEVPFFF\CFPKFFPWI*AFP RFFPPFPPPP*RG*IFFF*\DGVLLCHP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GWSAVVQFWLT
510	14411	A	516	1	163	NTREKLSGGGGTQLS*/LLGRPRQKNHLNLGGGGCSEPRS\HCIPAWMTE*DPVSK
511	14412	A	517	1	390	RIVRVYKHL C/Y*GSVNPKEKIDNFLDTFNLSRLNQBEIETLSTPISSSIETVIKSEPT\KQKSPGPE
512	14413	A	518	47	312	EYTGILRLYIE/LFTTQH*KQKALNQA K*LAKGLNKHFIKRGCMNDPKHMKKSSA SLAIRKM*IKTMMRCHYILT*MAKIENK TESTRP
513	14414	A	519	320	1	QNPINKQ*KKNKKYRLV*HKKPPPFPTT QPHQSNQH Q\PN**PQKHT*TKNHHTPP PPP*SPPPSLSPSPPPSPSSSHPP LLSPPSPPPSPSPSPSPPTSP
514	14415	A	520	1	368	LKTOQEANNLILKWAKDLNRYLIQK/VY RNVKHTKRCPTS\RELQIKTRYYYISIR *RVKYKKRDNTKC**GRETGTGLVIHYS *EYKMV*PLWETV*QFLTKL/E*SY/P* DPAITLLGIYSKELK
515	14416	A	521	2	264	GKKIPMLYFABIEKCIKLFV\KRS*KAK *ILPKNNKAGGLKFPDFTTYKAAASKH QVGGWLKELRSTLQAQQTWVPREELRST SPS
516	14417	A	522	1	408	LEKMSTSLAI/RVMQSKTMMKCHYIPIR KAKI*NNNDIKCWQ*CRETGPLIYCC*E CT/LVQPL*KTV*QFLIKVNM\DPAFVL IFIPKK*KHMFTHKKCKHTFRAALFVM ANTRII PNIFQFVEWLNKLSYKHIVDY
517	14418	A	523	320	3	TYIYIKTCPRMFT/AVMLTITKKQKQPK YPPTDE*NV\YIHSNAYYSEMKNREVL I HATTWMNPKNIMLNKASSRKRPHTI*LH IYEMSRI IQMVLCNCLLLPSMF
518	14419	A	524	426	9	AELPASPTPGTCTPQPLGSGRDQV\GA VGGTHPGGSGLAGSPP*GGLGMAGCKS* ALPRGEVTEAWRQFKCGERRQASSTGGP GAPSAAGPGAKPLTAWGQRHQPAAPSA GPAEPLPTQNCWPASNPGRSRLSLHT
519	14420	A	525	13	461	ICTWRKMNILLPYTKLNSRWIADLYVKG TTIMFLEVSVREHLHDSQKKIF**DAKL MNQKE*LDILDSINIKSFVH*KAPLREN KGKLOSAIHIYEKGLVSRIVEELQ\TY KETLKANKKKIDNP I EKWAKNLNRHFTR GCPSIYKHVK
520	14421	A	526	288	570	ATGSLCCPGWSIVAIHGFNHSAL*LLTP GLKHPPASASQVAGTAGMSDCTQLCKIN FFFVFVFL/RRQSLAVTQAEVQ
521	14422	A	527	3	438	AVSHDCTGLQPG*QRETLYQRKKKGTF SPLPPSPGIGGKPALEFWGPKTWPPPG IPFFLFSPPPSQSGGGRPLETLAGSF SQNPWNLRDGAPPPPGGGFFG/CPFGP PGGLG/PPGAPPPPLKNFPKKKGGGGF LFPPQAKG
522	14423	A	528	2	616	FFFDTEWRSVAQSGVQWRDLGSLQAPPP GFTPFSCLSLQSTWDYRRPPRPANFFL YF**RRGFTVLARMVSIS*PRHLPALAS QSAGITDVSHRALQVCFITTL*LSK/H QFKKAGVT/PHLQCLHEIGLDCVLHKKH /WSVHHSPE/HKTNVC



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
523	14424	A	529	57	485	RHSSLGNKSETQSOMKKKKREKKKGKET SFDPAISLSI*PKENKSLYQKD/TCICM FITALFIIAKTQNPCKPSTDE*INKRV \IYIYIYIYIMKHYSPIKKNEIM/SF AATWMELEAIIISSETMQKQAKYCLFSC I
524	14425	A	530	399	3	FFFFFFFFFENPPPPPK/WRGGGKKKAP FKFFFKYKK*LFFF*GGGGGHQKKKKK KSSSFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF F*FKGFLLGTHASAHASAHAS
525	14426	A	531	491	4	SKWIKDLNLRK/TTKFVEET*VKIFMN LGLGNDFLSMTPKA/LKIDKSDFMKIKN /FCSSK/TIKEVKRQHTWVKIFTSYI FDKGSTSRCKEL/RKQQKNKPIQKCSK VLNRFFRFREDIQLSNKLMKGCSTSLNH
526	14427	A	532	184	509	PQWPAHSFLPALGSSGTGPY*VVRQIFD SKDKESSQ/WSHETSDRPKPADHRRRSR PSLATSP\PRLEPHPSLPNHSGLPILSS LPWGAVALAPTHFSALAWP*RPLPCNSQ GEKFFFWFGFF\ERESH SATQAGVLGHD LGSLKPPPWGSKGFFCPSYSGG/WNQKN HLSP
527	14428	A	533	401	3	VIREMQIKPLHIQ/PGWL*SKSVKKY*Q GCGQS/NVLIHY/WLKT*IMGPFWKIVW QFLIKLPYGTVILLSGIYILWRMEKKPP KFCTQIFIAAFFIIQ*PKSENNPNIHQP KNQ*DVHMYIHTMEYYLAIRMNIIH
528	14429	A	534	419	93	SLAIRQM*TKIPRYTRVAK\IEKSHNT KYWKRHGATGLIHCWWECKMA*S*KIW *FLIKSNINLPFNPVILL*GIYPREMK CLYKD\CM*MFMAVSFIEQNGKQPKCL
529	14430	A	535	414	2	NFLARGYINCGPQFFFFPFRKNLKWGVP LSNFPPKL*KGGIFGEGPKVKKNFFFF FLFFFFFF*KKPPCSPRLKAK/WKIFGFL KPPPPGLKKFSLTPKKNKDKRGGPPRR GNFFFFFFLVLVKTETFYVVGAGLK
530	14431	A	536	32	435	DRATALQLG*KSETSSYKKKKKKKKKK DGGAPLKKNPGGAKKKPGEKKKNFSPKR GGKKNPPGNFEKKTNFGGKGAKPPQK KKT/AWGKKKNLKGKRGKKNPKTLGAKK FPPRG*KKKKKPPAARPGKASS
531	14432	A	537	348	1	EYIKSTHQMKNYPLKNTVSSGQVQWLS PVISAQFAIAKWSQPKPSLNEWIKKL WCV/WCVVCVCVCVCMMEYHSAIKRNE LMAFAVT*MRLETIIISEVTQEWTKHR MFSL
532	14433	A	538	523	66	TDQTSHNIPLSQSLIQSEVPTLFNSVKA E*CEEA/AEHKFEASRGWPTRLKERSRL RNMSV\GEAAGSPEDPATV/INGGRTQ PQIFSVAEATLNWKKTPCRPFIGREKSM PGFRASKDSLTLCRDFKTHLCLVFHYWN AKHVQVYILLKVTAKI
533	14434	A	539	413	2	RDKV*PCCRSWSQTPELK*STRCLCPKC *DYR/R*APAPGFLL*VHRHVSIFKSG PLSCRCSNFQD/HDSIKPSFPTIQYAHG NKFQL*TPDTLIFFLKWSFTFVAQTGVQ WHNLSSLQLLPPGFKRSDAWADAWADAW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
534	14435	A	540	385	2	MASKHIKT/CARQLAIREVQIKTTQYHV IPTRMAKVKK/DNECWHGC*NTLINCW WDCKMMQLLWKK/SVWHSSRGKMYVQLP CTPAIPLLGIYTELKTCSHK/T/CT*T FLAALLVIAEKWK/KCPSAEW
535	14436	A	541	44	398	RPPFFFFFKRPLWKKKGFPFPPA*RG IPSAKK\PLGPVSGPGNPPGP*KE/PQ NPPPLGGSPFGKKPPLDIPFPGGPIK KWGGPPLAGGATTKN/PPPGNFWKGGK APFPFSQKF
536	14437	A	542	370	10	FFLRTKVSLEFPRVEG/KVQSQLLAAPP WGQVIPPLQSP*LRQKDPFSPGG*GCS EPCSCPCLPAMTEPNVSVKS*KKRKK EKN**KKKSFINTTGKIRFRIH
537	14438	A	543	1	370	FLLRHILLCHPGFCSVATAYCSRDPGSS D/PLPPQAPLPDQ*PRLQA/WHRLAPP SANFF**RQGFTVLARMVSIQPCDPPH WASQGATATKADDYQK
538	14439	A	544	50	395	IPGLTRQWLLDPCASPTTPPYT/P*VQP STPQNSSSPKTHNQGLPMLSPTPKP STAWKKAILEHTSSSSSSSSSSSTCRNR NGYTYTVPEHRPARGHTASQTRKQVLA THKP
539	14440	A	545	1	370	LCSVTQAGVQRRKLNSVQPPPPRFKQVS CLSLLEFFFF*KRVTLEPRLEGRGP FNGSPTLRG*GDPPV*ASKELRKGGPH QGQLINLF/CLGATGPTYGAQGGFKSPG LRRWAPLGPPRA
540	14441	A	546	178	365	YKKTDATKTKMDK*DSIKLSFSTVKET INKGNR\QPTWEKIFASHTSDMGIISQ ICKELKQ
541	14442	A	547	11	236	KGTTKLVLKLSDFKSYFKAIVIKTVRN/ WHKYK\HIDQWNRIQNPEINPHIYGQMI FKKRAKNQWKDGLHKKR*WSNDFQET CQEQTMEKGRSSQEKMM
542	14443	A	548	355	3	IKKKNLGRKRCFFQEEKTWP*TPKKP LENPGGVFPNPGFPPFFKAKIPEGFPFG V/SFF*RGGFKGYPPLFFFFFFL*DG SLCHPGCSAVAQSRLTASSASQVHAILL RHVDEGR
543	14444	A	549	1	373	CFLICRHTSHMWRIWFQTTAINQIWQ*K ESQKVVSQ\LYI*KLHLLYEVO*HFV*K YTQ*LLLENADTK*AHAVGKMVLIDLLK AALSLIFNL*KNK*NLKNWPGMVAHACN PSTLGGQGGWLT
544	14445	A	550	446	2	NIDKAPTVLGKMVSIPTSRSPPLGPPK CWGHRREPPRPAYFGI*ILFLTPP*NPL NNSPQHLSGKISGIFSDPSLVFFSSFF FAPPPKFMCLCF*PFFFFFF*DRVSLCH PGWGAVERSWLTAAPISQ\IR*SFHLSL LSSWDHRHA
545	14446	A	551	342	26	WAPPFFFFFFPYKRSQKFPFPPGENNSR GF*IFG/RGGFFKKEGLSQFFFFFFLKKV FFFSPGGEPQGYFPPPKASFLKRIFFPP PPIKKGDPGRGSPRGNNNPFF
546	14447	A	552	3	167	QPHLQDCL*QQNPFVAVG*AFSSHPRDSL NNPW\WPGAVAHACNPSTLGGRGGRIT
547	14448	A	553	3	413	TLITALSSH*FFT*VGLEINMLAFIPVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						TKKINPRSTEAATKYFLTOATASILLI AILFNNILSGQ*TITNTNQYSSLIIM AIAIKLGIAPFHF*VPEVTQGTPLTSL LLLT*QKL\APISFTYQISPSLKKK
548	14449	A	554	441	1	SSPPPPQARGEIFF*KNPGEETISQHNKKN EVFPPPPP*KFFFSPKAFIF/RGGGGPK RPPPKKKFFPKKTPRVFYKPPQKKKKFF FPPPVKFGPPRIFFKSPPPLFFFFFFF FFFFFFF*FRMGCDRWHGKFWIL RDGF
549	14450	A	555	3	455	NTNSSMYVCIYVFILRQSL/DSVTQAGV QWRDLSSLQPLPP\GSWDHRHLAQ*YL FNVLLLEV\FVYERGTIMVPIL*DCNVN CRVFGTRLSVYCVMGIFYRC/HBSML CDRCFIFFDIGSHSVTQAGVHWCNGL\ MKPLPPG*RNFSGLN
550	14451	A	556	1	299	RRMRQENRWNPGGTGCSEPRSHHCTLAW ATEHDSVSKKKKIRSSLGKKT*FYHNI LKAMG/CTGIHKGPEGAWQREGHFTPP QGPKKAPQRGQTYDP
551	14452	A	557	3	391	PVWWSFEASSGWLIGFKKRSCICNIKV QGETASASVEAGVSYPEDLAKITDEG IKQIIFNVDKTT/YY*KKISSRTFIVRE KSMGFKASEDRM*FLGANAASNF*LK PILICHSKIPMTFKSRAKS
552	14453	A	558	337	1	TRFPPFLGGFSTKFFRPLRVFPL/RE RKIFPLPPVFGGFPALGPFWGFLFFN FSKKRPFGFFWGFFF/CFPKFLPKPFL GFFPSFRGFFFFFETVSLCQPS*SAVV Q
553	14454	A	559	117	419	IPPLLLGVGLFFFFFIRKKRGVFSRWR GGGSNFGLETPPLGIDPFSGLTTPKSW ELRAPPPPIKF*KFLKKNF*WVSPG GLEISALLVFP/ASQ
554	14455	A	560	347	1	IYKELKQLCRKKSNYLIKWKAKNPNRHF SEEIOMANRQMKRCS\TTPVIREMLIK TTLRYPASPVKMAFI*DR**MF/WQRC GEKGT/H/CWWECKSVQPL*RAVWRFLK KLKILLP
555	14456	A	561	2	375	IPPLQNGEKIFMI*TGAEKAFYKIPF PFPIK/TLNKVGIGKNFPHIIRAL*EKP PAYIFHGEAESFPVRSGLRCLPLLLLF HPVLEVLVRAICPLK/E/IKGTQIGKEE
556	14457	A	562	391	2	ASGSKGKKYPPFLRGSPPLPGNPLFFL EGGEGKFP*P/RNWGPPKIFPQKQGN PFFFFFLKGPKGFFFPQGEKGVGFPL PGEKSQRP*GEKGVPPP*RKKPPPF FFFFFFSETVLLLPKLECS
557	14458	A	563	384	3	ISDSGVHPLGLPKRILLCLSYHVP*P KCFC/PHLCLFMTLFQPP*GLPSVCAPS KQEEHGCFFISVARQRC*PLFPKNLDT* HFVGNFLKFFFFFF*DGVSGLHGPWSAI LTHCNLCPLGSSNSLPQ
558	14459	A	564	522	120	SLFLPTLECNGTISAHYNLHLLGSSDCP ASASLVAGITGMCNLCPLSSIDPSTAS *VAIDLK**GARGNCPVS/VLEKGWPE AEMGRGESASWDPRLGRPGVAKRICRR HCCPVQQPVSMESPSPASN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
559	14460	A	565	73	264	KDRHIDQWNRIESPQIKSMTIHLWSFDF FLQGY**KDRHIDQWNRIESPQI\NL*L YIYGHLIFFYKGT/IQWRKKTLSSKWF WDNWIFKCKQ
560	14461	A	566	413	1	EKKKKVPSQVLTPKPQVLGNFRFSEEQ *LSLVPVSSSLPLQSLSGKNQGP*ARRVA LCFGKSPGSQQIWF/RLP/EDIVTTVQA SYSKKRLFLSLDLDFQYVLQRREGAVNSA NLSLAPW
561	14462	A	567	397	1	FLGQDLTVAWARVQWCSHGLKPRLPGL KGSSRSATG/SASPYLVPMFLSNLFWHV YIL*LYKTMGTI*MEM*FTPSCPMYSVV RDV*IFFSFETEACPVQAQGLQWRSLGL DQPPPPGPKRFSCLSLTSD
562	14463	A	568	437	1	KFSEDPAKLIGEDGYSKQQVLNAN/ETA LYWKNMLSSTFLARKETSMPSKLQGTG* LLLGANAAGDFQLKSMITCHFKNPRALK NYATSPLPVLHKWNNKAWMTVHMTALL TEYFKPTIKTYTYHNTTGSLLTTPHASAH ASAHAS
563	14464	A	569	234	1	FFPPFFPKASSPPQGTSSSRGVF/PEFF PPPKKGFFPKIPPGSSSPFF*EKTYFR FPPFFLAPPGVFFR
564	14465	A	570	2	396	FS*AFYHFGALALTPQLGGDWSPAGITQV KSLQVPVNT\SGLLASGEEIT*ADHNV IQNNRNRRIQALLITVLLGLYFTLLQAS ENFKIPFTISDGIYGSTFFECAGLHGLH VIIGSALLTICFIPQLTFDC
565	14466	A	571	3	403	HASGLPSSWDYRRPPRPANFFVFLVEM GFHHLNKAIIKSFACNEIQPLSAVSAG LVGCV*VCKCLFPVL*Q*LFQF*/S/HS IANWMREWPLRLSLF*LIC*GERMSGFA TQSRRDPCSLPGFLYQVLSLAKFR
566	14467	A	572	100	371	YKSNDFVYVYGILHFLTT\FFFFFFKKK KFPPVFQVGGQGGNLS*LNPLFLGLKGF SCLKLPRSWNNRGAPPPPNFGFFSKNG VSPCNPG
567	14468	A	573	371	1	REGARES/TWSSSHTPVQKGLRYGIILF ITSEVFFAGFF*AFYHSSLAPTPQLCG HWPPTGITPLNPLEVPLNTSVLLASGV SIT*AHHS LIEN
568	14469	A	574	353	103	SLQLQPPGLN*SSHLSSLSSWIYRHKFP CPANVRFFVFFCRDGVLLVAQAGLRA/S ASQSAGITGVSHLAQLVNPLLFYFSRAG D
569	14470	A	575	1	206	FCIKKIIGFIPGK*GWFNISQPV*SLTN RIKEKIHISMTAEPITSIITEKVFDKIQ HPLILQKPFQK*EYKFLNLKIGICEKN /PIPNIIYNGEILKQCLLSPFLFNIVL EDIVIQSVKIKEGINIETQELR*SLTNR IKEKIHISMTAEPITSIITEKVFDKIQH PLILQKPFQK
570	14471	A	576	157	255	YISFTPPFPDLPF*NYLPNPKLTSPAP NFQIY
571	14472	A	577	365	3	PPHPSVFFF*KSPPPPPPLFFFFPPPPFL FRGGPLYYSPP/SPPLFFSRRGKDTNPP PYSGLSVAGQTPPPPPRRTPPPLVSPPPP PFFFF*RGGPKNKKAKQTITFKSPPGT

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						NKPKHKNDRI
572	14473	A	578	2	323	VGSWEPDEKVSHELLLSFLFYPPFFSHI SS*ETLIDFALTSTDIWALWHAENQTV VKYINFE/HVWVT*FCHPTSPQAISC*E DERPGAVSHACNPNTLGRGRQIT
573	14474	A	579	369	1	AHLKGTLLGGFPDFFPINLEFRGGTSC NPLNNWE*R/RPPPPPGKIFGAFFFFF FKVETGFHRVDLLVLIS*PCDLPASASQ SAGITGVSHRARPTPG*FKKKIMTF/CL *KWWSHYVAQIG
574	14475	A	580	394	125	AAEGEQGREGWRNRPRGRERASDRERER VR/ERGEERERGEERAPQ*SERWR/E/R SRERERVRELWSDSDRALEREALLR
575	14476	A	581	416	1	KQDLYGEV*KVLLKVIKQVLNKKWDMS CS\KINILISFPPIRIALKFFF/ELDEI/ CSFV**NKC*RIAKEVLKKQ*CLGHL /TSPHIRRSYNTTFSQSIWCCYRTKQID *WTRTQNPEKDLRI*GDLIYDLRCCSSS RA
576	14477	A	582	3	403	NCFSQFNVIIMEIPAKFFIDINKLILKC FCKGRSILKKKR*EDS/QRRNFLVIKTV WYWQRECHIDQWDRINNPEINLHKYSKL ILDKGAKAIR*TKES/I/YSK*C*NWKF CM*EK/IDPKLNPLYK
577	14478	A	583	402	121	QSLIHSKALTLENSMKAEEAAEGKVEAS RGWFMRF*ERNHLHNIKQVQEATSAGVE AAASSPD*GKTTDE/GGYTTQQIFNVD ETAFYWKTPMS
578	14479	A	584	255	517	IYIFGFTFRGRVLL/CTHPS*SVVLQS* LTAALNFWAQVS/LPSSWDYRCTPPCLA FFFFFCRKGGSTLCPRLVGNNSNPLKFP LGTPCF
579	14480	A	585	1	414	SSHSCCSKA*SSMGPSAFYKLVPLFLC LFIWDGVWLCHPGWSAVVQSLLTAASTS Q\VHPSS\CLSLRNSW/EYRYVP
580	14481	A	586	392	43	CWDYRCEPPCLA\TETGSSYISQAGLEL LASSNPPMVCHPKCWDYSHETMHSQNF FLKGIS*F*LCCSHFTHNHLWLKVIH TYTHAHTGLEKYKTQCLDVKCIYSDLLD GAIK
581	14482	A	587	1	394	GTR/YGINLFIITSEVFFAGIF*AFYHS SLAPTPQLGGHWPPTGITPIEPLEGPLL NTSPLLASGVLTIT*AHPSLIENNRNQGI QALLITIVLGLYFTLLQASEDFEDPFTI CDGIYG*TFFVVTGLHGLHV
582	14483	A	588	190	3	DGINLKIPGGIFFFLKARSHSVTEAGMR W/P/NYGSLOPRPPGLK*SSHLSSLSSW DHRHAPPSC
583	14484	A	589	157	387	TKRGRVGGVWIKILGINLTKEIKDLY SENYKTSLEIKER/DTNKWNIPCF*T ERVNTVKMSILPKAIYRFNVIP
584	14485	A	590	891	0	PPPPFFFLPALIFFPPPPQ/PKTPKK KKNPPPPPP\PPFSHIP*QFLSPPPQ HHHFIHPPPPQPPFHPFYNNPFKFFF* NINVPPPP*K*IYFF*TKFFFFIPNIF F\TKKIFLSPPPKFPPLLTNLSLPIL IKNLLSKPPPPQI
585	14486	A	591	1	496	GTRAYQIVKPTP*PLTGALSALLMTSGL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PMRVHFHSTLLILRLLTNTLTIYQWR DVSRESTYQGHHTPPGQKGLPYGIMLFI TSKGFFFAFL*AFYH\SSLTPTPLGG HWPPTGMTPLNTLKDPLNTCVLLASG/ VSIT*AHHSLIENNRNRIEALMTIV
586	14487	A	592	175	2	PFFFFFFLLRHSITLAQAGVQWCDLCSLQ PPSPGFKRFSRLSLP/H*PGMVANFCIF SK
587	14488	A	593	107	733	AAAAASKVLM*REGQLPGAT\GTGGVQA *APGSVA/AEGASVEGPGFDTAPAHG LSPTRSHGQGGAGRAS/SSQGSPPGGRG DGASEVWSGAL/SPGGGKDGASASVPRG PYAEAEKGGWALRGLGGVAAPGPPSRAG QAPSGS/YTGPNARPAWPIPGQGGGLR RDQAG*VSSWTGSTPEGAHTAHRAPGHG GKGGSPQQPHPGGPGQIPT
588	14489	A	594	10	435	FKWLLKSHAICFWTRS*SYCDNVCVPSL WAHHLGIRTEIPEFFLSKFLCTSIIPH TYRRQLRLIQGST*EA*EDKLEQK*AL GAAQFTLPMDVFCVFCF/CLFEMES HSVT*ARVQWCDLGLSLPLPLGFKQFSC LGL
589	14490	A	595	437	3	DEPKKWKTI PCSWIERTNI/VLKMAILP KAIYRINA/VPKLPSTFFTEVGTFSQN *KTTILKFRWNQ\KRA*IAKATQSRKNK ASSIT/PDVASNYKTTVTKTARHWYNNR HVDQWNTIENTEIKLHTYSQ*ILSKAGT SKQWGKEHV
590	14491	A	596	2	498	FFFFLGKTKPPTHLFFFPFPPFPIFFFK IFFGGLFKKKNPPK/PFFKRPPSPKNF FFFSPPPPFNPLFSKAPPIFFFFFKKI FFFFFPPLFKKSPPKTPL*ILGFFPSFP FFPPGFPPFSLF*GGVSLCHPSWNPVVL SRPSSKLASAFRMPPEV/SPFPSP
591	14492	A	597	1	311	RRVSSESRSLSRGRSLEIQGRMERP RCQRFRENSCVAPRHCKGPGGKGLQALF *VPVAQLGEPGAQLGDPGAHGEATVPEV QGE/PAALLPGTAK\PGEGSPGFIPPR HCRGTGEEGSPGFTQGRETSKAQQTGC LLSCRGCLCLSVSGDS
592	14493	A	598	302	2	FLRFFHHKKFTKALNRHFSKDILILLSS NHMKGCSMSLVIRD/MLLKIT/MKYQFI PTRMA/IIKKTDRYWQKN/CEKI*TFIH CW*\NEKMWQPSWKAVWQFLRK
593	14494	A	599	3	386	HTWPPPPRSPTAPPARTQPPSLQSALPA PQPGKKKALRNEKG*NGSKKG/RGQPR PPPLRGPNRTRSPAGICKGGGFCPGV SKAQGAPRPGGRETVPGFGRPLPR GPGPPGLWTSRHCPLR
594	14495	A	600	374	53	EGFFFFFFPRWVGQRALFWSPHFPFPGV KIFFPPPPPGWGLRLPPPPFNFFFL KKKGFSPPCPVFSQLPPAGVPPPPPP/ TGLDLRG*PPGPPPPFFFFFFF
595	14496	A	601	393	1	VSPPKGCVSENKIPPHNYFAKTFVHV KLFQVAPLFLQILF*GFLTISRGLIL\ WIPYSPGY\TLTLLIAPRHFLRTIIPVF RSVLKTYLGLSGMPRRYSDDPDYTT* NIGAFRIARESUVGRKLDL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
596	14497	A	602	1	155	FCFVT*SGVQWRNHDLSLQPLSPGFK*FS/CSSWDCRHAPPHLASFCIFRSTRP
597	14498	A	603	170	455	KPNASLKRVLILCIQLQSSRQKNNPT/VKKWAKDLNLFSTEDL*TVNRYIKKYL TSLVIKKYHFIPTRL SKMKKTEHSKCWE SCGEIETLTCSW
598	14499	A	604	3	449	TLLSNLEEAKKKKEDALNETRES*TKLK ELPGVCNETMMALWEECKPCLKQTCMKI YARVCISGSLVGRQLEEFNLQSSPFYF WMNGDRIDSLLENDRQQT HMLDVMQDHF SRAFSIIDELF\QDRFFTREPQDTYHYL PFSLPHRRP
599	14500	A	605	169	435	KYENTKINRR/VAPN*ISLSPEKKKKKK KKKKKKKKKKKKKKSASSSKASPSRSGG
600	14501	A	606	453	29	TSPPPPPPGENFF*KKPP*K/HFFPPPOF RFFPPPPFLKIFFPPPSLFFFWGVFPHF PPPPKKVFFPKSPRGFFPPPLKKKFFF SPPLFFFFPPGFFLSPPPPPPPPPPPP FFFSPPPPPPPPPFTVKNFYLLCYFYKN
601	14502	A	607	170	408	NEYDHFSTIKERRDFIVCVFFFIISR*S FTVVTQAGLSSLOPPLPGYKRFSCLSFL CSWDY/RVVHPQGSANFFVFLVEMG
602	14503	A	608	2	448	SLHPVIYSEGIKSRQSPCWR**KTVKKK KKKNPKNQPKKKKN/RPKNPLGGGKFF *PEKKPGPGKKILKEGKKICFPPOKK NFKILKKKKKGAPLKNP*GAQNFPGMK KINFFP*REVKNPIGIFKKKPLFWGGP IGANPPPENL
603	14504	A	609	441	28	GGTFLKGIKSAPKI*KGFFGWGGARFPA RDPQFGG/PKGGGSLSPRGINPPGPPG *TLFFFKPKLTGGGGPPPLIPALRGVR P*NSLYPQRGGGAQIPGPPPPGGRAP CFQKKKKPRRKEKKK
604	14505	A	610	445	1	LWLKKNNTGGGGSPPLFFPLGEPKRD/G FPRGRGFGPPPPPIKNPFFFLKNQNNPG GGAQPGIPGPWGG*GGEFFLPP\SPGFH *PRFGPPPPRGTKREPPFQKKKIANC FLLSDKSLLEAWGQVVGPSPLEPTVA PKPNPRGKAQ
605	14506	A	611	253	437	KKKKVQDMFSENFKML/NEIKATLNKWK DISYS*VRRLCVVKMAILPT/IQSYRLN IPIKI
606	14507	A	612	186	2	KKKKVQDMFSENFKML/NEIKENLNKWK DISYS*VRRLCVVKMAIL\P\KQSYRLN IPIKIQ
607	14508	A	613	37	453	KTPPPGENFFLKKPKKNFFPPGNWGVF FPPSPLKFFFFP*TFIFFGGVWPNFPPP KKKFFFKNSPGVFF/SPPP*KKIFFFSP PRYFWPP/HGFFFGGPPP
608	14509	A	614	1234	0	KKPPNTPN**WAKDLNRHFIKDSSTKDD QYY*SLGQCKLISQYNFTCTRIAIKKT NNNKSW*GCGETGNLIH/WIECKMVQ
609	14510	A	615	327	188	FFSSSLIISIPKFNVTSLLRLNK*AM LGSSHL*LQLLRRLRREDHLSPGVSGCS KL*SH\THCTPVVWTE*DRKGLAGDGS HSVTQTGVQ
610	14511	A	616	103	446	KKKKKKKKKKKKKKKKKKKKKKKKKKKK

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						DGGGALKKNPGGAQKNRGEKKKFFFF*G G\KKKTGGFWKKNPFLGGGNFAPPPPK KKKPLEKKKNF*GGRGEKPSPLPCGKEK FSHKKK
611	14512	A	617	3	429	GLLSIIYKELLQINKISNLVGKWTKDK/ NKQFLKKEIHRLAK\YMKRYSTSLVTIE M*LKTRYFYFHPLNKIKHDNNIHC**GYK EVGILHILLEA*IGKPFWKAITVTVLNA PVFCL*FCFEMEFSCCPCLKRAFTSF IGAS
612	14513	A	618	427	6	WGPPPPPPIFFFFPPPP\PYPFFFLLQ ALFS*RVFFFLTTPPPPNFPFP*GPFP PPPPPPFCV\FFPFFFFFFPPPPFFFF PPPPFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFLVENCVFINSITSDIEQKISI SC
613	14514	A	619	68	434	YSKD*PINTKKKKKKKKKKRGGAFFK KPGGGKNGKGKKKNFF*KGGGKNPRG NFGKTLFGGGKGGEKPPQKKKSLEGKK KI*RGKGGKKT*np /CGGKKFSFGGF* KKFPPGGGGKY
614	14515	A	620	454	90	NFTPEKFPGPPQGNL*KAPPFFFF*KGI PPFFPG*KQRGGFKSPQKPPPOGTIFR PHPPKKGPPQGPPPPGGKIFFFLEF\KK KGGFPG*PRFFFPGPSKPPRPCKAG IQGETPRPGP
615	14516	A	621	432	2	PEARLSSLLHPAGEKFFLKKTPEEKFL TAKKYRVFLPPFLKIFFFP/LRALIFL GRFAQIFPPQKKGFPPKIPRGVFFCP* KKKNFFFLSG*IFAPPGIFFKGAPPFFF FFFFFLDRVVLCTPGWSAVARSSTS
616	14517	A	622	422	2	GGGPLPPPPRRGLPPPK**KA/VGGGKK PPPPAPL*NPPPPKKKIGGGGGKNPPP PLLACFFFFGFFLP PPPPSFWGGEKFFFF FLSGGPPPPQKKKKKKKKKKKKKKKK KNKKKNQTKKKKKKKRRAARDPRVRPRV
617	14518	A	623	176	401	KFSNFILWKAYITLCVCVCVCVCVCV VCVIMYLFISSQ/RRLCLFGEGKICISIS LTVLRRSRVCV*SQDLVC
618	14519	A	624	1	355	HSSGLDNLTALAHSLLLCCGV/CLCFVL VCVCVCVCVCVCLVCVCL/CLYPGPQV PK*SKNSSTSCLLFHTSARTICP/CC/ CVVECFCEFA/CYTCL*ILTCL/AIC TASGVCL*ANKYSM
619	14520	A	625	2	400	HTRLFCDGVLLEC PWLQTPELKSLL FSFGFLSLFFFLLCPDGSHGP\VG PNLG*WKFwPLG*KQFSFLTWRGNT\ RGPPPPPLVFWF*KKTGFCFVAQAGL EQRFPGDPVWASOGAGITGVP
620	14521	A	626	307	3	VFRILPTQQGLFACFCPPPPCRFFFS FPPGSNSPFPF/L*KLNFWAFFPPPF FFFFSILFKDRVLLCHPGWNNAVVS** P*TPGLN*SSHLLTLP SG RV
621	14522	A	627	1	391	NPPPLGGAKEGGPPRARSNPPPYWET PFFF*NPKIFPGGGGHVIPSPFGG*GR KFELPREGGVPL/RPNFPF
622	14523	A	628	191	375	LILIFKTI FN FLINFN*SGGATQAGG OGRNLG*LQPPPPWLKRFSCLNLLSSW\



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						DYRGWP
623	14524	A	629	3	382	HHCQIRLFILLITASEVLFVLFVFFET GPCSVTEAGVQ*CN/HLQPLSPG/PPTS AA*VAWTADVHHHAWLFFVCLLI*DGWS VTQAGVQ*RDPSVQPPPTFGLK*ASC\P AFQKCLDYR
624	14525	A	630	396	2	CRIENVLKKKKLEMSNLSEEGMLKANIG QKLSLLAPQQVNVNAKESLLKEIRSALPL NTQMIRMQNSLSADMEDIL/VVWIR/DP TNFNIPLSQSIIQSNAL/TLFNMKP* RGEEAA*EKFDAISG*FTTFKERS
625	14526	A	631	47	392	LHSFFFLFLGKKIFTGGGGGGQKPF* NPPPPG*RNFFFLPP*KTWFMGPAPPPR KIFGFLKKGFPLGGL/SIGTPPRGT PPPLPPRGCGYGGGPPPPFFIFFFRTFK NFSN
626	14527	A	632	39	382	LEFSPFFFKNFFFFFFGRFFFWGGVAPIF PPPKIIFFSQFP/LQVFFFSPP*KKKFF FPPP*IFAPPKTFFSIPPPPPFFFFFFF FFFFFF
627	14528	A	633	2	213	LDKPGKHSKISSLQKI/HNGVCLQS*LL GWLREQEDCLSEGS*GCSEL*FYHCTPAW ATK*DPVSKKKKGFLK
628	14529	A	634	2	206	QENGMNPGGRACS*PRLRYCTSSWATER DSVSKKNE/TNKTTLREI*HFVGGPNG KKGLLKTVMGGLT
629	14530	A	635	205	2	KRSLGLLAQI*/VQWGDFTLQPLPPGV KQISRLNLLKKWDY*RGPSGLGKFW/IF L*KQGFPPQFFRVFN
630	14531	A	636	3	399	QVQQTASCPDLSDLSEDEDLQLAMASM TFPKKKKKKKKKKKKKRGAP*KKTRGG PKK/IRGKKK
631	14532	A	637	122	373	VSNILWTQSLFFFFFFLKGSSLFVPPQG GQGLDLG*TKFPPRGLKEFSCLTLRISG NYGLAPP/HPG*FCFFIKKGVFPCCPGW F
632	14533	A	638	390	3	LLVLFLPDGWSPPFAFPHEQKLPEVSPK ANAAMLVPQPAKP*AHPTFFFY*FPSFR FFFARMG*SS\YFVPNLTKLSEILKGPI NDMREVFFPIFRLLILFFFGDRVLLCGP GWSSVQ*L*LIAASA
633	14534	A	639	392	42	PSGPGKPGGKTFLRKPPFQEACKRQGFY PLFPPKPLKNPKAPQNRKNLGPICPPPK P/QGPLRISPQNSQSGSL*GPNKGNCFP A*TWGPPGAP*RGPPKPPPPFFFEKVME AMGLA
634	14535	A	640	390	1	LSFSEEGMSTAEAGQKLGPLCQ/TSQVI NAKETFLKEIKSVIPVNIQMIRK*NSFI ADKEKILVV*I*DOTSPN/IPL/SQCLI QSNVLTLSKKAEERGEAAEBKFINF *RLRKEAASADREAESYPEDL
635	14536	A	641	368	3	KKGGYGVPPPPFSPPPGFLGEGSFLPPKI KVQKTL/SWPPPPPPPGGKKKTPFFKKKK RKNFLTGFFFFP*KKGPPPPFF*CPVV* KFWGGGFKPIFFFFFF/RDRSLCCPGW SAVV*SQFTPRV
636	14537	A	642	134	413	QKDQRNRIESLE/IR/PHTHTLIFDKG VTGFQYKDSLFNKWCWDN*RE/ITQNL

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						SLDPAHTTTNNVLKWTCLKARP/VKTL VENMGENLRD
637	14538	A	643	2	436	GRVESINLPLGCRFLFKKRDNIKCGQ\G* RAGGSLIHCW*EC/EVVQPLWKRIQQFL IKLNIHLPRDSTILLDLIDLDGHPKTSAL FIITHNCCFIHNHP*LEQPKCPSTDVW MHKDPWPIHSMHYSIAKSAAVWDNFKGI LL
638	14539	A	644	446	75	LDLLTS*SACGLPKCWDYRSEPPRPAF NF*/STTK*SLWSSHKQDYICRFLLSYT ATQKFSTLTTY*SHLKT*NAQMPRLYL QSLILGSIF*KSNLPR*FQCAAKAENH* *SDLYCQIMLFSFM
639	14540	A	645	318	1	KGVPRKCKNSYVGPSPGPPK*ILFF*I F*DRISLCSGWNARVFS*LPV\T*TTG VKKWWPLSLNI*GYKGVPPRPGIFFFF FFFRDR/SLTMLPRLVTWVQVIFQ
640	14541	A	646	3	348	QFSSFFVLIYFTLPFMVSFCF/WCFNSL VLFCEIIFFLIFY\YSLVLSFFYCLLV LFLSKLSFF/C*YLNITVFICSMTSFF* RIL/CCLNFIKTSFNELL**FGMVLESC FFFFFFFWP
641	14542	A	647	2	553	AILIPDKIDLKK\VTGDKE*NVTMIKGS IHQEDVTTINIYASNSR/APKYMKQKLK GKEKQISP*K/VVGIFNTPFSI/DRAPR QKINQEIEDLNIIIRQIDLKDIYRTFHP TSEYIFFSSAYET/FSKIGHKLKHKTSL NKYK*TEIMQSMPSD/HHGMKLENNE/N VGKLTNNMWSDTLVSDWLGAHAHA
642	14543	A	648	388	1	GPPR*SPPFGKPRGAVPQ/GGGGLKPPG PQGENPFFFKPKI*TLGPGWGP/RNPPP LGG*KGKIP*/PPGGGSNKNPFSPPSGP PGKQKQNFSSQKKKKKEKKKEKPES*C PGTSPQPVTDGSAINASSIS
643	14544	A	649	387	25	PGMRGGFPFPLKNFFFPGP*/MSGGG GGPNGPPPKGFFPKNPPGVFFSPKKK KIFFSPPENLGPRLKGPPLFFFFL QKNPGVFFRAGQGNPPQKIAKIFPLPPG GGGGAVRHI
644	14545	A	650	918	2	LGLKGLTIYKILHSTIADHTFFSSSHGT FAMTDHILGHKIHLSSTFSKE*EIIPSTS FQ/HHSRNLN*K*INNKNVWKP\K\FWR LNKTLNNT*TKE/GLKRHNILS*TKN ITYQILWDAGKAVLRGKFIVLT*IRKE ERSK\TTSFNIRKRNKKLIINIRTEINE IENRKSEKILN\TKSWFFKKKSIKSIK TLARLNKRKRKETQIPKHQK*RRGITTG NMANKKIKRNIHEQPYTHKLGNDNIGQ FLEKRYLPKLQGEI*SGWAYIN/SKEM ESIINTLPKRKAQDLKMFSSQSE*YQTFK EKK
645	14546	A	651	282	265	GVFFLKKRPTVF*KKKI*LGPHPQLKGP PGVFQ/HFPI*NFGISGRGDLEFFFFFF FFFFFFFLRLRQGVSAQTGAQWHNQGS LQPPGLK*FS
646	14547	A	652	6	223	LYAHKFNNLDEMDQFLQRHNTPKLIQEE /HRLTVIK*IKSIVINLPKQKA*GPDGF SGEMYQLLKEEIIYNVF

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647	14548	A	653	128	337	FXXFFXXXXXFXXXFXFXFXFXFXFX FXXXXFFFFFXFFFFFFFXFXFLI FFXFPLFFFFFFLFF
648	14549	A	654	238	2	MAAASTTLLALVIISTTF*LPQVNGYIE KSTPEECGFDP\SPARVPFSIKFLLVGS PIQTHALDIALFLSHTRALPHTHT
649	14550	A	655	325	3	CSEHKKNVF*LRAKKTNNPNLKWAKDLN RHFSRENIQVAEKHI*ICSA SLGLREM IQTTKC/WHPVWKTV/WTILQN/LHTRL PYD/PAILLGLIYORELKTCSHKMYTS V
650	14551	A	656	3	1655	FFLGMESSPSVAQAGVQRCDLCSLQALPP EFK*FSWLTLSSWDYRRLPPCLANFVFL VETGF\TMSRMVLIS*PCDPPTSASQS GGITGVSHRVQPALLFFLSCLCVKMIVH APLVKTCRPSTVGSC/SVPAFWE
651	14552	A	657	519	84	SRVRQQA/QMGASHLGYSGVRDPLEE AVFPFSDLKLHAGITTTLFKA VRQGHL GFAKF*RPAEQ/GT*YTSKLA/STKQN ILHEE*ITFVLLPKHEGIWMPSVPPKP FLFFS*GMTNSGSAGILD FVNHP SKDG *HYVLITSH
652	14553	A	658	38	383	EKCIFFFFLERGFTFGGPPGGRAQFWF NKTPPP/HKKREFPALPPP GGNNGLGP PARENLVF*KKRGFPLGGKRGLNPRPQG NPPP*PPKGG/GNNGGGPPPRQKK
653	14554	A	659	98	394	KPPGKKRETFSQ/NKKKKKKKKKKPF PPRGKKKNPFKKKRG*KNPP PRGGGKG NFPPVMG*RGKNLPPRKPLFP PPQGGG KN*KK/RA*KNSPQNFF
654	14555	A	660	214	567	GFSVINIGLKMMMMTIIILRDSLTVTQI GVQWHNLSSLQPPPPPGFK*FSCLHLLSS RDY*HAPPCPVNFCILS/ERQFHVHGQA GLKLSASSDDPTLAPQRAGITVPSHQ
655	14556	A	661	463	392	S*HFHPSSSSSSSSSVINY*/FGLLL C/QVAHFYNSIDQQMIQS QRFMMLQSL AFEQI IKVNGLLILL
656	14557	A	662	205	242	GTGWQGGGLDG*QMTLGWP GSGVGGSA P*GI/GPGLPLPAPPASP
657	14558	A	663	63	351	QSETPSQFKKTKQIELLYEP AVSLLGTY QKERKS VLKKHYTPMFTAALFTI\VWDQ PR/CPKYM KR*NVMY/HVYTHHTMEYY SATEKNEILF/FATTW
658	14559	A	664	1	358	FFLRQL/DSAAQAGVQWCNHSSQRAPP LGLGRSSH\PASLAGWSAVA*SRLAATS TFRVQVILLSQPPE*LGLQSCSITQGV QQWRDLGSLQPPLPGFKRLSCLSLPEN* DYKRLAPP
659	14560	A	665	10	257	GMNERGNITKEIKKIWEYYE*LGTSQL DTL/ELNKFPERYKL/PRTNSQS IENMN RTITSDYISNFKRLPKKSPGLDGFTGEF I
660	14561	A	666	360	2	ENKKIFNSAPPPGSPFLFPPLWEIRPEG FLKPRVLNPPWP PN*APPFKPPMPGPPF PLFRGV RVGDPLSPGPLRLP*PGLPP\G PPG*PWGQNP TFSSKKKKKSWLDSSGFL EPNISVNF
661	14562	A	667	328	1	NLFAENYECPENKKKNFKKKKIHOIWON

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SEFMKVTEYKLNQON/SQLYLYMPEKNT *KV/ILEKHPL*PQITKYFGEILKKDVL NLYTDDKYKISLREVKGQNKWNNVSS
662	14563	A	668	405	566	IHCQWECKTEQILWKTVWVFFTKLNLIL PGDSAIMLLGIYPKELKMYIHTETCT
663	14564	A	669	218	2	LLMLESIMFVPPFPSPFSEKWAHL*TY/CH GAHANFLPSFPSPFPFSLSFYFYNRV FLCCPGWSAVVRSQLT
664	14565	A	670	2	210	NFGQEEENSEMNSLCSYLHNLEKGEQTRP KASRRKEIKI*AEI*K\VORSNRENK* KKWFFEKINKIDKPLARLTKKWRT*ITI VRKETGTITKDPADTKRIMKEY/YKLLY MHSF*NLSRNLKRYREVIEKINERSGSL KRSIKLTNL
665	14566	A	671	200	3	SLCHLPHVASKATLET/GLVEHMM*DFP CFFETESHCIAQSGVQWQCNLGLSLQPLPP RFKLFSCLSL
666	14567	A	672	94	374	PKFRPQETTEQTSQFLQINCKGRKRQG KRTYRLGEIQKQSQPMATFELYLD/H*F *LAKETL*LGAVAHTCNPSTLGGQAGWI TRSGVQDQPGQ
667	14568	A	673	312	3	WKMQLPGRPQLPQLSQEKILSLNSPNV FKKKKLLK**NILPKKKRPDCFTHKFYQ TFKEEIIIP/L/HKLT*EFKKEILLKS F\YEGSVV*AAKLNADINKKTTTH
668	14569	A	674	34	438	QLT*PD*HFIKYSTQQKTFFSSTHRVF AKLGHNLVY\KANLNKFKWLQVISNMFL DRDRIALKINNKK/PSSPLKYLQTHLLL NDPRIKEGSKREIKDFALNDNATY*NL WCL*NGTLRKVYTTKCLFRKEGPQM
669	14570	A	675	3	349	QKDRKSVRPSS*NPPLAVEKIPI/LKQN PERFNGPAFFKIAHGLTSSLVFCLANSN YERTHSRIIILSQGLQGFIAIKTRKLL ASLANLALPPTINLLGELSI
670	14571	A	676	346	1	KMVKLL*NIVWKLK/GLTEVPHGSAIF PFFIPIFPKEMETNVHKTCTWAFPAF FPMAKKKKQSGNNPTTDE*IQKK\W*TH IIDYYSATKRNEILLTHATSCNITLSKRS QTKK
671	14572	A	677	357	6	AAGDSELKPMFIYCFQKPMPL*IMLKST LLVLYKWNHKAWMTACLTAWFTE/HCK PKLETYFSEKRFLSNIT*LMKASGHPRA LTEMYKEINVVFKNPSNTTCTLHPMDQEV ISTFNSY
672	14573	A	678	401	155	YYSVAQAVVQWRDLSSLQAPPPGFE*FS C\PASWDYRHKLLTSGDLPASASQSAGI TGVSHCAQPLSLFVFLTNQRFVAALS
673	14574	A	679	292	395	Q*KISFEMLLIITNVPGHPRTPMEMYKE LNFF\MPANTSIP*PMDQGIVLTFKSY A/RNVFCKAIAV/DSDSFDGFGQSKLET FWKGFTI*DVINKNIDL/WRGVKIPILT GVWEKLIPTLINNFVFKASLEEI
674	14575	A	680	275	3	WPRQASLALNT*SIHTYIHTDMRTHAHT YIFGMKSVTQAGVQWHNHSLEP*SPGL RRSSHPSLPTSSEHRRTPPR/LADFLHC L*R*GFTML
675	14576	A	681	330	507	GSV*FVNLRNCQPFVQSGCA/SLHSHQ E\WYMCSPHPRHYLVASVIFILAILFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LRRSL
676	14577	A	682	390	43	HHLPIRYICLSISSILCLSFIMYLS/IYLSIYLSIYLSIYLCQRCQIPLVFLCLLLS*LS*IILLNFSCFFVGRTIVLS
677	14578	A	683	396	63	ADPTEIQRIISDYDQRHTNKLENL*KMDKFLKTYNLPRLN*EEVETLIRFIANHEIALIIKSLPIKRSPVLGGFSGVF*HIDKEELTPVLGLFQK\IKKEILANSFYESR
678	14579	A	684	1	396	EETLPLFADDMILYIIKKKQKTKKTKTESTKRY*N**M\NVFGKVAGYKVNITQKSI N*QYTI*KVKLAS\FSSSPQKNKIGINLTKEIQNVYSENYKTLKEIKDLNK*ESIPCSQIRRFNIVKMTVLLKLIYR
679	14580	A	685	283	3	NCVESSNTHLWEPSPQKPLSSSVSLTDVCP PMLSAALFAIA\RSYTLPTRSSIDE*IK KMWYIHTMEYSAFKKKRIMSFLMPRME LKIFRVNKLIR
680	14581	A	686	53	324	HCFCDRIRAAFCFYILDCCPFFISITHKL I*IFFFFFLERESIFVPGVGGGGPNFGS LNLPLPRLRRFSCLTLPRGGDYGLGPPC PT/NFCVF
681	14582	A	687	39	208	NIFFCREGFAMLARLVNS*NWPGKVTH IHNP/STLGGGLGRITQTQEFETSLVDA GA
682	14583	A	688	47	341	SSGRVFLFCFFETGSHS/VLFRLAYSG GISAYCSCHLLSSGDSPIATR/GTTGM CCSAQLGFCVCVCVF/IPVF*VKIGFC HVAQAGLELLDSSNPPTS
683	14584	A	689	229	1	GRVDGRQIACQEFKARLASQSAGITGVS HRAQPFCCFC/LLFVVFEMGSHSVTQAG VQWCAPGSLQPLPLRFK*FSC
684	14585	A	690	339	1	KKGPPGGPTKPEGGRFPRGPPGGGKEVF PPPPPGGKGEKKRGGAPPPFFLKKKRK SGKGG\N*FFPPGGGKGGQKKKKRVFF PKKKKKKKKKALSLSLSLSLSLSLSLG
685	14586	A	691	372	0	YDLYIYIKKL*N/LREKIDKFLDTYNLSR LNQEETENLNTPTITSNKIETVIKSPPT\ KQKSPGPE
686	14587	A	692	117	297	APLLESSSASYLHFSN*DLQMAH/KHTK RCSTSLAFREM*IKTTRHHFTPTKMAT SKRHT
687	14588	A	693	122	322	EQTNSWSIDFFFQRCNSNAMGEKNCLFN KW*WDNYVAI\AKMKLSLFPKYIKTNS K/WIKDLNIRAKT
688	14589	A	694	21	342	RSHFRHLNEYATQQGNSDVHPLLHNSN ISTAIIWQLQRQERRKEKRLKEVKNEKA LKEIFFLRGWLLCHLGWSPVVG*S FIV TLN\FGLRQSSHLSLPSSWDYRPV
689	14590	A	695	2	343	KFVPLHSLGNGRSQKQTLQRKKKKGGV FVAWAKVQWHNHG*QGP*TLGRQSSCLS L*GGWVKL/PGGRHAWGFHHVKKVGLE LLTSDDAPSSASQKAGITGMSHTAPGPK NLV
690	14591	A	696	336	3	IPPVKS PKFPILLKKKKFSLFCFSGAPF PCYSPPPRAQKKGW*KIFSPPPK\QKKPG ALFFSPKPAFFPPPPFKKKKKKKAKEBGH YLMIKGLIQQEKIILNIYASNIGARRRG
691	14592	A	697	374	2	AFY*KKMVSRTFIAREKSMRPFKASKDR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LTFLLGAGNFKLKPVLVHSENTALKN YAKSTLSVLYQRTTKAWMTSHLFTWFT EFFEP\TVETYCSEKKIPSKILLTDYA PRHPTLMEMYSC
692	14593	A	698	361	3	PQMCPPPPR*QGIIFL*L*THCFCTVK ARLFLFPF/S*RKGGFFFE*RKFFKY FGWELFQIRFKVFFFCDRVSLCCSGWSA GART*LTAASTSPAQASLLPLTLPSSWD YSHVLPRLV
693	14594	A	699	75	362	KDCAYGICSKKQKGFCLTGTGAWQQYEE I*GLET/GFSRSVHSMGQRRYWDYRHAL THPANFVFLVETRFLHVRQAGIELPF/S SSQSGGITGVSQ
694	14595	A	700	2	277	FFLYTSNEQSEKKI/RETNWFIITSK** NRNVNKEI*DLYNENSKTFLKEIKEDLN KWKGILSS*TEKLNIK/PTAI**FNAI LIK/IPMVFDK
695	14596	A	701	1	407	GTRKHFSKEDRQYHKSIRKQIKT/TVSY CFTPTKLTTVGKTANSK/CWAGCKVIGT LIHCQ*ECEMVLLWT/SVQQFL/RNVK LYETAIISLLGICTREIKTPLHII\IIA KKWQQLRCLSTDEWINNM*YIHTMEYYS A
696	14597	A	702	209	3	SLNRRLSFFFY*RQGLALLI/EPGWGAV ARSWLTASN\FELQRSSCLSLRSSWDY RRVPLHRVSLRFSC
697	14598	A	703	308	3	TTGLKRFARVGGPKCWDRYCEPPGLATS SVLKAFQPIGSVPPRLSRILSFM*NQ\* YRMLITSTKYFPRMVISRPCDLPALAS QSAGITGMSHHAELVPLV
698	14599	A	704	603	2	PLPP/GLQVESP/CVSLPSSWDYRHAPP RPAFVSF**RRGFTMLAKM/VLIS*PC DPLASASQSAGISGVSHHAWPKQT*LLD TDKTEGIFLTNHLRLIPPPMFYQYILIK VLESVKETKDKRKSVSSTLYRCL*ILF IS*AYIKFTTFFFF\ETDSRSATQAGVQ WHGLSSLQPPPPGFK*FSCLSLSSWDY RSMPPREA
699	14600	A	705	3	366	ARVTYYSGKKEPFGYLGMA*AMISIGFL GVIV*AHHIFTVGIDADTRAYFTSATII MAIPTGVKIFS*LATLHGSNMK*SAAVL *ALRFIFLFTVGGLTGICLSNSSLDIVL H/DYYVGAHF
700	14601	A	706	358	3	GFHHVGGAGLKLITS*SARLRLPKCWDY KREPPHAPDRKYFSPVLFARDNFVPQG P*\HVWINICLSQVKAATGIYPGEAGAL RNRLHPH*RIFWPQRPRVPIKSPWTLRV ISTLCSC
701	14602	A	707	358	67	QLSSTIY**KN/RIDQWNKIAQNTSVH RKLISDKVTKPIQWSKDSLFNKECWNN* TSICKK/LSLDSALTFLTNTNSK*ITEP GSAHTCNPTTLGG
702	14603	A	708	34	363	RTVFFFFFFFFFFFFPKKTPFFFPGRGG *IPPEKKIFPPVFRGKFKKPPHLDPGG GNFPRKPPFFFLGP\SFFFLGKTLGGGG WIPFPWPNNLFFKKIFWGAGGSPSF
703	14604	A	709	1	380	STCKRMTLDSYFTPYTKINSKWNKDLTV RGRTIKLIEENIGVNLHDLGFGSGFSDM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TPKAQAKRKIN/WDFIKYLFCA*EDSERV/N/RRSTEWKIFANHIQ*GN*NIRILKLSKL*ARLKWEDL
704	14605	A	710	382	30	PGTTGVHHHTRLTFVF/CGRAKISICWL VWNS*AQSACLSLPKCWD*EPQHPARFV SFNTRSGIPIISTNPSLSLAFPSQGFV FLFPHFPASHPETALAEFFLGTFSLSPP GPFTPAS
705	14606	A	711	1	377	LLVICGMQMKITVRN*TLNKTATIEKK TAKCC*HYGGLKTLIHQWCKSNMVQPLC KTV*QF*KKLNIQLLYLLK*KKAYIHPS NCTQMFTA/ALFSVLAPNWKQSAY
706	14607	A	712	1	390	LKYKIMLGMAAWACNPNYSGGPGNITA* TW*AYMALTRLEPGRGDHTAALQPRQS TTPF*KKKAVPFRA/RPVKMREREI*KP FSPE\RTYSCAQEGPGRTFGSAQDLEAA GGRGHHRMGAVWQEPHRLLG
707	14608	A	713	2	393	KVRRQIINVDATDTSIGIKWIIWKHYV* LYANKFNYLAEMDTYVERYKLP\KEIDV MNSLVPAGEIIVVVKILLTKTPDPHIPT NEVYQTFKEYY/PVLYKLFQKIEDERTF LSSFCEAGINLISICKRFFF
708	14609	A	714	219	1	PRPGAVAHACNPSTLGGQGGRI*TQSSI IKACCLIHDLAIQTQKQMT\WPGAVAHA CNPSTLGGQGGRIITRSGARDQPSQHSKT PSLLKIQKKLASVVAGACNPGYFENYIQ KLLRGPQT
709	14610	A	715	381	126	IIAGGGGVCT*SQLFKRLRQEDHLSPGV RGYKEL*SYPCTLAWTE*DPVF*KKNY /TLNTSPKETNKK*GVRICKTGKVLIFV AAG
710	14611	A	716	417	1	CYCCWGATNKILLTNDASGRQIVLMDM YKKNNVVFVPVNTSRFVQLMDQGIILNF KSYLRN/TF/HKCIAVINSNSS*ESGQS KLKALWKGFTVLYAIQNICDSGQVKMPT LTEV/WKEVILPLMGDFVRNRTSEKQNY KLS
711	14612	A	717	406	122	MFSRDAVSLCCLGWS*TPELKLSSLSL PKCWDYRGEPPCSAAKDF*IIRKR/HSC RNIIRNSDAWQR*TTLVSYDRNPP*FPS PPNSPLCPAA
712	14613	A	718	535	1	HNLNKIV*NLHVENYKMLVKDKKT*ISC LWVRR\LVKIPVLPKLFYSVIVFPIRSL VRYFIEVCTFTLKCIPEKDLKQPNRF* KKKKKVHLFPFIKVYY\KLQ*YIATVIKT VWY/W/YSKIDKAKWYKTEKAEV*PHEY DQLILAEVQINH\NLFNKCY*SN*TTIG KNMNLNLSFTSYT
713	14614	A	719	255	1	GKLQPNKGLISLIY\NL*KLVRKSNPKE KWAKGMNR*LTEKGIQIAFRHMKRCSPP FIMKAMHIITWSYHFSSKRKTRIQRLT
714	14615	A	720	381	0	KFIAVNEYIIKEIDLPINNLTLYLKL/ EREELTLCKASRAEVI\KIRAKIRELT PIRKTDNQSWFFLKIHKIGQ/PFKLD*L QKKKRVREKVPITKLRYENRVIITNFTTE /IKRIIREYYDH
715	14616	A	721	3	381	IYREWRDLTRDGTQGHHPGEGK/VC RYGIILFITSEGFFAGFF*PFNHCSLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PTPQLGGPWPTGTITPLNPLKVPLLDTS VLLASGESIT*AHHS\LIENNRNQLIQAL LLITILLGLYFTLLQA
716	14617	A	722	56	455	KTITINIKPPATIQYQTPLFV*SVLITAE \LVLLSLPGLAVGITILLTDRNLNTTFL DPAGGGDPILYQHLF*FFGHPEVYIIL PGFGIISHIVAYYSGKKEPFYIGMV*A MISIGFLGFIG*AHHIFTGGIA
717	14618	A	723	398	3	HQLPVFWQYNKKAWTTRPLFVDWLH*CL VFEVSKYPASKGLPFKVVMLDNDAPD/H PTQNSMSS/DSKGIEVIYLPNTMSLI* FLDQGVIRTYR/RHYPQYSMQRSIRPMQ EISNKENIIVWKNSTTDDAIVA
718	14619	A	724	318	14	TPFFFLNIPNLFFLKFSPPPPPVFLTKS LFFPLKLPKPVFGK*SLSKF/CPFPKFN PKPQKKNFFPPPPPPPPPPFFFLRHNL/ VCHPAWSALAPSQLTATSAS
719	14620	A	725	2	371	APRCKRFSCLSLPSGWDYRCMPRPVNF F/SIFSRAGGLES*PPMIPPA*A/FPK/ CWDYRHE
720	14621	A	726	430	97	PKKNPFWKRA*NGGAQKDVPLSLF/SW AGGSPWGPFGF*PPLGPKGGPPFSKPPG GVGPFILMPTPEGGGKLA*DWPPGFNP PVSIFLPRPPRAGGKKGTPFPKKKKKEK
721	14622	A	727	406	1	GGAPPPPPPPFFFIKKGVFF*QEGFFF PGLKN/LPP*PPKKVGVKGGSPPPGGFF FFFKKKVFFFPGLRTRAQIKVPSTLVG QG*KILPPQVSQEGGVKREGPQAQLFFF FFFFEMESHFVTQAGLQWRDIGSP
722	14623	A	728	98	368	KPHKNAKCPIRVAIVADMENNKYW*GYG EMGTL/LHY*WEGNIEQPWE/T/VWQLL EKLNTLPCDPATPLLGIYPKTLESRDS NRFFIFFFSF
723	14624	A	729	19	404	VCVISICLATEILFFLHTRPCVCIYVCV VCVCLAVWGTLVCYVVCIESVCVCFHLT GVLC/V*VCVISICLATEILFFLHTRPC VCIYVCVVCVCLAVWGTLVCYVVCIESCV CVCFHLTGVCVCVCVCISSVCVCPPT CGTVVCVVRPPGVLCVCVCVQAANVAV SMCLTP/CPC/VVCVCVCV
724	14625	A	730	432	12	FFHKPNFPAARKGRLEFFIYPSKCLISP KAL*F\FGGVGPPFPKKGFFPKVPR* CFFRPLIRKKQILFLPPLNAPPVGI*M /PPPIVFFFFFKRDRVSLYCPGWSAV A*S*L/TAVRTRGLK*SSCLSLPKCWEY KCEP
725	14626	A	731	332	7	NKTRKEKFLTRSISR/CFPPFFPKIFF FPLRA*FFWGGLPQIFPPPKKVFF/PKI PKVFFKWPPLRKKIFFFFSPLILGPPRV LLKGPPLEFFW*VFFF*DRALLCHPY
726	14627	A	732	70	294	FLRFCVETAINKIAIILANF*NFL*RWG \FTMFPRLVSKL*DSSDPPTSVSQSVGI TVVSHHARLNFFYYQNSRR
727	14628	A	733	1	355	FLLRHILLCHPGFCSVATAYCSRDPGSS D/PLPPQAFLPDQ*PRLQA/WHRLAPP SANFF**RQGFTVLARMVSIQPCDEPH SGPQGA
728	14629	A	734	50	395	IPGLTRQWLLDPCASPSTFPYT/P*VQP



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						STPQNSSPSPKTHNQKGLPMLPSPTPKP STAWKKAILEHTSSSSSSSSSSSTCRNR NGYTTYTVPEHRPARGHTASQTRKQVLAA THKP
729	14630	A	735	451	0	GPSSSPTNIPTPVSWNSFK*SSQVAGAT GTCYHAWLI FVFSVEMDFY/HPVA*ASQ SAQLCQYFMI FLRQGVSLCPPGWSAVAW SKLTT/CLCLPGSWDHRCALAH PANFLY FWWR/HSC
730	14631	A	736	2	477	PSHVS NKRLISKIYKELIHLNSKKVSNP I*K*GQSLNRDFS KASFLPP*KC\QMVN RYIKRCSTSLIKEMQIKTTMRCHLTPV RLAIMKKSKDNKPSLVWDC*IRVLHLF/ CK/WICQYVQL/FWLLLSNFLVKQPF\Q LPAPPNSPTLG
731	14632	A	737	3	2344	AAGGPTAQSPAQLAGRALRLARWRAVAV GACRPGAGSPCSVQGGASELSPRPQTW IGSLKP*TFGAAAG*AHRCGGG SALN* ATPRPAPGLPASPTSSQALPAPLGAWGH SDHQPRAFP*SPQASTAIRKEKKQRAQP GRASVCPASNPFISSRALPVLQHGPPAI SGAGSAVASQAPGSS/GSHAESGSPALA HTP*GS*EPHSLIVESTRKS\ELPSSSQ GRLLLPLLT PGVAS/PVGTKLPGATAAT AGALHQPGRLRLSSLQGVGGAKNKQTGCC CLQLPTTGLPQAPGALRPLGRLGPAAAP GEHRQRTSPQGTVPYGGIRQGW EQPRL RAYGTALPPHTPPGSSGP/RQAPGCRG SGAGEAAGIRDTGGGGPGRRAPCSQASP GRGGWQAQVGCETCRGCAQSS/GGGAVQ PGLPRKPYPHS/AR*ENLVVFPFCSEPT RAQEPQTQGE/GVEGPQGS PCAPGAVR GRGIQLSSEPGKLARQ/PASGDGP*EG TGQEPSQAFSSARHPWPSEARMPDTAIC RNQAA*QLTSSQPSMGFPQLRKSLPATP QPNSYWDGNSATLGRTTNTRRHCGMSN FGARGDLLGTVP*QPLMQRRKEKPRVG GEPVQSHTVCG*\PAGVSRGWPLRPMPL ERWRPLSASSGSQGRPLHPPSLA\CGP SSSPHRTCSP/GLDPGLE DAGSIKPPSL VGAGQGAGST/GLD/GPGLSLLSPGKSL LPPSSPATGLSGLGWAQSAF*SLLTVA* WLNVPVNGPSDTADCTPAQAPTAPAMLE NQANKSDFFFH
732	14633	A	738	37	450	NQKKWPPPRSSKPARPLFFFL*QKYIKD P*KTYQGCFFFSPPPKKNPPPKGGGF FFFF*KKKGGGPPP/QAKKRGGGPPQK GGAKNPPRGFTRVFKGPFKKRGP
733	14634	A	739	2	426	QEFVLGSAPGCGCWVGGEGRVSSPWGDR KVGGPSNSRHWKAGAPSCPPGPSLAAG LPGRRAGSWAPVLW\PGPP*GLAQLPSP LW/PPSPPOEREPLPD
734	14635	A	740	21	392	AQEFKSSLGNMERPLPYQKKKKKRP GG GA/RPLETQPF GPGGGEKKGGKKTSR P/IRGKPPFL*KKKN\CLAWGGGPAL*P QFFCGVGEKKT FNPGGGGLGKPKPPFFT PTRGKNQTPQKKKKK
735	14636	A	741	1	408	PSSQGG*EAGG*LEPRSSRPAAWI* RDP

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						/GSPEKGKKKKKKKKKKKKGGGGFKK TPGGAKIKGGGEKKNFFFKGGEKKNLGG ILEKKLFFGGGKNGEKPPKKKKGLREKK KF*RGKGKKAENPGGKKIFQKKKK
736	14637	A	742	394	1	RDPLEEAVCFPSDLQLRAGRRTTALFKAV RQGHLSLQRLRLRFVCLCPAPRGAYRS RQASLNRRGGFHPVRAVLLCLPKQASEM AGAPSPA*LPPCSLISDCCASNQ*DSVG /VGPSEPGEGYNLVVRFLS
737	14638	A	743	384	1	FTGPYLKNNGYSFLFLYPPPSVLGNWQP PHPGRVFP*DVNFNQWIFVSL/ISSLK DEPAFSSSTLYSF*QHFFITYLPPP/CF FLIESCSVAQGGVQWCFNGLSQPPPGY KRFSCVGLPSSWDYRCV
738	14639	A	744	2	410	TPLNPLEVPLNTSVLLASGVMSA*ADH SLIENNRNQIIQALVITILLGLYFTLLQ ASEYFESPFTISDGIYGSTFFVATGFHFG LHVIIGSTFLTICFIRQLIFHFTSKHFF GFEEAV*YWHFVN/VRGLFLYGSIIY
739	14640	A	745	393	1	PPPPPRGRGSPPPPSRKGGPKGKPPPP GNFFFFFKRVFPF\CPGGFKS*V*GVP PPFPFKIFKFKGGTFFPGLWSPLKSKKS QFFWVPKPGERKKLFPFFFFFFLRRPCL SLSPRLCSGAISAHRL
740	14641	A	746	2	290	KNLCRENYKYE*KKLTKMKDLCKEYYKV *MKKIKENM*KDKLMNFK\NNIKISTLI KVIYKFNAIPKIPMTFFAE\LK*ILKC V*NYKRP*IVKAI
741	14642	A	747	59	364	CRFFFFFFGLGGGGGGGGGGPPPPFF*KNP PNPPKKIPNWGFFFRGPGFAPKKKKGPF LGEPPPWGAPLYNPPPFPGGGGAKFPPI FFPRAGGPQKRVG/RPPPPPPPPPPRPK KKKNLH*LECVEGTEEPTRPPTRP
742	14643	A	748	2	371	SSCLDLPCWDYRHELLHLAHLVLGIF LLLLFCFVLRW/RSCSVVQTGV*WSDLT SLQSLP
743	14644	A	749	339	198	IADMEKV*AF*TEHKTNHISLNQN*I*S KVLTLFNSMKAERD*EGPEEKFGASTGW FMRFQEIISQLYN/IDV*GEAASADGEAA ATCAEDPAKIPDEGGSPK*YIFNVD*AT FIRDLSWIFCTSCCSFSISTCCFTLHVM L
744	14645	A	750	249	2	KIFKPPAFPVSFPPFPL*DSSSPPEP*I SGGRVGP\I\FPPPKKGFPPKNPPGVFFS PPLRKKILLVPPPLNLGPPKGLKRPDP
745	14646	A	751	1	288	VVNHMTDEGLVSRIY*QPLQL\KRKTEN PVQKWTCPNRRFSEEDQMARKHKQGW PASRAIRGTQSKIIMRCHFTHTMARIK KEKEAGPGGSCL
746	14647	A	752	494	2	ETGSWFQGPQRLEVQVWIKSSLPQ*PPW APVILPPQ/LSSG*DRHVPSRPG*LKK KFFL*RWGLTMLPRLLNNLPTSASQNA AITGVSHCARASVFLILRQGLWVWEE/ GAQW*SALSHLPV*/LSR*WCQP*PLG* DSGSGSPLWRRLAYLPLCALWKEVTMCS
747	14648	A	753	1	533	YLSPLRECSGGITAHCN/LRPPGLK*SS QLSLQ\SSWDCRPAPRPAARLIFFCRF EEGRSHYVAQACLKLPGS\SNPPTVA/

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FPKCWGYRCEPPHTGLCS/GLSEFGFCL WWGACSRSSHKNPGCGTA/CPAVFLHSV GYASHPSSSTRTAFTLGWVLVVFVRDKG LTVFSQAGSTVGVILG
748	14649	A	754	1	346	ELSKSTLPALCGGNDKAWMTAHRFIWAF TDYLKPTVENYW*EKKIRLKVLLLLIDNA PGHPKALLEMYTEIHVVFMPADTTSIL* PTHQGVISTLKFCYL*NTFHKVQ\CYID SDSS
749	14650	A	755	1	323	EDQTSNVLNLSLNLISQKALMLFNSMEA E/R/SEEAVEEKFEASRE*FMRLKERS LQNIKVGEEASADGEPACDPEDLABI TDEGDCIK*QIFIVDKTAFYSKKMPS
750	14651	A	756	1	344	ARQQFGDPARGGGGRRL/QPRQAASFC TGTLARARHTCEGAGVLRPADKLASLN *HFSQKKKKKKKKKKKKKKKASSSS KKKKDSSYSSSSSRGGSSSSSSSPPPP PPP
751	14652	A	757	119	317	NRYFPFLRVKKFPWVEGPPFFFLR*SLTL LTLVAQAGLQWRNLSSLKSPLPGFKPFS /PSA/LSRWDYRR
752	14653	A	758	2	363	CILAIKSAINRIAN*YI*KCSMSIITK RQA/IKRKNKTRRYQLIPVRMTLIKKKK RW*RCEEKGRLAHCWF\ECK*RQPL*KT K*RFLKKLKP\FITAIALLDIYPKQIK SE/CKKH/CAILFIALFTIAK
753	14654	A	759	358	1	KADFCFPPTFSRVRKKIFPPFPKKWG* KGP/LPPPGENCVFFFFKKKRGFSPLGG GFFYFFPPGFPFPWPFKKLGFKGLTPPP GPPQKILVFFFFFFFFFE/DGVLLCRP GWSAVAQS
754	14655	A	760	316	2	KATRSQDIRRIQVKLKEIEPQKPLQKTN KRSYFF*KH*NRTLTRVMENKREK/N EIDPIQNHKEDITDPTEIQTIRKYKH LYAHKLKLEEVDKLLDTNTL
755	14656	A	761	3	321	FPLGLWGLGAKPEGQAPLYPPTLSKRV VPLC/DKGRSAVTFTNTVYSSGSSRVVFP PPCM*YRLCIKGRSSDPEQKKKKKKK KKKKKKKASKKKKAPKDDSSPKT
756	14657	A	762	315	2	KTERW/VFEKINKMGQS*DGLTKKNREN /V/QINKIQNERGGLSTGSTEIQRVIRG FCEPL*AQILDNLEKMD*FLQPFHLPRQ NYKKKKII*KKPISKVIELVIKNL
757	14658	A	763	226	329	NPTTLEGQGRISKGPFF/CSRDEVSPC WPGWFQTPDLWRSVRLGLPKWDF/RR* APPPGLNLFFRMLSTHGSW/CQHPCFKF PTSAFQYIYIYIF/SFLSRSTFVAQAV VQWHDLGSPQPPPGFKQ
758	14659	A	764	335	1	QSQERPDSFQVMNLTLPRAPSMFLVSPR TELSKSP*\PPAFLCPCVWPHSTLLSQT LKY*IKYP*SPTPFPSFVLF*RDRVLLF HPGWSLAGS*LTAASNSWAQVTL
759	14660	A	765	100	310	HFGRPKRENCLSP*V*DQTLHTHTHTHT HTHTHTHSRSENGMRLTPHIPERVRW\ GIIC
760	14661	A	766	315	3	IFPNPPRIFIQNPFPFLGFFPKKKEGE KNWAMETPRFSPPLGGKKAPTGFPPPP IGF*GPKPLIKGRGP*/PP*KNTKIFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFF*DRVLLCHPG*SAVARW
761	14662	A	767	1	309	KEPYKLTTELHNEIRVACGHLSSKKKKTW VSDS*ASCPKTRGNFIGPSAGSRAPSE KLEAHFHGCGSVNRVHLT/CK*HKRRPL GVAHLEVSDQKSGRTSLALD
762	14663	A	769	1	316	GRAPPPPPPPPTPRVHTSSKSESEPER /DGRE*EPTRSLERL/LFFASYFCLEAR QSTSALPPLPLSPRSGPT/VLLCPSPPL PGERPPNPTKLSREKQTKQTHRAR
763	14664	A	770	2	366	ARHIIILTF*QMITFLNTKGR*SLILA SLIIFIATTN\LLGLLPYSFTPTTQLFI NLTMAIPL*AGAVVIGFRSKIKNALGHF LPQGTPTPLKPIILPIIETILLIQPIAL AVRLTANITA
764	14665	A	771	2	364	NAFPVISGAWTEYPLSHFIQRCRQKE/ LNLQIGKEBEIFLFKDAL*IESPKES VQKRLDVIYKFSRIAVCKINIQKSNIVV YVWNTQFENEVKTI*DPQ/DIKHWGIIL SQRKKE
765	14666	A	772	3	376	HEPLGKLKLSLLFILATYSLTVYSIL*S C*ATNSNYALIGALRAVAQTISYEVTLA IILLSTLLRRGCFNLSTLMTTQEHL*LL LPS*PLAIT*FICTLAETNRTPFDLAER ESSELLSC/FNIEYA
766	14667	A	773	3	350	HEFFFFILKMYLGQAQYFICLFFFLGF HLK/HKSCSVTOAKVQRRHLGSMQPPPP GFMQFSVAEIKDVHHHAQLIFYIFRIFI F*F/NFLRHSALVAQDGVQWRDLGTLO PLPPPG
767	14668	A	774	1	359	GTRYAAMLSALGFIFLTARGLTGIVLA NSSLDIVLHDTDYVGAHFHYVLSIGAVF ALIP\GFIH*FPLFSGYTLDTYAKIH\ FTIIFIGANLTLPPQHFFGLSGMPRQYS DYPDAYTTW
768	14669	A	775	2	369	ARGSICLRQTELKTVIAYSSIRHIGLVV TAILIQTP*SLTGAVILIIAHGLTYSLL CCLANSNYERTHS\RIIILSQGLETLPL LITF**LLARLANLALPPTINLLGELSV LVTTFS*ANIT
769	14670	A	776	2	353	ARGTGA*VDS*LTTLHGSNMK*CAA\LL \WTLRCKILFTVRGLTGMAITNSTLDIA LHDTYYVVAHFHYVLSIGAGFAIRGFI H*FPLFSGYTLDTYAKIHFTIIFIGVK ITFFPQ
770	14671	A	777	3	353	HEGLHL*LPKAHVETPMDG*IALDAGLL RLRGYGIHVTILNPLRKHILHPFLVL SI*GIIITSSICLRQTDKSLIAYSSIS HI\SLEVTAILIRTP\SFTGADILIIS HGLTCS
771	14672	A	778	367	2	FCPI/CPNQKFMGVGAVGPALYPNPFGG LGGLV/TPGAGVLNPAGPPG*TPPPKN PNLGGGPALFFPPLKGLGWKIALTPEAK GSINPNSPALPGGPNQTFSSKKKRRK LMLVYSIELTSRA
772	14673	A	779	3	432	HEPLHWLSSCVCPACVVCVCO/CLWLQ VGVO*CNYSWQHEPLH*VHTRVVCVC LCHSVAQAGVQ*CNYS/CTAACNSW
773	14674	A	780	213	466	DDILPVWNYISFLFFFNRAFFLPPGW

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						GAGTQL*LPASN*GPKGPSRLTLL*W\DNHRHGPPC/LDNFIFLQKKNLTLLPRLALN
774	14675	A	781	304	373	R*VFFFFFFLKKEFHFFFPQAGGQNGEMG*LHPLPPGAG/RF*CLTPPHSWDNGEGPPREPNNFCFFRGKNKVSPCGP
775	14676	A	782	389	1	PPFPKN*CRVNSRPNVKHKT/QLLEGNLGASVDDLEFGDDFLDTIPKVQSMKERS/WDFIKIKNNVCFAKDNVKKRGPATNWKISVKDLNKGGLPKIYEELKLNNTET*R
776	14677	A	783	1	383	LT*KWSKVLNRQLTRETRA
777	14678	A	784	1	389	GTSP*PLTGALSYLLMTCGLAM**HPHSITLLILGLLANTLTIIYPGRGDVSRQSAYQGHHTPPVQKGLLYRIILFITSEAFFFA
778	14679	A	785	374	1	GFF*SF\YHSSLSPTPQLGGHWSPTGIAPLNSL*VPLLNTWRLL
779	14680	A	786	1	363	GTSIVIPTGVKVFN*LATHGNSNMK*SA AEL*ALGFIFLFTGSGLTGIVLANSSNLIVLHDTYGEAHFHVLSIGAVFAIIGGFIH*FPLFSGYTLDQTYAKIHLT\IIFI
780	14681	A	787	1	361	GVNLTFFPOHFLGLSGNA
781	14682	A	788	1	352	ELNAYWNVMNLQNLINWAQPLSIMQIFQILIKSQIQNTLVVVISIDTGYLPGIDKWN
782	14683	A	789	365	128	CI*LKILCIVKVTINRRAMPVIDWENTFSTYTNDKGLIPKYKELKHS\KQTNNLIK
783	14684	A	790	217	257	KWAKGLHSHSRA
784	14685	A	791	2	363	GTRLYHANTN*KKLRVAILISEK\TDFTVKKIRNKEGHIYIMIKRSIL*EGITILYV
785	14686	A	792	2	362	GTSPSNRVVNIYRQKLIKLPGEIDESTIILRDFNTPLSVIDASTRKKISKKNIVESNN
786	14687	A	793	2	360	IISQLDLID
						GTLFSSSERKNPTWVSLNQKLEMIRLIBEGMLKAETGHKLRLQLQ/TSQVVNAKEKFLKEIKSATPVNTRKTRK*DSLLADTGKVLVACIED*TSHNVLF*SLIQSKALTLN
						CMKPERGE
						GTRNYAKSTKSCLYRWNYKAWMTAYLFT
						AWCTEYFKPTVETCYSEGL/SLKILLI
						DNASSH*RALMEMYKQINVVFLDNRI
						LLQPVQD*VILTFKSYLRNTFHKALAAR
						DNDSSD
						PLDQHGETPLLLKIQKLARRNGAHLYSQ
						LLGRLRHENLLHPGGRGC/SHCTPAWVI
						E*DCLKNQTKTKAPRRVSIHSA
						WSGGVAHPVIPATQEAEBELSLGGRDC
						SELRSCHS\CTPA*VTQAGVQ
						LATLHQTVS*FVHAKKEFKWDDL\KSAT
						PVAI*MIRNLNSLYNLIMETV*VV*KED
						QTSHLIPLS*SLTQSKALIFFKAMKTD
						RKGAVE*KFEATRGWVRLKEKFCLS/H
						HIKVQG
						GQKGLLHQTVSKFVNAKEKFWKELL\K
						SATPVDI*MIRNRTS\LISDMETV*VV*
						KEDQTSPLIPIR*SLTQSKAVNLFRA
						MPVRGKGAVE*KYEASRGWFMQYKEKSC/
						RMCNIIQGG
						ARAGSTMAFKNYAKSTLPVLYKWNKKA*
						MTAHLFAARVTKYVKS/YCLNKKIPFKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						*VFIDIVPSHPRALIGIYKE/INVFMPA NTTSTLHPTDQEVISTFKCYFKNRFRK AIQLPYSNSY
787	14688	A	794	2	359	AREKLYLSILTPLQRSLVIAFAATELTR YYILFETTLIPSLAISTR*GD\QPERLN AGTYLLFYTLVGSPLLLIALIYTHNTLG SLGILLLLTLTGQELSNS*ANNLI*LAYT IAFIVKIP
788	14689	A	795	157	365	GIIEEKGYLPEQIFNAKCSGMISAHCSP RLPGSSYSTSA*TDF*CQVQWYDLSSLQ PPPPRFLFYLSDPSTWDYILAPP/RPS **FVFFVEMGFRQTPE
789	14690	A	796	224	372	IFFIFIFIYLFTEWRQSFALVA\QAGVQ WRNLGSL*PTHPPRVKRLSCL
790	14691	A	797	482	1	NSFFFFFLFPEAKDHDKDFSPFPFVFK KLKGFCA*APP*VQKPVFYLKSF/CLKDY MLSFPEKVNFPSPFPFL/SPSPLEFVGD PPLPPETYSFCF*DPHSINFFLPPGPF LFHFFFFLRWVLLCHPG*STAV*SLLT TS\VK*FFHLSLPSSWVYRCTSC
791	14692	A	798	1	415	NLGGGGCSELRSYHCSPAWATE*DSISK QTKTL/NKDHTRAGWERA
792	14693	A	799	2	401	VQTGFHHVGOAGL*LTSGNPPASAS/Q SAGITGMSHRARPO
793	14694	A	800	73	307	PMALEHHGCGMCLDFLPTFGKSHCFVLR CAEMETRSLFSPWSAGA*Y\CLLQPPPP RFS*LRLPSRWDIRHLLPCPAN
794	14695	A	801	87	401	SLIEIWTLLKKSTCHNLVNVLS*HSLKA IVLARHS/VESLTHVLKMCLV*NFVFAF S*RLCFFLKISRPVVVAHVCNPSTLRG *GCHITRSRDRDHPSQHQEIPS
795	14696	A	802	3	354	LRHYTP\PG*QSETLPFKKKKKKKKKK KLSFFPPPKFLKKKKGLFKNPFKKKGKI FFNPPPPKKKGFFLIVNPPPKKNPPPL GGGGPPKKIYF*KTFFFAAPPKFENPFF FFSPRF
796	14697	A	803	1	830	VETGFLHVRQAGLKLLTSGDLPTLAYQS AGITGVSHCAWLFFFF*CLAVTQTEVA PS*LTIASN\PGLKLSFFTLPHHARLI FKIFSRNEVLLFSR\PSQTPNMQSSCL SLPKCWDYRCEPLYPAESLSF\FIKLSC MLKCLEVKCNDVCNLL*NTLIKWINEWI EGWIGRLTCVKQIEKNVICRI*VMLKAT QPVGTEPS*ESRSTNSGEAMW*SKDNTP FPVFVSFVLRQS/LCFVAQAGVQWVSHL SSLQPLSPRLK*SSCLSLSSWDLRARA
797	14698	A	804	389	3	FIWPFKGAPENSFFVFMWIKGHKCPKKG FGRKKNLGPKIPF*KKKKKGAPPLWLK RFQGPFFFFFEMEFS\IAQAGVQWCDL SSLQPLPPRFKRFSCSLSPSSWDYRHAP PRPANF\CVFSRDEVSPCW
798	14699	A	805	161	21	RGGGCLQSQFR/RRLRHENRLNPGGGGC TEPRSYRCTPAWARE*DSVSK
799	14700	A	806	405	82	FFLRWTL/DTVTRGGIQWCNLSQPQP/ PPRFKRFSCLSLSSWDYRRPPPCPANF LYF**RRGFTMLARLVLPN*PRDPPASA SQSAGITGVGHRAPMPIFENRFDL
800	14701	A	807	938	2415	KITFWETFWITTVHPLCKEREATAGIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						RRWS*NNW/MIHTHTKNLNPYLTPDTKA TFK*IIGLT*RAKTMQL/LESFCQKENT GENLSDLGVGKDFLRHKKHGSIKGEKIA KLDIFIQVKNF*SLKDTFKMKMKYALGWE KIFAERVSDRGCVSRRYKEL*L/IELKD NPIRKGNNLNKVVHQRI*MANKHMKRCP KS*VIREI*I*TIMRYHCTILPRMAVMN/ SD*SHGDKNGGSSGTLIH\CR*ECEMDQ LLWKTIGQFLSK*M*CHTDSSIPFLII QEK*NCISTKKTCTQFTAA/MYLLLVIA KNWKQLPYPSVWI/QQIWCYIT\MEYY SAIKRTVDTLNN\QMDLKIIRFNE*S/H NLRRVHCMI
801	14702	A	808	414	1	KPKAKLFVVRQVVNAKEKFLKEAKSAA PLN\RMIRKQTSLTADTEQV*VIWIEY* TSHSIPLSQSLIQSRVLT\SMKAETGE KAAEENLEDSRG*FTRLKEKSHLHNIKV QGEAVSADGEAAAGYPEDLAKIIDER
802	14703	A	809	399	1	TGPPPRNQPFNPKAGNFWLFLFFFL*F /CNFFFFFPTGAFLSLFGI\LV*CLML VWGNFSP*PFKYCFTFSFFLSFIFLIFL WLLNTCLYICYTFCSYLTVL*CSFLFS SIFFLLYF*FWRLLLIHPPPTRP
803	14704	A	810	1	392	ILLAGAIEDAEPGSG*TGYPITLTGSYSH PGAYVYLTILSLHLAGDSSILRAINCI\ TTLINIKPPAVARYLTPLEV*PVLDTAM LLILSLPVLADGVTILLTDRLYSTFFD PAGRGDPILYQHLL*LLRH
804	14705	A	811	66	411	RETRAGAQGLSRFSPWGNPSQKIFLGP GFKKNPGPQKGNFFFF*KKFPLVSPG GRGGGNFRSLQGPPPKVPPFFCFNPPRK GG*/MGAPP
805	14706	A	812	3	392	LSVPQFPFFFLKKTFRNCPFFCFSPNPI LGFPLKGSKK*GSFFPPPPPNYSFFWF PSYSF*NQPCLTRGPF*NQKFPRL*KGV PILRL*SPLFFGPPPHSF/IFFFDRVS LCHPGYSAVAQS/LLTAASS
806	14707	A	813	690	153	IISIDAKKAFYEIPPPSVISSSSPTDSL YYNLGFLKNFKKGREVKYLNIIKYIEK PTANIIIFISGKLKAFSLRSGTRQICPLS PLQFNKVLEVLARATWQEKEIRNIHIEK EEVKLSLFSNILCIENPLKMP*KNSSN **IQRVAGYKTNI*KIS\AFLYTKNKL CCLSHPIYDIPL
807	14708	A	814	32	376	LFGLARSYITEGGRLPENPTIPHG*REF WELCNKCD\TMRPKPSLHCSRCHCVTR MDHHCPCWINNCVGEDKH*LFLQLCFYTE LLTCYALMISFCHYYYFLPLKKRTLVRN VYI
808	14709	A	815	2	423	YPLYPFKIFIFPKGFNFCREVGPICPPP KIKVLSKNSQVGFYTAPYKEKNNTLPAR VNFPGPKDSLKRPLFFFFF*RDGILL CYPWS*TPGLKQSRCLGLLKHWDYIC* PLHPASF*KKHYSRLILP/SLLADAW
809	14710	A	816	404	54	SLAHFFPPPKGFFPKIPRGVL*PPP*K KKFLFS/HPPVNLGPPRDFLKGPPSSS SSSSSSSSSPGG*MIFY*/P**FGPAL VQPMACYCKASCKVKAPFFSTHSGLMVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PPTTAQS
810	14711	A	817	3	410	DAEVGGSLEPG\SGGCSEP*SCHCTPAW VTG*ETVSKKKKKKKKGFFPPFFFKRGP FFREIEKKFGKKFFSKKKKKKKKKRGG PFKKNFWGGKKNLRGGKKKFFFLGGKKK KPRGFFFEKKTFFWGGKNWATTTQK
811	14712	A	818	1	404	IPINSLTSKINKLLKRHLK/HLNQEET DNLTRTIPIT*INIF*YKQNTGPDGSIS KFY*TIRKT*Q*FYTSFQIKNEEVLPN SFYEASTPLASPKKKKKKKKK
812	14713	A	819	421	2	LPPKRRCFSPKPPRGFFFPAPS*GKKNI/ CFPPR*NLAPPGVFLKGPPLFFFFFFF FRGRVG*SWVPAASPLQGQVFLPPQ/SS *VGGSPGPPEHARVNFFFFFFFFF*F** RQSLTMLPSLVNSWA*TILTPQPPKVL GLQ
813	14714	A	820	84	418	ILTCHNARLGEKSQIVTMQASQNNPKLV NICEVFLVFFFWKPIFFGTQVGGQYFNL SSL*VRLPGYTHFFCLTLPKSWDYRPIP PS\PIFFCFFNKKGVSPGYPGGCNLLVF
814	14715	A	821	290	3	FSPPPENLGPPRNFLKGGPPPPPPPPPP FFFFFFFFMFCVLIY\FIFFCTNLLFLDF CIT**T*NWFISSKAVCLFLFLPLQPAS QKTKNRCRKSFF
815	14716	A	822	416	2	ITKLTEEEKKIWSGKRKNQVVKYAGASQ YTAVVLRPQSMITLKDSSERKAPHWGEL NVV\HVHHFIWKER*PEV*YIES*AI DGLASWSGPEKNKIGKLGAKKV*RRDMK TDPLECTQININIFGVCLFGDRVSLCW
816	14717	A	823	409	45	PPPPFLFFF*KKKAPGGGSGQPKF*P PPPPKGGKPPFFKKKKKKKGGGPPNP PPKGGGQK/QFFPPQGGNFNPKSPPPQ PPRGQKKKPPPPQKKKKKKKKKRLNVTG PQFLQLESGTY
817	14718	A	824	1	408	IFSEHNGIKL*INTKRNFNCTNIWELS NMLLNNH\*VNKEN*NKKFIKTNE/NKN ITCQNL*DTKVVLREIYSKKCLLQKKK KKKKKKKKKGGGALKNYLGGGQFYGGE GNFIFFFWGGAKKPCGWIFRRRPPFW
818	14719	A	825	259	274	YL*YLLLYRRYSA*IP/LGYLKKRKL LYQRDTYTPMFIAALFTIAKMWSRP*SP VV
819	14720	A	826	422	105	FFFSKIPWGNFFPPPPKRIFFPPPPPKI FFPPPPPPFFWGGFSPSPPPKKVFFPK SPPVFFPPPP*KKKFFFP/HPPLIFFPP GFFFKPPPPPPPPPPPPPPPPPPPP
820	14721	A	827	15	402	IKSLGKNIGINLGDVLNNGF*YTLFKA QATKEKIDN/WDLAKAKNICA*KDTIKE VERQPKK*QQTFFVNHLEFDKGLVSKH/N EL*LINKKTNH\HL**WAKD*NRACSK DVHMTDKLMKDVPVSLVIREI
821	14722	A	828	420	3	KDAHTCPPGCKGGFSGHRALKAI CRNQG FLLTTFEFLTHKCPPLPGQEPWGHQGR DSPRRVSPAPGTWQPPCHRRERACLAPSA VE/GPS*IQEQEKSLLFFFSLLRWSL/ NSVAQGVQWRSLSLQPPPPPRFKQFSC LS
822	14723	A	829	1	269	IKIKNLARHGDSCL*SPLLLEMLRLLEN



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LSPGSRGCSSEL/CQPARQGETLSQTNKQ TNKKPHQVQLPCFEIINFKEFITCLVLR LPGNSW
823	14724	A	830	432	1	GYNNQQIFDVDQTAFY*KKIPSRTSIAR EEKSMLGFKASKDRLILLGAKVAGDPK LKPMLVDPSKTPRELNN*ARCTLPVL/V KWN/KAWMTAYLFTV*FIQYFKPTVDTY C/FKILLLLIDNAPGLPRAVMDR*EESNV FMPVNTTL
824	14725	A	831	1	233	KKLQIKYLGINLMKYTIHVVSICQKLLM KEINEDLNKWRDVLCLWI*RLNNMSILH KLIN/RINLLQLRI
825	14726	A	832	3	477	YQTKCEDLTQMLLKIFQIKGEGIIIPNS LYDASIAMMPKSDKDRKKF\NYRPI SL MSIDAKILNKILPNQIQHQHIFIFIPE MKG*FNIRK*INLIHLITKMKTKTPMII SIGTEKVFDDIKY/PPFITTLTKLGIDG RSLDAIMVARE
826	14727	A	833	3	402	RYQTPLL\*TVLITTALLGLSLPVLTG GITIPLTDRRLDTFFDPAGGGDPILYH HLF*FFGRPEAHILILPGWGIISHIGTY YSGKKEPFGYTGMRAIISIAFLRVIV* AHHIYTV*IDRDTRAYLPSLHN
827	14728	A	834	7	395	DPQRVSCMALSSNSFFFFFWERKSLFFP GREGRGQIWNVTGTPPLQKRNSPASPPG GGGITKKAPKLHPPKKGWGGGLEKPP*N QRGGFGI*SPGGKKGFAGG*KQGQSKG GGKKKGRA\DP*AYIPLK
828	14729	A	835	41	444	DPVRVKKERENLYRSVSIKEIESVI*NF PTKKI*GLDGITSEFIQILPKKKPK\IK KERTFSNPFDKTNITLI/SKPETTFTKK EN/VRPVSLMNI/DCKILLKVLNCTL\ HI*REIHDS/INFIPAIQISFNIQKTN
829	14730	A	836	3	415	HAYYIVKPS/PWIPKGALSALLKTYGLT M*MQFQSIKDLRLGLLNTLTIIYQ*WRD VTRKSTYQGRHTPPVQKGL*YGIILFIT SEVFFFAGIF*AFYQSSLAPTQLGHW PETGNTPLNPLEDPILNTSGLLGIGVS
830	14731	A	837	378	0	TPPKGPGGKIFLKK/SPGRKIF*PPGNG /PFFSPLSPLKFFFFPKARNFWGGGGPQ GPPPKKGVFSQNPPPGKKRPPQKEKKNF FE/PPGKMGPPQGGFF*RAPPP
831	14732	A	838	383	38	GPGEKIFLKKPREKKLSPPGEKAKFFPP SPLKNFFFPQGVFFLGGGGPKRPPPKKK GFFQKTPRGF*IAPOKKKKKNFPPRGKF GPPQ/RIF*KGPPPPFFFFFFFFFFFWSL
832	14733	A	839	59	418	TKISSKDQKQY\TTPGW*MAEISTTFED AEIIDALIFPNLPIWLHKKPDCSWKVS VYCKLK*VVSLSISATGLDIINT\LLEEM KRVSGTWYIATDLAKTFYI/PDQKEFA FSWYG*KDIF
833	14734	A	840	5	335	IRHLF*INKFENLDKMDTT*KLTVEGIE SLN/RII*NF/PVVKSLGSGSFTSEFYS LFKEEITAIYKPIWRVEKGGI\LPTCFA TRITLIPKETCIMRKNKCGPVLPMNGH F
834	14735	A	841	1	38	RRLKLEDHLSLY*KINSKWIRELNIR/P

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						ETIKLVKKDKGNV\QDTPGKDFMVKTT KTKIDKSDYIKLQSFYTANETVNRVKLQ PIE*GKIFKNYSSGKGLLSMIYNELKQQ HRNNNLI*KLEDHLSLY
835	14736	A	842	2	424	GRVGSIPLSQSLIQSKALTLFSFMKAET GQEAEEKKVEANRGWFTFRKERSGLCNI KVQ/GAGGDTAASSPADPAKINDEGGHS /KQQIFSGNETAFY*KKMSSGTSIAREE KSMPIFKASKDRVTLIGANAAGNF\KL KPMP
836	14737	A	843	281	3	FFFFFFFFFFFFFFKTFLFFGYWFSIFFP LLFSISLLLSFSGSFVTFAPQPPF*VSR YHYQHFNSTF*FL\KL*FIF*IFFLISI LFLFHGYNF
837	14738	A	844	409	1	RCGGTCPWSPVLRRLR*KDHLSLRG*GC SEP*LHHCTPAWATE\DSVSKKNKKKGI SCRQHIVGSFFFHLKMCLLNGLLSFFTL NVIYVVEFKFTILLFLLYSICSLSHLF SPPAKSWINSKFESLFVCFNSFS
838	14739	A	845	63	451	KNQEQESEETLPNLFYKASITLIPKLDT QK*KKRKEKKRKKKK\EN*KPITHRNIY AKILNKILAHQIQYIGIKIHHQVGC P/GAFDKIQVRCMIR/TLOKMGIEGTHL NIIKAIYIRPTDSIIENREKP
839	14740	A	846	60	460	RNNEPFLDQIVTYPEKWILYDNR*/PT QWLDGEEGPKHLPKPNLH/QKKVVTVW WSASLTHYSFLNP\ETITSENYSQIDE MH*KLQSLQLASVNRKGOIPLHDNPRLO VAQPVQLKINELGFEVLPHPPYSPE
840	14741	A	847	344	2	NFLKFHPGGETFLQKGYTFGYSPFP* K FFFSLKPLNPLGRVGPFPFPKKGFFSK IPQGGGLISPPLRGKVFPFPRLNLGPPR VFLKAP/HPFFFFGI\PHGLQPRPMI*K PTRP
841	14742	A	848	439	132	RRVAAPPPSKNIFPPPGSYNCGGVWPQK SPPPK*GFFPKP\SGVKNPPQIEKVFF FPHARIVPPGDPIKTPPIFFFCFNSI NFSLRGAQLVWDFLGSGC
842	14743	A	849	94	470	LNHFLSFFLSFFLSFFLSGSLSLSLSF FFFWKGSPPP*GTK/QKPLCKKKKKK GGGGGQNFPTPPGGKKNPPPGGGGGGS PAQKKK/EGGGPPGSKKNPPGGGFKKK KPPKKPRGGGKPPFP
843	14744	A	850	2	396	FFKKENIQMANKHVKTYYTLLVIREMKI PTSMRYHFTSIRVAKILKTDNTRC*QEG RTIRILMLC*LQNKMVLLL/WKNWQFLT KIKIFLF\FDPTISLLGIYPREMKTYVH SSFIHGNSKNRTGNLNVHN
844	14745	A	851	369	36	SKGASDILEKPLF*EVGLPTTSPPLGE KMP/FNYKGGPGKGISLLIFPKKFP GGHFPFPF/PFFMDRVLLCHPGWSAV AVSQT'TTSASRL\K*FSCLSYSEG*DG RIS
845	14746	A	852	1	367	PPPKIKSPSGPGPPSKRGSPGAPPRGG KFWFLSQKGWGGP*FPPPPGVKPE/NIP *PPRGRVPL/HLNLAPAPPPGPK/PPK PSP
846	14747	A	853	1	378	AMLATLISNS*PQ/CDPPALAPQSAGIT

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						GMSPCARPTSCSFYF*ILLTVRTFTKIR NFFFFFDGTSNFVAQPGEGHDHG***P QPPGPNKSFNLSLPSRWYDYGAPPFCFVI LCIFCKDEVSSCGSG
847	14748	A	854	369	1	SACFGLPKCWDYR/R*ATTPSLEIIYYI ER*EKTTSFDNANRFDVTKLHHYDCSVM DF*KAL*NGDDFPVLMKMHMQSLNII\ FVFCFLRQGLALSQ/AGVQWRDHGLPQP QLPRLQPSSHLSL
848	14749	A	855	380	335	NPGGRGCSELRRLCHCTPAWAT\SETLSQ TKIQPKQEV*LL
849	14750	A	856	373	1	LRIKILNKKGLANLIP**R*KIHSQVE FIPEMQA*FIIRK/TPSIKWPIVRTKKK KKSQMLISIDTEKIFDKIQHFLVKPVI KLGIEGTFINFIKSIY\KKSTTATIISG LNASPLRLKTRQDF
850	14751	A	857	369	44	KVONLYFEKKLLNKKIKVDLNKW/NSLCT RFRKLNIANIIMFKLIHRYN/SKVKIPI KIPANCFGEIDKLILKFI*KFKRPQIAK IILKKNKDGYYLPDFKTYIYIMQYHLC
851	14752	A	858	1	348	QWHAPAS/LARPPPPRFK*FSCSLSPNS WDYRHAPPRLANFVLCFVVG*GGIHL
852	14753	A	859	1	366	CTSPTFNQKLEMIKL/BEGMLKAEFG*K LCLLCQKV/QVVNAKEMFLKEI*SASIV NTTMI\RKQSFTADMEKV*VV*IEYQTS HNIPLSQSLIQSKALTYSSMKAEERGE AAKEK/LEASR
853	14754	A	860	12	366	PSTLGLRRASCLSLSRWD*RHMPPHPA N*KNFFCRDG/SLTMLRLVL\NSWPQA IHSPWPPQ
854	14755	A	861	424	78	NPRPLEGQTASFSLAPNF*TTLGKKVNP FF/SLKNPPPPPPPKIWAPOGPGPPS PGGLNGGFFLPVRVKAPIIHKGAPPPQF PPQKKKGPRVFPKKKKKKERKKEGMTR AFCYP
855	14756	A	862	327	3	SHWFFFAV\GREISM*AMAPDQTKKICP RSAEDAICYFLTQATGSIILIRALFNN RLSEQ*SI*NTTNTQYSSLI*IMAIKIV GMAFFHF*VPEVTQGSPLTSGLLVL
856	14757	A	863	1	341	YDRNKWKDIPGS*IERLNVKLSMLPTV IYRFNVILIKIPMTFFAETEKSIKFSR DYE*PKQS*KEQNWKTHTP*FQ/QFFTA TVIKMVWY*NKDRYIY/DQWNRI*SLGI NPCI
857	14758	A	864	32	324	LVWPPPPPPPPPP*KKKFFPPPP*RK GK NFFFFTPPPGLNLF/CPHPLKWEKR APPPPN*FFFFLKKTGFFFTQKGLNF PPLETPPLTPPKGLN
858	14759	A	865	350	3	RVKNRPFWGF*MVLKPLSFFSKKTN*I LFPLKIFSPPKTVPWGKIFLGAL*NPFF CFKNPLWFFGF*KL/SFFFPPLYFF*KP LAPLKRFSFFFFFLL*DGVS LCRPGWS AVARS
859	14760	A	866	342	118	GSVTQAEVQWCDHGS LQPETPGIK*S/H PPTSSYQVVGTTGVCHPGLAMLSRLVLS SWPQAILSPWPPTVQGLQV
860	14761	A	867	1	354	VKPSP*PLTGALSALLMTFGLTM*IHFH SITLLILGLLSNTLTIIY\Q*W\RDVTP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						STYHGHHTPPVQKGLRGIILFITSEGV FWAGSV*TFYRSSLSPPTQLGGHWPPTG ITPLN
861	14762	A	868	3	344	QIKNPDNISC/WIRCGATGMFLHCWEC KLLQPLWKTT*HQ*SRR*AVPLSGMFP/ NRYSSCTCPASI*KTFLSALFMMTPL/C LSRVEWIK*SWCNQKL*Y*SVMKRSEEF SLKNA
862	14763	A	869	345	1	KQAGLKNVKITG/EGASVNQSR*VS/YL GTIKKITEEGYLPERVFNAGASAVF*G KKLPQRTFISK/EEKQAP/GSEVGKDRL TLLFCANMSRFMISTALLYKAADLQSLK GKDKHRL
863	14764	A	870	340	45	FCSFCRDRVSLCCLGWSRAPGLK*SSCL SLPKC*DHRC/AA/VPANFQRCILEKKN QIY*CAERIL*SERPHTRHLDSSVTNIL PCPLSKVIFWKKKNQIY
864	14765	A	871	209	72	KLWDIHTMEYYSIAIKRNKPLKYTTWMD LKDIMLCEKANLKRSHTV
865	14766	A	872	3	353	SFFLGPPPPPPPPPPPPQPLPIFFWRRFF FCFSPPKKPPP/PFFL*GGSPPPPF*RG FFFF*KKKGGVFPFPFFFPSPKVSPPP PKKGGGG/PPPPFF
866	14767	A	873	3	267	DFTMLARLVNS/WPGVVAHTCDPSTLG G*GGWITRSGVRDQPGQGEI
867	14768	A	874	1	346	PRRPFFFFFLLIVFIYFKCVYLF*DKV LVCHPGWSAVPHHGSQP*PLRIKQSSH LSLSSS/WDHRHAWLVFVSFYRDEVSPC LANFCIFL*RQDFSMPLRQ/VLKAICLP WPPSL
868	14769	A	875	1	172	KLSSGSPPASASQSAGITGVSHRARPG LLNFFC*CAFSVPGPCLGYPDTFTH/LC PPSFHQSVIASLDFSCLS*L*MSP
869	14770	A	876	1	348	LLFCFNYSFFHGVKPIPAFFVFGPGC LPHFPFPIITPAFFFLDRVLLFPGWRE MGPF*APPTFSPQG*GVFPFPPQ*LGP RGPPPPQGVFFFCIFGRDSA/LAILPR L
870	14771	A	877	1	203	GFHYAGQASLEVLTS*STCLSLPKSWDY RRGPP/*PGLSYFLYPLRS*FICAMSI HIPFIKKKASD
871	14772	A	878	343	102	EWEDCPSPGGRGCSEPRSHHCTPAWVRE TLSPKKYLFLOP*KLKNTKIYLSISIP* ELET\ILKILHFKMMNPLHSYNFF
872	14773	A	879	2	359	RDITKGDMMQMETKHM*SFSTSLTSGI/H NSPIRPSKMKNIDSTRYWRGCRAIRALI HCWWRC*MVQPFGE*ISSFSKLNMYLS YDERPTFRYEK*K/P*VHPKICV*MFMA AFFLISPW
873	14774	A	880	205	1	FFRGVTEGL*EPYVESVI/AGGTTARR PLFFFFFFFLLRWSFALVAQAGVQWR DLGSPRPPPPGFK
874	14775	A	881	150	2	CRARVDGVPWRNPGSLKPPSP\GSSDPP TSASQECGITGAHHHTRLT*VF
875	14776	A	882	345	1	KGNQPWKTEKRALFC/TLKKKKIFKNSP PRGNF*KFFVKKKIKLKEKGFSPTWGK KKEFFFKKKKKKKK*AKDLNRNFSRE DVQMAKHKMKRCSTSLIIREM*IKTTIR

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						VHF
876	14777	A	883	2	355	DRLLFSASHLDLGLTYLLFGA*SGVLGTSF\SLLIRABLGQ\SGCLL*NDHIYNGIETAHAFVMDLFIVRPIIIGGFGN*LGFPNKKGADMAFPRINNISF*LLPPSLLLLLASAIVEA
877	14778	A	884	262	2	PTCEQSEREIKKTIQFTTESK*IKFVGINLAQEAKDLYTETIKYKTLLEIKDNTK*KNIIYV\SWTRRFNNFKMLGWAQWLMPVIPA
878	14779	A	885	16	318	ILRADCADLFFFFFFLGGKKGFCEPRLKGRGETLLN*TLIFR\VKGNF*PKLPKIW/DFKGPWPHL/AENFVFFLKKGGLTLLPGLVLS*IKEFFHLWPPKGVA
879	14780	A	886	298	322	KRRTP*YPPGEPHFPPPPQG*KARGAPPPPPKGGF\PEKKKKPGVMVQGTQKPPKTKVRVD
880	14781	A	887	353	3	FPFWGFLKTLFGKALWLFKGGFFFAHQKFFFLPSLPPP\LGFFLRGLT*FKIFSLP*KGAPQKGISHPLFFFLISPKPPPPFFFFFFFFPPPPFFFFFFFS\RDRVLLYCPGWGA
881	14782	A	888	22	341	IPCTCLKLHGKVDHDSQSLWPKPQEE MRTLENNLAVLQSIQLQWLDIELPYDRAICAREIKTV\QONCT*TFMLALCITAKKW/KQLKCPSTDEWVSRMWTCTR
882	14783	A	889	51	338	ERSQLQWLMPITPSLFFFTQFLFCCPGRAWAIFKIFEFLA\PK*KQFSCLTLQTI*VYGLNPPPRKNFVFLKERGLFHVQSGRDLPPSGDPP
883	14784	A	890	1	225	GRLRPENHLNPGGRGCGELRLCYCTPAWVTERDTIS/RHTHT*NYFY*GSI*QLANSCCNMLNKFNVICILRWC
884	14785	A	891	357	164	GKGCSDSRLCHCTPAWAT\TKTLSQKKLILKKQNKFRS*LDD*INMRCTVWPCFHVFLFIRAAPLEFSDWLYNK*MNRNT
885	14786	A	892	207	302	EPFSGIINESIHQEGIIVLNVYTSSNRPSKYMKQTLIELKGEKVKSTIIVGD/FYTHLLVIDRTSR*KR
886	14787	A	893	86	332	VMRVSCCCLKD*ISLCHPTWSAVVQS*LTVASNSW\VKQSSFLGLPALWEAELGGSLEVRSRLRPVWAT*TP\FCKNKKL
887	14788	A	894	2	336	FFFWPPPTFLKNPGGPGPKREEGPGGS PRGQKQGPGLHLTGFGGQPGG*KNPEP GPGGRAPKGETRGEggGPTRPQIP/QLI NGKSGKPPKVTLNGAWGTIKIFLIKTPV G
888	14789	A	895	1	214	ARESLASFLPPSLPPFLGLRFLPSFLP FYFSFLPSFLGFGSFLPST*VPSFLPSF LLFFPSFLPWLWFLPS/FLPSFLPSFLP SW
889	14790	A	896	131	352	TLHESDSESVPDRDFKISDALAVEDDQRS PGTLNAAELS/SSVRERKKKEK/KPEPGL*DSIKESDSYMVSGRIQ
890	14791	A	897	3	184	CSVAPAGVQCHDLTSLQSPPP\SSSNPP TSSNPPTSAP*VAGTTGMCHHAWLIFVFLVDAA
891	14792	A	898	327	264	NRAVSLMNLDAKVL\KLISASQIYVYIK

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						KMIH/HNQIRFTMRM*GQFTI*TAINIY HKLIK*GRKHMILPIYAVKIFEKI*YHN IMIKTLHLK*IKEPPGSFIYSL
892	14793	A	899	3	313	TKAASHSQ\LANLQFLVGRH*HLKSR TISPGRVGATAAVNSTAILEYLTAEVLEL ARNASKDFTVKHTTPHYLQLAIRGDKEL GSLFKSTIAGKGVIPHIHKS
893	14794	A	900	340	1	HLCPHKEHLY/LLQTSCLPAII*FISTI AEHTKAPFDMKVESELVSGFNIEYAAG PFALFFIAEYPNIIIIINTLTVTITFLGPT YVALSPELNTTYFVPRKIVVVRVFIIM FV
894	14795	A	901	1	252	LTFPPQHLLGLSGMPRRYSIDPDAYAT* NILSSVG/SSFSLPAVILIIIFMI*EAF SKRKVLIVEDPSINLE*LYGCPPSFPSF
895	14796	A	902	326	1	LGPFPPLKEPPGVFPPIFF\*FWNFGPV GPF*KILIGPLILDFFQFFGGVSQIVF PPF*GKIPFF*KNTPPFF*GIGGSIPHP PLFFFFFLL*DGVLCLLHWSAVA
896	14797	A	903	1	352	KGIFPVWSCG*KGTQKKGGLSQGGQGNV PPCGIHVFKEFLGFPGAQLLIS*GGRLLI F*KGPKKGFLP*TVFG/RAQFEAPR
897	14798	A	904	325	2	RLBEKLNLDYWNEMKVKNTFYPLNLVE DIQKRPDQTVVQCDACLKCRK*PYGMDQ HLEK\WYWCNNHDSQFRYCMVPKDPEDM DLVHPNYGKPKKPSKETYWFSQMP
898	14799	A	905	1	329	IGLAIHGAERIVRGQTAKSLAVHN\VCE QKKIKKKKGPGREFQNLKWNPKNPGG SF*RLGPQSNFFYLKQ/RLGFFF*KKP PKI*ILAMEPPNKKIF*KKNKAHFFF
899	14800	A	906	148	2	DVDKLFLLRSLPTL*RPEYGSYMIETG\ TGQPYGGTMSEFNTLEANMRIR
900	14801	A	907	384	1	ESKRISIFGPPNPPPPGFGFSRHAPLWL RSREPPHKAGVKKGFPRFRPGS*MPIP* SFLQNCPLQRVGFPSLPPPGAPFLKISL FLRQESRSVTQAGV*\YGLLQCRPPRLK SFSCLSLPNSWDYNR
901	14802	A	908	3	297	TKIKSL*INHLIRAKTVKLLLEENMGINL HDLSSGRQQPFRYDTFQ/SMINTAIKEK IMKLSFVKMGSFISQRTPLRKERQLTK* EKIFADVYLIIGRRG
902	14803	A	909	169	373	ASNILSATDISNTFGPPSGQFGSGREAY VEAGTYTTFNSCLGQVKVF*YWMQLIVS IVLL*LL*VTQKL*L/GPRQEKVF*YVP AST*ASLPLKPCDPGGPKVFEMSVADS/ DV*SLWLALIGESKFRCLVF*SKFLPSS AYTYSPLKELFILLGCFVMICFCFCFL RRVL
903	14804	A	910	132	368	GRIFLFVGOEKGARVSFLFLF*DRVSLC HPGWSAVAQSQLTTS/TWTQNNSSHLTP P*VAENHRCA/PHTPNVLFCLC
904	14805	A	911	2	339	NSWAQE*AGITGSCHHTQLTLEF*AHDR QMMFFLFLKTNFTFCPPA*RPWPGLGL TE\PLLPGLKHFF/CLTLPNWDKGHL P/HPYQI/CGFLRKNGASLISG
905	14806	A	912	3	381	LNFCDTHTLTPRPVSIQRQCLPLVEAGI RWRALISPQLHPPT/YSLSSWDYKHAA PHPANFFFFFCKGSLTMFPRPGS*IF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IYLLIYLERESY/AVAQAGGQGPNNFNSG QPLSPRFKQFSYLSLLR
906	14807	A	913	394	1	MSKKGIG*KLG*KFAQKVSQFVNAKEKL LKEIKHFTLMNT*MI*KRNS/LIADLEK ILVWNIENKTGYSIP*TQNRIQSKALIL FYSMMTERGEEA\KKFEARRDYFMRPKE RSRLQNMKV*DEAANADGEAA
907	14808	A	914	326	200	HNWLSIWKKVKSNCFLMPHTKINSRWIK DIKI/R/LHRIKILQENVGNHIYKI*RQ KRS*PRHNFHLKNCCLVWHKTNK*NH* KIYL*CI*KTFVFM
908	14809	A	915	3	334	LVVVRVKGPKFKFWLHHQLGLYC*VISFF INKMKEYVLIHRIK*DHKNIF*MGYKKL *NVNIW*LVLFGFSSKNHL/WSGAVAHT FNPSTLGDGRRRITQGQEFQISLTNMVK
909	14810	A	916	14	299	YQKLPQKKSPEPNAFTDKFYKIFK*LTA ILQ*LFQKI/E/KETPLPK*SNESNAL I*KPDKDIT/SKNYKPISVSNIAKILN KI*GYQVQKQLYSK
910	14811	A	917	3	339	SLQPQSCRLKCSSLSSCWDYKHKPP CLA/NFF/VFF*EKGICTVKN*NGDYPL GRRVTKRDHERGF*NAGKVLVGV/CGF ETQSRFVPQAGGQGRNLCSLQALFPGLM PFSC
911	14812	A	918	2	321	GIISGIYKELSQPKMTDSSIKK\KDLNR NFTKEYVQACKHMKRCSASLVIREIK\ IKSTMR*H*\TPTRMTKIKD\DKNTKCW *GYGAVGMLIHCQW\NTKMQPLWKN
912	14813	A	919	51	326	FFVFCFLSLVFIISLNCGLF/PTFFRIPS L/PYLQLI*YLYFFY*LKPIFLKFFRDR VSLCHPGWSTVA*S*LIEASKYW\VQ*S SHLSLLSS*DY
913	14814	A	920	239	2	DSLILSAVQ*HDLGSLQPPHPGLKQ/FL PSNWHYRCMSPCLAYFLFLVETPFCHV TQASLELLGLSNLPASASQSAGI
914	14815	A	921	1	242	PRPRRRLKYFILFNFLRQ/RSRSATQA EVQ*HDHSSL*PQTPRLK/HPPASET
915	14816	A	922	249	1	ALFCALKKTLGCTLMFIAALFIIAE\SR HNQTQPTCLSTDEEINKMWHRRHAMGNYS AIKRNEVLIYAKI*MYLENIMLSEII
916	14817	A	923	404	1	SRPQKKLGELKCS*RPKGLNKKNQKPKG TFFFFETKFHSFCQAGVQWVYGC*SHPY LLHIIFP*VF*MFLILITV/PSRNKDL IGNSEKQIHN/WSSLYFYF*LFFLRWSL TLVPQSGVRWRNLGSLQPLPRFK
917	14818	A	924	6	358	FFCSLLGHGGETPNNSPLPHPWL*ETKS PPKPPHPLKKKKHSLFFKIFILKKKKNG PPFFPPAGENPRG*NPFPQ/RPPKGPP PPKEKINPPPPQGNFPKGRPPPLGPF PKKGGGY
918	14819	A	925	268	2	HMYAFVKIDLTAHLRFSAGKKEIPAGKL YF/L*RKNPKNQIGNQKKKCLPRAGRM VAHAWNPSNLGGQGAGTT*SQALETSMG NMGKP
919	14820	A	926	74	338	IAGITGVSH*ESKNSY*KQFL/WPGTVA HSCNSSNLGGQGEWIT*GQEFETSLANM VKP
920	14821	A	927	339	1	LRLFACPPLPKWWDYRGEPPRQIFFSWH

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						FFKKQGFICPIEKGRELSNCCFQKEVLI *KKVILKI*PFFFFFFLMBSCSVA*AGVQ WHDLQPLPP\NSWDYRCPPSRPAKFCIF
921	14822	A	928	3	416	RCWENKIN/PFWK/S/VWPCVTKVNIH SPYDLTISLQYLPYRDEYLC SYKNLMFL IVLFIITKNYQPKCASVG*WLRILWYL /YMENYSAIKMNK
922	14823	A	929	344	69	YKRSPLL\KSA*DGPANWKS LPRS*YKR SPLLIKAKPDQIISGWASPLII\PRAL LQKLKPAASKF*W/NPKKKRALIS/KAI PSKKNKAEGIMFPNFKV*YRDTATKTA* WWYKNSSSL
923	14824	A	930	378	1	HGKKIDPRFIPYTKI/NLKWFDLNVKP KTIKFLE*NIGE/TIFVIDHKK*NP*KK KLVN/WDFIKIKSFCFVH*KPAVGK*KR /QP*TRRNVQTHTSRGLISRICKELF *LNSKVINSIRKWAQSLN
924	14825	A	931	479	83	SRKGLGRGLKRGGFFPPPPKGLPGGVA PGFEGFFGSL*KG/DRG*PFLKGVKGE KGRKI*EGG/EKGGGFLPPPPQKGFSSK NFLGFYAGKKENP*GGSPPPPLFGPAQK ISLGKGENKVPPPPGNLFYLFIF
925	14826	A	932	36	440	TTYASLDEAQLPRAKFNALTTTF*HIK NGFILGKIGRKYMIADQ/GHRMKNHCK LTQVLNTHYVGPKRILLTGTPQNKLPE LWALLNFLLEPTIFKSCSTFEQWFNAPFA MTGERVHLYEETILIIIRRVHKVL
926	14827	A	933	8	398	CLQGKEETLTNTNWHLRYP L P P P P P P P K KGARKNGGRPPGGSPKNQAPCPKPFEN PGEKTPQKRGFPPPKPCPGPGPGPTGGQ GKPP/HPQRPQILPFPQAGPQGRKGG* WNPPPPG*KGFPAPTPRM
927	14828	A	934	1	441	TRSHPRALKEVYTEINIVFMPANATSIL QPMG*GVILTLKAYYLRSTFCKAIAAVP SDS/SSDGSQS Q L K T F L K G F L I D A I * NIGDSWEEVKISTLTETMWWKLNPIFMND FEGFKTSVEEVTADVVKITEEVQVESED GTEFLQSH
928	14829	A	935	3	383	PGFKASKDRITFSSGNNAAGNFKLKPVL IYHSENPRVLKNYAKSILSVLYKWNKA WMTAHLFTAWFTE\PYVETIYCS\EKNIF FKILLIDSVPSPRALREI*KQMTIVY MP/STTTTILQPMNQ
929	14830	A	936	417	1	CFFSRDEVSPCGPGFSPSPD/HHDPPPP PSQCWDYRRDPLWVPPHICFLIHKKRS SHMGSSMYDP*KPPHKWMKSPPPVSVLY GSIPVQVQIAPPPETNPVYFFSPPPFFW GGGRVCVCVCSSEVCDFFGGDENVIV
930	14831	A	937	412	3	KPTRVKKINPPFFKNTKNKGRVGGSLY SPFFGGLQKNGFTPEAKGSINLKFP PKSWGTTQKSLFKKKKKKKSILKFIWNQ KINPKQIKQS*GITLPE/FKLYYKEATV TKTAWYRYKNRPIDQWNGTDRNKATH
931	14832	A	938	1	416	KNRHIDQCSGIERPEIDSHKYSQLIFDK GAKVI**RNDNLFNKWYFNNWMSTC\RK INLDTDLTYLFQNGSQT*P*NIKLLENS MGGNLDL/GMSQ*VSSSSSSRRIDHKK LVS/WDFIKIENICSEKGIKRMKSQTT



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932	14833	A	939	4	443	D DFDYNHDHDAELGTRPGSVGQGSFDPQ FTPSRMGREGEGTHSIL*CSSLGMGVIA DLSTDPTLEKRALEVAGPDGQASAI SP ASPRRKAGDGGHRRALPGCTSLTGETTG KSGEAGQDGKPPGD/GPIGPYSLPGSGP GSGESMMG
933	14834	A	940	3	404	LFMFLEFFF*KPRSC*VSQAGMQGCYLK ALQAPPPRFTP/SLLS*DYWSLPPPIA NFLYF*ETRGTGLTRMISIPQPTMPG LASQTAKLIFP*K/HRVLVES/HG*SAR AVHRGDLHILEP*TPGLK*YS\CISL
934	14835	A	941	397	1	FVENSQVANAKKKFLKEAESTTPVLSGI RKQNTFAADME*V*MVWIKDQPSYSIPL SQSVIQ/SRALTLFDCTKAERNRRGKLQ WEPAV\EGSKGWLRFKERSHLHNIKVQ DEAVSYPEDLDKMDAVNTKHQI
935	14836	A	942	441	29	SVTLCKHTVHVPTFLRRGKRCPLFGQCQ PWSPG/PHPLSMSPV*RPQ\PIPLHS APPLALGPFPMLSMAGLFPFQGSGLR NWKPPFPQPSLLQ**HFPKLPKPIRGLR PFPSTLSIPLPGTRPRAKLGVMSRRL
936	14837	A	943	2	397	ARDAAPEPGEHLLQGLSARHGLRPPRDS RPGPD\PP\SPPHPLPFAVPTFVSFG DSWLL*SPFFPAPWASEGGACAPNPHAL VPSPSGQASGLRGGAPSWKAGLDTDQQ AGRQSPGPAPPSPPLPPSQC
937	14838	A	944	3	449	LRQVWHEGEMPNKTTLYHYTPI*ITNI KNTDNTKSLWGCAEARSFTHC/WMRIKM VKPLWETVQ*YLI**KLQLPFNPAVALW \SICPRKVKT/CHRNKTRS*MFIV/A LFVTAQTKN
938	14839	A	945	380	175	RAPAVPATQAEVGG/LH*TWEDRLNPG GEV/CSEPKWCHCPPAWATKPNVSKKK KKKEKRINHQHDEK
939	14840	A	946	21	331	VAPLKYGPSKETI/IQSVRQSTECKKIF AYYPSDTGLITRIYEEL*RLNRKEKLS SVYKYAKDLI*PFSKEDTQMANRR/H*K KCSTSLIREMRFKTTMRVDAV
940	14841	A	947	365	1	GGGPFWFFFFFLLGGFLKIGKIWAKKKT GPSFPQKKKRGPKKKKPPGFFFFF*K GFVAPGGQWEGFGLQPLPPGVKQFFC PRFLRW/DSRFFFFFLIKSNAEQPPTL YAGVRMRYIK
941	14842	A	948	357	137	ISAHCELRLPGSHHSPALLCSPGLSRTP NLKQSSLSPLPKCWDYR\LATVPGQLLL F*ARHCISIDPSLHLNNM
942	14843	A	949	53	352	REDNHKCI RNKMINRKWANEVNRCSFSE EIQMVKKHEKLLASPPIRSMQIKRY\LS NSLA*KKEKSD\NTKLWQGFGETKSV* RYIIN/PYDPTIPLLLGIY
943	14844	A	950	937	3	KVSPYKINIHK*VAFLECTNNIAQKK/M NMVLFITATNKKI/SYLVIH*IKEVKYL YNKNYK\LLKKNRDNANK*KGTPCS*I* RINIIKMSVLPKATYRLSAISLKL*MQL FMELEKE\TILKVIWNKTAHLAKATLT \QSNPGLTLPGLYYKATVIHITW/HCY KNTHVDQ*/NRRESPEISLHFTQLFSD

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						KVNRSKQ/WKNCLSNKWYVESWLIICRR RKLKLYLSPYKKCNK*IKNLTVKLKA KIVEHQKSTVLVTGLWKGFMNTTIKVNA TKIKVKN*HLIKLKNFCTPKET/T*QIC RQORVWNKLFNSNF
944	14845	A	951	246	1	AASTKTGVQTKTCT*MLIALVITVKRE KQSKCSSVE\E*TMWYIHTMEYYSVTKR NDVLIRTTWMNLENSMLSKKDSHKG
945	14846	A	952	2	255	QGCGEKGTFLHCWWEYQPLWKTWV*FLK DPETDIPFDQAIPLLGYPKEYQSLYYK DT\AKTWNQPKCQLMVDGICKMWYIVDA A
946	14847	A	953	343	3	GSIYTKEMEPKVNNLQK*KASCTDGL*G EFY*TFENEIPILYNLFQKTEAKGTLTN SRDEASIIILIPKPEKCTRRKENDK/P/I SLMSIDAKLLNKILAN*IQQSRIYSRHT RLIQ
947	14848	A	954	1	349	AQPPFILFILHP\IYCTFSS*S\R*QKT LKTTFQGFIFCFFFFFK/QAKSCSRIK GRGPPIAKGTPELPGLRDPPTSPT*VAG TKGGGPHQTQLKFIFIAK*FYISF*HNGK FCSRRGR
948	14849	A	955	2	351	GLKNYAKSTLPVLYKWN\KA*MTHLF TAMSTE*FKPTVETYS/EKKIPFKILQ LMDNAPSHPRALMEMYKEINAVFMPVNT ISILQPMDOGVISTFKSYL/RNTFCKA IGAIDSDS
949	14850	A	956	336	3	PTKENFEPDGF\TG*FYQTFKELIPPQT FLKTSREYFSSSSSSSSSSSSSSSSSS SSPYRPI/SLMNTD/AKILNKILTNQVR LHIKRNTTHDLVGFIK\WPNIRKTDQS NN
950	14851	A	957	181	1	RWDLTMLPWLVSNS\GLRRSSH/LPKCW DYRFEPPTA*GWFLIGPHWNVSTVVG PRISRQ
951	14852	A	958	3	293	GGLTSPHVKTYYQATVIKTAWNG*RGVC MDQ/YNKTEPETDPCKYSQLMFSEVTK AIQ*RKDSLNIENWNN*MSIHKSSSR KHLNQYLTPYTKL
952	14853	A	959	350	3	NKKKGQSLVFRSPTLFFFFFL*IEMG\F IMLARLV*NS*RRNMTTSGSQSVGITGV SNHARPKRKLFLFSIITIGWAGV\WWL TLVISALWDYRREPPRAVLLPFHIQRS RMPLSN
953	14854	A	960	349	1	GGFPPPLFFFPF/PPPWGKPPPPFFYQ\ SFPPKKKGGPKPPFFFGSPWGVHKKQFL VKSPLPFFWKKKKPPPPF*KKFFPP\VF QKQPGRVKKPPYERNSWLLGPPTKSPK KSTGS
954	14855	A	961	379	160	PGPQGEPPFFLKNPQKLVGQGGRLF*AP LLRGVRQKNSLNPGGGALKPGS/HLWP PSWGGKGDFLF*KKKKKK
955	14856	A	962	184	2	TFFSPKKLFPFFFFSKFFPKGTFFSR ENFFFFFF*DGV*L\CHPGWSAVVPS RLTATS
956	14857	A	963	1	328	ARLVLS*PQ/CDLPASASESSGITGVS HCASASQAGITGMSHHIRPKWISLYLG FWSFNKNVLHFFCASSLEGESMNNELLS

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						KKNWEFLDKKLHGSTKLGGNHVCVNF
957	14858	A	964	1	334	HPLGGRVGGVPLGP/VVLNPPPPQ*GTP FFLKKPNPNPGRGAKPVIAPRRGG*GKGF LLPPRRG/PSMNPNCPPAPPP
958	14859	A	965	206	360	QKSMSLHQQ*QDIHSSQAHKNSSW\PGA VAHTCNPSTLGGQGMQITRSGDQD
959	14860	A	966	10	332	NFFSPGAPPPPPFFGGGFFLKKGGPPFF* KKKILGGPPPPKKNPPGVFPFSP/AKNL GFP PPPPPFFFF
960	14861	A	967	1	282	RKCAKDLNRHSTKEDIWISTECI*HC*S LRKSTLKPDMPHIY*ND*LYKKND DIK CW*GYGVGAVFHFHWSRMVQPLLNNW TVPRNVKFTL
961	14862	A	968	339	195	FFFCDRGVSPCCPGWSRTPRPKQSTCLS LPKCWDYR/RL*ATVPSLDYLF
962	14863	A	969	3	342	IKKGPHQLKKPPGVFPVFQFKKSYFPP PPPLFNNPFFFR\DKASLCHPGWSAVML SYFTAAYTSW\VRSSSHLSLLSS*EWRH TQPCLEFF*F*FL/CRSK
963	14864	A	970	384	6	GRKNVAGFPLSPLYTPPHGHGLGPPQTF GAGPPAHKSHQKVGRQKRGPGFVPPRP AFLFFFFFFKE*SVLEKKENLYNSLFAY KILNKVQGETQCEGRAHIC\VCVCVCVC VSVCTCVHVCALAIC
964	14865	A	971	427	109	LNSQFELQEKRI SNLENEKII*SEKES KNRMARN/E/QSLRETWDTFGYTNIGIM ECPEGE EK/GKRKRKTIKKKMAANFPHL MKNINLHIQKAL*TPTRITCTGPYGG
965	14866	A	972	389	145	SLQP*TPRLMLSSHLSLSSWDYRCVPP HLANFLYF**R*GFAMLGSSNSSA/SAS QSGGITGVSHHAPVVF TKKKLVADT
966	14867	A	973	170	419	VSFLFFFFFLERQFYFFSPGGGEGGEFG LIEPFP\PGFGNFSCITLW/RRWD*GAP PPLPAYFGFLIK\TGFLVGRGGLDLRP SR
967	14868	A	974	212	3	QNSMIRYSRMSRSLCTTILILSLNRS LKSPR*/WPGVVAHACNPSTLGGRGRI TRSED*DHPGQHGETP
968	14869	A	975	28	356	VFETSLFRNKKEIVKGTSLPDFRTYFKP LIIESI*CLHGIGQNNAWNVRGNLQIDA /ECAENLIYEKGGISIQW/SLFNK*CWS ITIHKEEKKIRPLHCIKIKGTDFKKLS
969	14870	A	976	350	1	LFCKEKVSLLCPGRFEPFGMKKSTLLSL PKMRGYR/RLAPPPQLEIFFHFLT SKA TPL/CLGRSLKRLNSQMFSPPFSEGVSL CSQAGIQWRDFGSLQPAILWFK*FSCPS ILSSWN
970	14871	A	977	4	343	PLHSSLGNIVRPHLLNNSNKNNDITTKCW* GCEKPGFLIHCIWEYMMV*LLKTDWQF LIKPNHLPYDSAVAH LGIYPR*MKTFL QKL/CP*MFIAAVFLIAKNGQLRCPSV SK
971	14872	A	978	3	424	KRMRRQATDWEKIFAKGISDKELLSKIH KELLKLNKKKSPKQVACFKMGKQT*TAH LH*TIYR/CRRVTHRKDHSTRSWLLREL QILNT
972	14873	A	979	114	325	QQQQNN*IKKLAEDSNRDFSN/EDIQMA NK*RCSTSLVIMEMQVKVTVRYXYLTLI

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						SIATIKQKKQNPKK
973	14874	A	980	339	2	GPTGFKFNQGGPPPKGSFFL*KISPPS* NPPFFFGPQKGFKPFFPPPYLNPCKNFF SKKPLFFFF*KKGFFKPPPPPPPPPP* GRVSLCCPGWSAV\A*SRLTVTSTSHVQ T
974	14875	A	981	2	377	QMANKHMKSFSTSSAFMKM*IKNKMRSH DTCIRMANINTNDT\CW*GCRSNKILMH SW/WECKMVQLL*TMV*KFLIKY/DTYH DEAISLLGSIKKSKFCT*/T/CKILYL NVLFIMNPNWKQSNWYSMG
975	14876	A	982	1	457	INEIARNTEKFNKTELTSSSSSSSSSS PLVGLTKRKKSQN\NEGDITTDITIEII/ TIIDYSE*IYA/NKIEQASSSSSSSKT YNLSGPHHEGTESLNRPMSEIEISLSQ NLPTNRSRADSFTGKFL*TSKDELPT LLK\FOKTEQERTLPR
976	14877	A	983	332	2	TPKAGQMQLVLPQYGSKVARAPFSVVAL PEPPFFHFHFCFPQPHCSLPPQIPPPFS RFFLQVKSSQGGPPPSLLGWGEQ/NTLP FFFFF*SHSLALLPRLECSGAISTAA
977	14878	A	984	365	2	KSSKLFNYPPLFFFLKNGFKKK/SGPF FCPFKNFNRVPGPNFNKGFFFLKKG PTVF*IKKFWWGPLPPLK*PSGVFRFFH FLIWDFRDRPPPPPPFFFLVERGFHHVG QASLELLTS
978	14879	A	985	1	153	GVQWCNYSNL*PRFPG/SGDFPTSAFQV AGITGVHHHTRLFFFFVGFFNF
979	14880	A	986	225	1	LYIYRERERDRDRDRDVSHTHLYIHT RTHLDNILECHPGWNAVA*SWFTVALNS WV/KSSSRPSLPSSSDSS
980	14881	A	987	2	375	GTDEYILIALIVMVSWVCLFFFEKKA PFCPPAGKTGANFGLRAPPPGIKEIFW PP*PSEEG\EPGRPNPSRGNFWFFKRG GSPL*PRLFG/HPRP*GNRPP*/PPQRG GNNKGDPPPPPGGIF
981	14882	A	988	55	335	HIYIDVFVSGSWLLTV/ISLLELTVFCY NVGAL*ASG/QASENRISVSDFLPSFY LPKAGL*SFPAFMMMGHKILPEKVIPIH MLEEE\TCTERP
982	14883	A	989	295	369	ILVTRNSEL*VLPEQRTFLEKAMALRS IPLLKR/NGRPGTVAHACNPNTLGGQGG RIKRSKV*DQP
983	14884	A	990	2	240	KKISMNLEHFMLSERSQS*KTTYMIIF T*KLQNRQIYK\TERIYIYIYIYIYL FFFFFLERKFLFLPREGGGPF
984	14885	A	991	463	0	GFRQLSCLS\LPSSWYRHMSPHLANPF \TF*VERGFHVGQAGLELLTPNDSPSS ASQSAATH/GMSHCTQP
985	14886	A	992	82	365	EICHQLYRSFLCSLFC/DHPSNKS*DT MNCVHFTIRLLNFSFFFEKKFRFPQV EGQGSNLG*LKVLPPRLKPFSCLTLLRS WGYRGPPPPPVN
986	14887	A	993	3	317	GLKQSSCLGLPKCWDYRHKPPCPHIF NTH*IIKVLNVFSFCI/PLCWSIALSD HVQ/PV*LYNMLVSSFLLLLLFFIEVV ILACLFPCVGPILFFF*YILTF
987	14888	A	994	350	139	LFRRRLRWEQHLS/QGGQCCSEP*SHHCT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PAWATE*DPVSKIQQKNQDTFSHTFIL ECRTSKGVSAFLAL
988	14889	A	995	219	1	RPRRPLIQTKAKNHHFTPTRMPIKDN NKC*QGCGEV/WN/CRMVQPLWKT/IQF LKMINTLPL*DRAIPLTGGKE
989	14890	A	996	3	498	CLPWAARQPPSAHPFPQPGP*LRTLA PDTATAVNQALQRQES*TCG*SPSGWPA VPTPVAPG/PPSAG*GVVDPRAWPRHNG PPGQHPKEKTYQPVPA*VQLSPTRQTP APMACSSLLPALPPAPAPARPPCPAPP FLPSRTSTLPPRRLSSTIKSKTPPGP
990	14891	A	997	2	419	ADTEAAASYPDNL\ANDESSYTKQIFN VDKTALYWKKTPTSRTSIAREGKSKPGFK TSKDKLTLGLGANAADDFKLKPLTYHS KNSRAHKNYAKSTLCFRN*NKAWTEHLF IAWF/EYFKVTVTNCPEKK/VLLLTHTN APG
991	14892	A	998	388	405	G*FFPLSASKFFFCP*ALKLWMEGCHIR PPPQVRFLQSSQA/GFISASLKGKGF ASMPANIGPPKGYL*PAPPPFFSFLRQ SHSVTQAGVQWRNSSLQPPPG/LRRSS HLSLPGSWDH/MPPCPANFCICTGG
992	14893	A	999	1	423	WILHD/NLRQPAQWLDQEAAPKHFPKPN SH/QKKVMVTVCWSAAGLIHYSFLNPGE TSTLEKYVQQIDEMH*KLQCLQPALINR RGPILPQDNARPRVTQPMQLRLNKLQCD VLPHPPYSPDFLPTDYHFFKHFDNFLQG KHF
993	14894	A	1000	2	406	SDLFRAI*ETTSVIVYDVSM DYLEIDSE MIRDLLNTFPV\HLELQQDSSGVIQAG ITEASTINAKEIMHLLMKNRQRTQEP AANQTSSRSHAVLQVTVRQSRVKNILQ EVRQGRFLMIDLAGSERASQTQN
994	14895	A	1001	290	3	VTQLPETVPHFLDRVSFCCSGS/DHSS LQPQTPGLK\YPPTSAT*VGGTCHIAQL IFIFLRDGS\SVAQAGVQWEDLSLL*P PPPGFKRLSCLNR
995	14896	A	1002	143	408	IKKKIKREI*KYLDISKNK/DTYQNLWN ATKAVL*GKFIGINVIYFKNRKN*NK*F NSTSGKLKLEKKEQTKLKISRKETIKI RAKINE
996	14897	A	1003	84	409	DKLAALPSSWTLHPGSPGLVTRAPPPPP PPPPPPPPRVLEPVPRSLYPGLAVPVV PRALH*PPHPGSLPACAPGILLGGTRQC S\QTILPKKKPPPLDADPANEP PPP
997	14898	A	1004	392	2	EKNAVHFDQKNLVSWEPLQVPTQVCTIQ NKTNSWGIAGYFFHFLKRNQRFNALKV PGPFSK*TIHLVNLKNLFFF*DRVSFCC PSWSAVVKS*FTAASL\IKQSSCLNH PSS*DCRHTPLLFFVRMRS
998	14899	A	1005	2	421	FVSLLLITSAIVAAGAPTGRVTYPPLS GNYFHPGAFVHLTIFCLHLEGVSSILRA INFIASIIISIIPPAITQYQTPFG*SGL ITAGLLLLSVPLAAGITI\LLTEPSLF TTFFDPPGGGDPILYQHIF*FFGHPEVY
999	14900	A	1006	1	428	DIHYG*TIIRYLHADGASIFCICLLHIG RGLYGSFLYSET*SMGIILLATIATA IIGYVLP*GQISF*GATEITYLLSAIPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IGTDLVQ*I*GGYSVDSPTLTRCFTCYF ILPVTIARLPALHL\LFLLTGSNKPIGLAS
1000	14901	A	1007	1	419	SPIVPIVMAMACMLLTERIILGYIQLRP GPNVGGPYRLLOPFADAIKFLSKEP\LK PATSTITLYISGPTLTITIGLVLTPLP IPNPLVNLNLGLLFILATSSLAGYSIL* SG*ASNSNYTLIGALRAVAQTISYEVTL
1001	14902	A	1008	411	27	GQPGQHRKTPSPLSIFYF/ELAGGGDAS T*FQLLRRLR*EARLSLGI*GCSEL*LP PCPPAWVT*DPVFGGRKKKERLSQLRK LRPREVKSLVQHYVAHKGNWDPNPGPM ATQPGRSCTTLCVPLCHR
1002	14903	A	1009	21	377	MSLGGQDQSAQTTRSPQFAGFFGQRSIP DRITGLGFHLGVCKVCACVQSVCKCVH MCACACMCTRTMCECVCQVCEVCVQVCR VSMCVQVCACVRVCACVCSGACG/CTCV T*MSLACG
1003	14904	A	1010	1	412	HKANTSTYLLTLVNTFSG*VRACPTTHK TAEVVASTLIEQIIIPRF/GPAFISKIVK QVTTTLDVNWKLHTPYHPQSSGKVERAN SLVKQHLIKLALKTRQSWVTLPLPALAW LWAAPQSPGTGINPFELLY/SAPLPLSN
1004	14905	A	1011	1	410	FRAVAGASRQENGA\TVILRDIARAREN IHKSLAGSSGPGASSGTSGDHGELVVRI ASLEVENQSLRGVVQLEQAISKLEARL NELENSSPVHRSTAPHTQOVSPAPVEP PAEKPATPT*DDVDDIDLFGDRND
1005	14906	A	1012	269	32	NISRIYKELLQLNNKKT\SISKRAQYLN RNFTKDI*MAKKPMKRCPTLLVIREMQI KTTMRYFFTPARMATIKKTDNNEY
1006	14907	A	1013	21	443	RIRKNSYPHYVKSIVAYTFIIRLFPTT IFMCLDQEVLIISN*H*ATTETTQLSLSF KLDYLSIILIPVALVATWAIQFSL*YM \NSDPNIKQCLKDLLMFLMTILVLSTAN NLCQLLIG*EGA*MISFLLIS**YARAD A
1007	14908	A	1014	1	309	SSRAAAIHGGACLWLQILHRLRWEG*LS VGGQGCSKP*LHH*TLAWATERDFVSQK KKKKPQKANP\HLETSCKKKKKPMGLP PKSQRKEGPKAPQGRTLWP
1008	14909	A	1015	3	256	EKNQILKWTMDLSRHFSKK\NMQVGNRH MKKC*TSIIIREIQIKTMMKYHFTPVKM AIIWPGAGITGMSHRTQPSPTLLTHVVA
1009	14910	A	1016	397	3	LEFSPPPKWGFFFFPPPRFFAPPPFFFF PPPPFFFFFCEKPPFFFFPPGGGAPPL SPPPPPPPPPPPPPPPPPPFFK/SPPPP PKKK*KKK*KKKKKTPNTPKKKPKKPK KKKKRAAARDLELVGRVGRV
1010	14911	A	1017	2	164	EKERRE*KREE*KERK\RKEGEREGGRE RERERKKRKRERKKDRCMFIVHFRE
1011	14912	A	1018	1	406	NSSPPKNKN*NK*QOHT*EKNFANYIS DIELVFRITYNELQLNKTGNPIKNSF*K NQFKNKGK*PNFYITQSF*RNKPI*KF/ AKDLNKRFSKED*IANKRIKCTPLA IRKRQIKTTVKSSFKA/IYMVVVKET
1012	14913	A	1019	302	2	IVEPLFLGWLCLFLQNRVKGPGPYFSK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GKANPVVFPTV\SKQPFKKPAFPVYQKQ LPLF/PALVDKKKVL/RFFFFFF*DRVLL \CCPGWSAMVQSWLTSTTS
1013	14914	A	1020	47	382	AKIALHSSSLGDRVSHTHIHKRSNEI ELVIKSSPKKKSSGLNGFPIEFYCSFK* ELIPIFLKLFQQ\VEAVGILPNLF*EVS ITLIPK/PRQEQNSNKTIYRPISLMNIG GK
1014	14915	A	1021	273	1	QSKERRQRTQOEMGKTFHNNRENGTLFG FSQSCLKDEIIIIIFETGFRSISQAGVQ W/P/NHGSLOPRFPRLKQSSCSFLPSSW DYMC*LPH
1015	14916	A	1022	327	1	KFLKGWPIYLKKGFPFVPGGGQWANYR SLVPQIYGVK\YPSAFASKINSTMGMC PAWVTFGMAQLINGD*IF/IFFLRQSFA LVAQAGVQWHDLRSPQPPPPGFKRFS
1016	14917	A	1023	3	407	THLTQR*/HNIQTPP/WV*TGTLSTVLM NFYLWM*FHFQSITLFLRLLTTLTMY QGWLDTVQORSYQGHHTPPVQKGLRYRI ILFITINTFFLEGLF*ALYHSSLFPTLH *RGDWT/PTGIPLKPLEDPLNTFE
1017	14918	A	1024	3	425	LPPQKKRGFPKIPREF*KTPPKKKKI FPPPGKNWPPTK/RFLKGPPPSRFIPFP FFPLSSSPSP
1018	14919	A	1025	430	1	GGFPPFPKNNFFPLSP*IFG/RGVCBK FPPPKKRFFSKNPQRGFNNPPQKKKKIS SPPPVNFAPPRDLLKRPPIPPPIPPPI FFFFFLFMHPSFPTSVPQWQITSFLCLL LILQCCVCVLIGMVVDQSESSPSHHLQ PRWL
1019	14920	A	1026	463	494	RKTGFPRLT*HLDLDFFFFFFFWKGIFV APRAGRGRNLG*LKPPPLGWAPFSGLT PPKSWN*GAPPPPPNF/CVF*RTGFP RLTR
1020	14921	A	1027	606	1	AGGPGPPKVVPAGFGWG/SLNG*S*LKG KSGKGAIPQSGPTVFPGGIPPKESPLR PPGGMQRRGPRWPGASGC/VG*DSVLR QP/GVTGEAPCPGASSPQASQAARRGSM GKGGAHSVWGGCVLSAAWPGWQPPGSH G*/PGRGGQSGCSCPKG*AWWRPCLAG SHSSAKHKGMSSEGPAPRGRAISPVSA SIGPIAARGF
1021	14922	A	1028	436	1	GGAPQGVLKRAAPFFFWKQNFNFVARI IKGKGVLSPRQFPPLGFKKFWGPTPL/ SRWGFKEGLKPPGSGFWFFKKRWGFSMW RWV*\IPGPKEL\PPPFQSGGIQGGT/ HRPPIIPPSLF/CFEMETHSVAQAGVR WRDLGSLQPL
1022	14923	A	1029	1	436	PPKKIIFSPKP*IFWGGGGPNFPPPKKS FFSQNPPGVFFSPP*KKKKIFPPPPENW GPPKIF/YKRPPPIPPPI
1023	14924	A	1030	28	366	EDHLSFGGWCNEL*LCHCTPA\WRQNK TLSPKEKDHK
1024	14925	A	1031	3	142	FDCSALQEFGTRLYCPSWSQIPELKRCT HLSLPKCWDYR/R*ATTPGLRIVLELQK KLRR*CRELLYTTPRSVTPNINDI*HWGG TFVTINEIISIH*YIALAGLRLSSSDV LTSASQNVGITGMSHTWP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1025	14926	A	1032	7	361	PALRPSARGQQYYDETCKNTLCRNAQND SYLPDPNPFSSRFSTL/DHSWHQLEAPDA *KAPFGLYWNCGARVCR\QGISA*TEA CGLGTIKPSFFLIPLKQGBLLGYPAYNE NLKKKKKK
1026	14927	A	1033	472	3	TKQQMLNVDRTAFYKKMSRTTFIANAEK SMFGFRASKEG*LLGANTTGNF\LKAML IYHCKNPRTPKNEAKSTLLVP*K*NNKA LVAHLFTA*FTEYFKPPIEIQIITADN APGHPR\MYKEMNVFMSAN\TSIL*PMY QGIISCRIPAARIEVKGA
1027	14928	A	1034	488	0	PLR*ILAQRSGTHSMKT*SGEAAAE*KS EARSSWFLRFKEKSHLHNIAQDKAAST DGKAAESYLE\TD*DGNTK*ICNGDKT AFY*KEMPSRMFPAREELMPGFKASKDM LTLILLANAVGDVNLKPMIYYTENPRA LKNYDKTQLC/PVLYKW
1028	14929	A	1035	114	491	NYFKNFTFSNKITL/CLL*LFLL*KLFN F*TF*LLC/I*HLA*NTNTLYSCTKIFS FFIFLFYKHFLKFIYFFYFLDFII*GAY *SLCYY*VVYFSCQFCQVLFHVFVWGLCC HVLVRLLYFQTDEPFY
1029	14930	A	1036	114	496	LLRAILTYLKYKISAMNLVSA*FIYLHL TYHCVF/DHPVQGR*LLNK*INELFCYR SFGF*WVFSYSHLSED*ALEEKYLRERS RWVK/DLNVTSSETVKILEEILGKTLLDI GLGKEFMMKTSQANITKP
1030	14931	A	1037	381	45	KNRGRKKNS*LGGF\SDKFYKTF*KLIQ IYKLFQKNEKEGTL\*NSRPISLINIE ANIQN/RAVLAMIIQKHKKIIRHNQVV F/IPGR*G*SNTCKSI\NVIHHIKQRRRI KSIEF
1031	14932	A	1038	134	394	SFCDKFTNCISESLCQ/SYSPTYIIKIF VLFKIRSGSITQPGVQWHDHSSPQP*TH SWAQTIFFLLSSQVVGTKGMCHHTWL/IF LFLFVF
1032	14933	A	1039	483	30	YDGGSEIINYVLESRLIGTEKFHKVTND NLLSRKYTVKGLKEGDTYBYRVSAVNIV GQGKPSFCTKPITCKDEL/AYVSTTIYT SETCTFVDL*DINKNDLPL*LQILAPP



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						AHTISQEKETKKIQI*YKEEKLPLFTSS SLFI*VKNLMEFAKKLLELINEYNKVER YKINIKNILLAKNTWTLKF
1036	14937	A	1043	50	457	TKYQLANKNMKICSTLPITRE/MQIRPH EISLTPIMMALSEEQKNKYWGSCREVE TLVHCWW*CKTVQSLRKTVHRFPK*LKT ELP*ELPPK/PGSQORDICTPMFIAALFT IAKRFWKHPKCPSTDE*IKEMWYIQS
1037	14938	A	1044	2	469	LKQSSCLGLPKCRDYR/R*ATVPG*FIL *NTTEDPNLTKN*ILNTNH/WCYSVQLI LGESNSTIKTSLSFSQASSHQNTTVQFL STSPSFKNCQWLAILPRK*GLTSLSCFA FERQGL/NSVAQAGAQLHHGSLKAQPP RLKQ/FLPNCPTLMCECYRLQP
1038	14939	A	1045	42	200	LICT*MLIVALLVIARNWKQIRC/SST/ DEWLNKLW*IPMEYY*AIKEPTIGTC
1039	14940	A	1046	475	36	LNVN*LNHPKIKRQKLAG/YVRKHDPTIC CLS\QQSRFIFKDTNRLNIKGWRK\TFH ANSNQKIA/GVAVYVSNTN\FTRNKE* NYILIKGSIH**CIIIIINICATNS*NLK I*NKLTEMKKEIHCSKITVED/YNTLF* TMDRQKEFHRMQ
1040	14941	A	1047	3	326	FFFFIIIIIFETERDSVSKIIIIKNNKK DLF*FLVTQVTPEITNQYISTLPLQSKT KWDRPGTVAHSCNPSTLGGRGRI/TLR SGVRDQPDQHG
1041	14942	A	1048	403	15	EVKNSSFSYRLMTEIMPGYVSKLYNCD SGS*LS*SFNVCKMNR*Y/LEERGNTS FKSILLMLWKLHSAIFSA*TPRGL*I YFIYMYVLETSWHSVAQAGMQWHNQSL QSPSPGLKEFHRTDIVYAR
1042	14943	A	1049	25	457	YMWNSHHSCMFTLLDFSSFPPLSLCFI LRSFLFLYAEPLAFLLVKDSFILFV*I MSVFHLILKLQ*NINHYFTILTIFKCT VQWH*VYSHFSVAKTAT\ISRTCLIPSS WDYRHMPCLANFFL*RQGLALLPRLVL TSWLQ
1043	14944	A	1050	14	478	FEPCYCRH*TRWN\CWGWYELVQSLWKA TEQYVLKPDICVF/LEPGVSLGMYSK LCTLC\YQKTRMFIAITLFAVKS**LPK SS*MVE*ITKL*YFHTMEYYTAM/KNE* ITI*TTIWMNI/TIILNERSQTQK
1044	14945	A	1051	2	465	GIDQPSKPIPL/TQSFTQTKA/LTFFNS VKAERGEAAE/ER/VEASSD*FMRFKQ RSHLNHIKVEGEAATADGETAGS\SYPE DPAITDEGSHTKQQIFSVDETACCWKIS SRTFAAKEKSMVSVKASKDRLTLLRAS AAGDLKEFPRLV
1045	14946	A	1052	392	24	DFAPRRKKRETRRSKINSLS**KELEN QVKTNQKGRKQEIITIKIVELREIETLK TFPKKKVNKSRSWFYEK\INKLDGTLAR QINKKRKENQ/DTIRNNKGDIIIDPMEI *TTIRGIPPLWR
1046	14947	A	1053	204	488	CAVCYTQISLTEWVDL*SLDPGFETVSH LFDRVNQ*DCRRVTDMLMV*NLHFVI LFFLFWF/DFVFLVLRQSFPVVTQAGVQW RDLGSLQLPPG
1047	14948	A	1054	498	2	SVVVCLFLSPGITSHTYVPMIFKIGAKK

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						VHWWKSILFNKSCWRNLSTCIRMKVDP M/LTPGKINTNWKDLTPSAESIICLK ENIG/THFHDIRLGNFWDMPKA*ATK EN*IPWITSK*QT\FCAKNTVN*VKR* PMD*E/RIFAKHISEKRLICVIYKEQLE LN
1048	14949	A	1055	28	209	IDGRSRGLWW\CVVLASQLLWEAEAGGS LEPKSLRLQ*AMIM\DCPPW
1049	14950	A	1056	163	479	TSFLGSQSAGITSVSHCPREVFFLKLI HWRQGGQVALLVATPHSPCCPQYRLAPI PRARHDFACASLIFVCILLVHVLMPRS VAGRGVGSLLG/CQAGR*L*TC
1050	14951	A	1057	2	1258	ELFPWHFQPSRAASLVAKAIRDKVPGT RRWPVPTDGRPEGFALSEPHHSLHGRH QGPERCRHMAASP*EAGNK*PKDKDGH GERTETAAGVHTGCGGKGPAAAGGR*AQ GGSGEAGAAAGGAGAAVGGAGAAVGGSA GGRWPAGLLGQHAGAG*GEGPCRQHGPPP GVSAGQAASPAKAGQPGPGT*GAAGQP GRG*GPAGPRGGAAERAGAGAMPAGQP AGAAAEPAGEARPGAGDYGPAANHPGA RTGAGGAEGAGAAAGGLPRPAQHR\AQ IHGPVPLGTGGRSSS/GGIPDNMSHRLW QRHRSHGEASAGQRHPHPGPTGGER\GL QSMLSKIREVAQQGGLKVGLRGRALGDO EEAPIQQQVFRLLCPGNLWR/RPPHMRP *AVLL*NIFHISRRREDVMDPMPSSPIC PL
1051	14952	A	1058	2	437	ERSVRTACCKQSRGLSSLLCPPPAPRLS *TGSPVGTSSALEPRSPHPQP\PSLRPR SPGPQPLHPLGPRSPSPSEQTVP SHPA RLPSLSPERTQG\PKAQ*SQLPPPSLAL AQPAPAVGGREEVASPACPSWKDKSRLR AVPGSA
1052	14953	A	1059	47	456	TRCYGTLLRLDAPGKLWTRKM*VVASTY ARTDRKSSASFRPLLPLPRGFQLSLHFS LTSPSCLAFSANTHRGLRGENYHITK/C DMPKV/HN*TAQAVVQWHDGFSRPPPP GGRSSCLGLPSGWDYSPLWHHEQIL
1053	14954	A	1060	484	13	FPTSASQNTGTTGVSHQAQPIIF/LFVE MGSPQV/GPASLKLPTSRDLPTPASRAA ESVSAHHH*FLNFL*RWASGFVAPSW* TFLL\KQSSCLSLPVC*DCRCYNHAWP HSVFSSQFLSLFPFNFSFLFFLSFSFFK DRISLCRPGWEFHQTVQWSR
1054	14955	A	1061	1	494	GSPGHPVCGRRRSALNPQGQPCSLQPGV VSGATGAIVRVQRTSSAWATAAMGAYV E/TTRFRYT*KAGVGCRLWGAWLKADG LGETKAEHTLHDG/PPEDALYGLIEGDD TNFTIQGEVVHCWYTGTLPDGTVFDTNI QTSQAQMM/NAKPLSFKV/GIGKVSH/G WDE
1055	14956	A	1062	3	395	SDPSPCGGIRFDEMEKFLFNLYNPKLKE /DKINDPTFVK*IGSMKIFHTVEP/PS HKCFTSEFY*TFKE*IAPISHKLF*SRG IMGTATPPVMFHLQENVIPK\PTTEKK*T YRPVSLMNIN\KILNKILTYK
1056	14957	A	1063	402	260	WYCPFKV/LLRFSVSSPPEVWAVGSIK

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						AELYMLRPLFPRTREVD*IF*ICPV/LK GSPKNKDFCP*GAKTFEYFYPATLGLNL KI*IFRQRW
1057	14958	A	1064	66	379	EFGRGCGEPKLRQCTPAWVTEEDPVSGG KKRKRKEREKT*REPSVSRPESH/PPSQ EAFWVQALSRPVLNPNFISGRSASGLGK SEAIKSLFLYLAVCSTTEEQA
1058	14959	A	1065	223	437	KSCMSCDSNKIFFLRQGLSCSLTQAGVQ WHYLGSLQPLPQGP**SHLSLLSNWDY RR\PPR
1059	14960	A	1066	414	65	NKSPDRNELAS*KCTQ*THTSIARDFFA KTIQWGKNSLFNIWC*DNWISTSKRIKL DPYIIPYTK\TNSKWIRDLHVAKTIKL LEKNGPGAVVCPNPSYSGGLLEARSRLR PAWAT
1060	14961	A	1067	418	1	LWVFFFSRQSL/DSVAQAGVQRCDLGSL QPPPPRFKRFSCLSLLRSWDYRCRPHV ANFVFLVET\GFTMLARMVLNS*PCDLP AAASQSAGITGVSHHARL*FCGF*YIHR VAQPSSQSI*DDHPIKKFCIL*QTPPFR S
1061	14962	A	1068	24	440	EV*NLYSENYKMLLKEMRGDLNKKWSIP *S/WI*RLNIVKMAVLPKLIYRNLPI RIPDEFFVKSTS*L/CKFIWNCKRLRIA KTIF*K*RTK/SGDLILTDFKTYKTMV IRTI*Y*QKDRCID*WDRIES/PEMNPY IY
1062	14963	A	1069	442	26	LRNQVSTPSSKTPRFFFFFLKRQTGAQ RHNHSSL*PRTPLGLKQPSTASGVSRTI GASHHTPLIFFYFFN*GKEGWGCSCFV AQAGLQL\RLQMILPPQPPLKCNW*RHK PPSLTYPIFLKRT*SCFSKEKATRIPP
1063	14964	A	1070	294	46	KNKLKRKERKENNKKKAKINDIKNKSML EKIHKDKN*FFERNNKIDKLLATN/RIT KKTQIVIFMKNKIRDIITYPTDIKNVKR
1064	14965	A	1071	141	469	PKKQGVQLTQNAPLPFRVGGKRGCPKK KKERERDREIISIIIIILKLPKKTPGP DGFTDBLYQTYK*LTSILLKVFLKKRRE CFL/PYSMDPAVPAIALNPPP
1065	14966	A	1072	49	472	EFQIIKK*NSFFADTEKALVWIENQNSH NMPLSQSLIQSKALTLENSMNAERVGKD AEEKLEASRGFWFMRFKKPS*HKVQGE AANLDVEATASYPEDLPEIIDEGGHGKQ /QIFNMDEIVFYWKMPSTRFPAREERSM PG
1066	14967	A	1073	82	419	LTVGFRRETRSSSWCSSSPKRALHALRF TPALKF*FFFWSFSRLFFFLDRVLLC CPGWSPTLGLK*SSCLGLPKCNW\RYE PP
1067	14968	A	1074	1	407	LEDGFFKITQSDRKEKKRI\KKCK*NLQ EVW\DYVKHSNLQVIEIPE*EVKCLLENL FEEVIEANI/PHLASYLDIQIAVQRTQ RGYIARQTSKPHIVVRLSKVNMQEKILN LPKEKHLITYKGNSIRLTAKPSPKPT
1068	14969	A	1075	3	396	LHAYHIVKLSP*PLTGALSE\LLMTSGL TM*FHFHSITLLILSLLTNTLTIYQ*WR DVTRESTYQGHHTPPVQKGLRYGILFI TSEVFLFAGFF*AFYHSSLAPTPKLGGH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WPFTGITPLNPLEVPLNLS
1069	14970	A	1076	250	47	VAACQNAFCFTSCYWL*NLICRK\MDLD ISLLP*TKVNSRWIAGFNVRALTIKILE ENIGSAFGNRHSQ
1070	14971	A	1077	2	393	PLTGALSNLLNSGLAMRDDLHSITLLI LGLLTSTLTITYQG\WREVTOESTYQGH TTPPGQEGRLRYGTMLFITSEGFLYTGF* AFYHSSLAPTTLQGGHWPPSGITPLYPV ESPLNLSALLA*GVSI
1071	14972	A	1078	2	500	LHVIGVSEGEEN\GMKQNKIFEEIMGN F/PNLVKYINA*/IQEQ*TPNGIHLKK TVHRYIIIFQLVRTNNKERILIVAREKWH GIFGGTML*MDDDFSSEFIKARKIEMMF LKYKRGISSAKHC*SRILCVAQISFVS KG/EITTFSDKRKLRAFIISRPAHRNAK GK
1072	14973	A	1079	419	1	LRWSFALAAQIVRWRLNGLSLQPLPPSS SNSPGSWRLQ*ANTAPLRSSLGNKNETL SQKKRK*KDNSEWEKIFANHASDKGLVS K*IKNSYNSITKN\DI*KWTKYLNHRHS KKD IKMANKHMKRCSTS
1073	14974	A	1080	468	2	KLPPPRGAGSSAP/PLFFPPTKKGFSP PPP*KFFFSNPLIFLGGFFPIFPPPKK NFFLKNPKGFFFSPP*KKKKIFFFPP*I FAPPKFFFKSPPPLFFFFFFFFFFFFFF FFFFFFFLRTGRTRGRTRGRTRG
1074	14975	A	1081	467	1	PTYKFNAIPKIQ**FFKKIENCILKFL /WNLKEPQIAKTVLK*NKVEGFTLEDFK \LTVTKTVWS*HKDRHRDE/WK*TESLK IKPKYDQFFFFFF*FSFL/HFF*YLTYSQHHKLI FNRMPKPFNKERLFNK*CWEN WISICKI IKLDHYLTPYTK
1075	14976	A	1082	387	3	LKQPPPHKSFVKNKNGVSLCCPG*F*TP GLKRSS\HFDLPKCWDFRCEAPVLSLLN NIKL*L/CGRGLIKPQPF/SVK*K*AP SWSAHLAETFFFFRQGLTLLPMPGVQWH DPGTVQPQTGPK*SSHFSL
1076	14977	A	1083	2	435	FHPPTNWGGFSPPPP*KFFFSKALNFG GGVGPNFPPPKRFFPKNPRGGFIYPPL KKKNFSPFPPPLKLAPRV/SFKRPPFF FF
1077	14978	A	1084	447	47	PSRKFFFLAPPKRGFFPPFLKNFFFP L GGLFFG/RGVFQFFPPPKGFFFKKPRG VF*PPPKKKNFFFPRENLGPPGVFLK RPPPPFFFFFFFFFFFFFGRRFVK
1078	14979	A	1085	438	2	AKNHPKGFSPFKKFSPPFGGGGIFIRGQ L*KSFFFFFFKPKFLV*KPPFKIFFF/I FFFKQRLAL/CPGGNGKVPQGPFFIF FSRVGKPLFENPPKNWGKKNPPPTPGKI FFFFCFFL*RQGLTTSRHLVLNSWA*A ILPLQPPK
1079	14980	A	1086	43	265	IKHKLEYIKIKNFCASNSNR/TERQPM EWEK\MFANLISDKGLIPRIHKQLL*LN/ TKQONSPI*KWVKDQLQWPYL
1080	14981	A	1087	11	412	IASGLHDFFNKKKKKKKKGGGPKKTP GGPKNRGGKKKIFSPKGGEKKTGGGFL EKNPFLGGGKMGQNP*PKKKPFGEKKNF *GERGEKKPKFPGGKMSPSQE/NKAP

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						RDDPRPPE
1081	14982	A	1088	2	292	RSIPASADSSSLVAASLAGVRDRVSTCW PGWS/AV/VQTL*SARLGLPKCWDYRCE PPCLAEAPSFMRSGKASCTLETVWEDKH KYEEAERRFYHEAT
1082	14983	A	1089	376	3	HIGLYIASCKTLLKEIKGS*IDILCSWI ERLNTVKKAILLKLIIYGFNTIAI/KILS GLFIETERMILKITGKCNRSQNTANTILK PNKVGRLALPNFKTYKATVIQTWVSWH KDRWYGFFCVPQTQI
1083	14984	A	1090	277	407	QIKAERSHHKQITSMRNVKHCSSSENYDS *RKPAPGYIIIK\F*K*LKRKILNSGR LKNRPIKEE*RYAYQDISETIKVRR*EN DIFKVL\KEKKSQPRLLYPLKIS*IEV KYFFDKSKLKEVITNRSVP*EMLNIVLQ /INYSPTYEP
1084	14985	A	1091	421	2	GHPGVLFKG**A*NEKSL*NCSFFNY*S SFSNMQTRIKNV/WPSTVAHACKPSTLG GRGGQIT*GQEFETSLANTVKP
1085	14986	A	1092	369	3	FLKEIRSVTPVNT*ENLIAD/IGEKVLV VWIENQTSNIPLGQSLIQSKVL/TFNS MKTER*/EKLQKFEASRGWFMRFKERSH LH/NIKVQGEAESADVEAGVYPPDAKT IVKGGYTQ*QIFNVDV
1086	14987	A	1093	71	506	FAEDNGL*LHPCSCKRHLAVFYGCTSF VLTFGL*PWFLTQS/FLNPLEFS
1087	14988	A	1094	118	385	SDLGKDFMAKTSKAQAATK\IYTDWYI KLRSFFSAQ*TKQSTE*RRQSTE/WKEK IFADYSSNRGLISSRQETQTTQWLKKIN KNALCTL
1088	14989	A	1095	419	1	DAKIPGQMVAR/RIPRPIKKIFCPDQVW FIPGMQGGFHIGKSINVAPHIQMG*KSF NNIQHPFMI*KKKNLSTGTTHEGDITQH /R*MLHEHTTNAILNREKLKAFPLRTGI RQGCLL*PLLFSAVKT*P*AMRQEKEI N
1089	14990	A	1096	34	464	NSSKKEKRKIPHDGLRLDMPKT*ST NGMMD/KDFIKIK/FCASKDTINKVKRE *EKLQIIYL/DKRLVPRIYKDSYYPPIRQ LKKWVNNLNKHCFKEDTQIANKHKECS T\SIRE*QTKTR*RSHFISTRVTKIKMS G/N/NKYWQGC
1090	14991	A	1097	458	28	RIKVDLMCTHNFDSLEEMNQFFKKS R*NR*FE*SYNH*RN*IHNKVSXSS GPDFTGEFYQTCEEELAPILQNLFPQKM ESIRSNSFYKVRITLIP*GDNGS/TKKE NYSVVSFMMNLDAKVLILAN*I*VFIK REFH
1091	14992	A	1098	41	500	FWIRHFLSRHKQRKNR*MDFIKIKNLYA SKDITVKEVKR*ST*WENYFQI/RMFDTG LVRVYKEFI*LSNK\DNHI*QWGGKAV SRGFSKGNTOAKKHMQRCSMFFVIRKM *I\KPKMRYHFTPSSMT*EKNKDNTCFK SDGEYGILIIYYWGI
1092	14993	A	1099	1	484	RRAPFFFFFKRSFFFWARAP/LQWAF GLVQNPPPRQIPPPGLHPF/SCPFPKK WGYKGGPTPGKILGF**KGGGPRLNKK IFISRPCDPPAPT\QKVGIGGGTPPPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PFFFFEMVSCSVAQAGVQSCDLRSLQAL PGFEEQFSCRGMPCLKWIGSHSPSPH
1093	14994	A	1100	144	260	ILILDSALGHPEPHEFNTKGIEVVYLPL NTMYIIQPLDQ
1094	14995	A	1101	265	457	DPAAPLLVITYTREI\*MYITKRYTAALF IKTKNWK\RPKCPKGE\*INKLWYICTM EYCSAIKNE
1095	14996	A	1102	387	40	RLRADILRLVYNNFLQRLKKQRYLFTG PQYRFLFLELWLCVCVCVCVCVCVRANF \*IISRDKVLLCCPV\CFCFLNPPCVCVC VCVCVCVRACAIINKLLVETRSCSVAQS GLR
1096	14997	A	1103	465	208	QNMTKTFQDYRPISLMKIYARKQQYRYR Y\*RMLHNYQMGFTLGLRGWFNI\*K/SII IHIN\*\*EKKIMII,IESERAFDKC\*QSL II
1097	14998	A	1104	57	250	MTCSRMQ/RNIKLLRYKSEKL\*EENSTS RNEITILSEEDSFTNVKLEN\*MKTVKQK KTSKKTGVYKMAIKKQISEFKGKTSNF Y\*EQINT\*EKKNFKENWSL
1098	14999	A	1105	2	378	YVDPQCGGILKGVLKGFTISNEKANP GRGSPSSVSKD/L\*CQNIKTIESKKTCL IQKLJKVKAIEYERESRKTMEIINETK/ SQFFEKI/NKID\*/PLARLTKKKKKTQV LKSEK\GNITTNHTEIKRV
1099	15000	A	1106	291	1	VSIYVSYNLDSCKGQIRIKSCDDQYIFK RLYFFEITFLKFLN\*K\*VLKKIRDNVLL C/YPGWPQTPLKQSSCLSLPSSWDYRH VPLHLAPINYFLW
1100	15001	A	1107	24	397	DIDHVVEFETVIFYHVGQAGLKLTSDDP TALASQSAGITGVSHRTRPSSGHFNTP EPPEASSLSSHPKLHKSPVT\*NGAGL/Y GSSKLLSCVLNGPISLVHSTLRLRKGGP QGNISQISLMAPP
1101	15002	A	1108	64	414	AQLTPTQPQGRAALHKGHV\*RKTAPTCL FMAEKNAASFFLFPFSPICINKE/HFK KKKKKKKKKKKKKKTRQKKKKGPEKPR KQPGGGLLISKILVAPPPGFLLTREGP PPIFF
1102	15003	A	1109	62	475	FEPLFYLMCLNLNLFPLQLPRHPFLFTV DLVNTWGCPLPSSPQ\*EWLLAAPHRSTP PPLSSGFPARRQLEPGAGARGP/HHTQA LHLSFFFVFLRRSL/DSVAQAGVQWRGL GSLQPLPPGFV\ILSSPLSLPSLT
1103	15004	A	1110	76	477	EEWKKLYRWRENISNLISDKELTC\*IN/ NQTFNIQPLKTKNPTKDVNDLKTFTNED TQKYTYIHQ\*R\*SHMKR\*SP\*LFI\*KMQ MSTALRFLYPPITMDRIQIPENIKFWRG CGILIHWS\*TRKMFHSL\*KAFWPF
1104	15005	A	1111	1105	3	KEERSETLAKGLIAAGA\*YN\*KEERSQ INNLTLLHLKGGKKTNDKPSKR/QE/I\*Q IRAEISRIRPRKKKEKNNEFVFLKINKN FKTHSYIKKKREISNTKIINKRGDSTTD ATEMKKITRD\*CEQPSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSPPKKKIPGPDNFTGEFYQTFQEEL MPALCKIFQ\*NVQKPEGDI/PNPFYQVN IYLVPEPDE/QPFVIKTLKELVIYGN/Y

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						L/K*IKIIEKLTANIILNGEKLKSPFLGSGIR*QHLFLPLLFTITVLEFLLRISQEKVIKRMQIGKEKV\KILFTDNRM*WV/ENP/VNSQNIQKIMKFNKVSQSGYSNTHKSVAFP*TNNEQSANKILK
1105	15006	A	1112	37	466	DRAAEFPPTENPLELISKASKVEEFNVSIRQPIVFLCISNKQLENEILKIQFH*/PISVASKNSKYGGINLRKYL*DMHIDNK/PLNKNRGGGLCSWSATSVLPLKIDNFSAISGNYSRFFFFGIEKLNLPKPIWKYK*VRVAKTVSY
1106	15007	A	1113	33	436	PGLN**CWKNRISTCKRMKLDPNLAPYTKITSKWIQDINIRPVTIKILKENRKGGLQH*MQQ*FF*I*PQKQE*TNRTKSDFIKTAQQRKQONERQSVWEKI/FANQISNKELLSKIKFRLLPLDNNKQLT*KWA
1107	15008	A	1114	2	391	PLTHSRMAIKKETK\NYKCWQ*SGGIGNLGNCW*ECKMF*PLWKIVLQFLEKKRNTELP*NPLIPILGIH/YKRNVCIQMFTEALFIITK/SWKQPR
1108	15009	A	1115	3	458	IRDPLEEAVCFADLKLHAGRTTTTLFRAVRQGPLSL*KLLLPFVQLSHVPRGGVYRGSQASLSCGGLHPVQAS*LLCLPTQASAMADAP\PPASLPPCSSISDCCASSERGSVGMGPSEPGMGYNLLVCRLLRPLEKPSIRVGVSLFSRYHM
1109	15010	A	1116	204	13	PKMKTDSRWILGLFF*FLRQSL/SSVIQAGVEWRNPGSLQPPPPRFKQFSLENOGIPPHGLVVS
1110	15011	A	1117	34	454	IHISVVEFLTSKLYGTLSQYNKKNILIK*MGKRFNAHFT*EGI*IVNKHMRKLP TSSVIREMQTKTTVGFRSVLTREAGIKQ TDS/NQAWVRKWSNSTLLCCWVKHRVLQPTWN\TAWQLLIYKMIWQLHFYAQKDIYVN
1111	15012	A	1118	83	451	CFLKFFLYRELISPFL*Q\FVRPSEAFRRKPPPWVAFFSDPS/FSFLVFFPKGIVFFLGDALKKVL*KNFFFFGRD*VLLCCPGWSRTPALKHSSCLGLSKCWNSTTRP
1112	15013	A	1119	316	441	FIFFFFLKTNFNFFAQVGGHNRNLG*LKLPLPGLKQFSCLT
1113	15014	A	1120	67	312	RQIDQWTRIES*ETDPREYSQLIFDKGANPIQWRK\LFNKWFHWNWTSTCKQIKKNLDIVLASFTKTSTSHRLRENLYRIHI
1114	15015	A	1121	27	490	GTQLHSREKKNSPFNK*YWEN*ILTCKRMKLDYSFIAYTKINSKWKDLNVSLGLLAKIK*SPKCKIQNY*TSRRK*KGKDLGQ*FLGYDTCKKATE*KNK/LNKWDYIKLKNFCIA\NKTINRMKRQPTVWEEIIANIISDKVLISRICKKTNR
1115	15016	A	1122	490	48	EHTNNKRDTLTVDIGKVLVI*TEDQTSN/IPSNOQLIQSKALTLFNSI*AERGEEATE/EKLEASKGWFMK*KERSHLYNIKVQGEAASADEEATASYQEDLAEIIDENG\KQQIFNSDKIALHQKKM/PREKSMPHFKVSKDRLTLLREF
1116	15017	A	1123	2	259	IYGQLIFNKGVKTIQ*RKNSVFNRQCYWD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						N*ISIWKR\GLDPYLTPTKINSKWK DLNIRTKTLICSSWRKKKRENFLKKRK KL
1117	15018	A	1124	206	24	CSIFFCIYLFYLYFYLYLRQSL/DS VTQAGVQWHYFSSSLQPLPPGT\GLF*RT SYSWDF
1118	15019	A	1125	3	351	RRGRGFTILVWAQTPDLM/HPPALASQS AGITGVSHCARPICLFFKROGF/NSVAQ ARVQWWDHGSLLQLQPLTLR*YYHLS\SW DYRRM/PAMLGFFVIFYAYPGITLLPRWP WISGLNELP
1119	15020	A	1126	2	349	STNHKDIGTLYLLFGA*AGVLGTDLSSL IRAE LGQPGLNDHTYNVIVTAHAFV IIFFIPIIIGGL\GWILP
1120	15021	A	1127	362	2	RVSLHCPGWSQTPELKLSSCLSLPKC*D YRCEPPHPAYLTSFITEDSKNFYVITL F*NNIY*TMFIEIPP*VHYIGAHLP*DQ LSTFF*SF*N*FFVCLFFRQSHSVAQAG \VQ*CDLGS
1121	15022	A	1128	1	349	IYFLTRSHSVSRAGVQWHSSGSLQP*PP RFRKRSSPPLSLLSSWDHRTWG/HMPP/H SSSFSSSLFLRSGWGGKGVLS
1122	15023	A	1129	367	24	INCVFYPCPGVTKKPWT/HF*RKGFII INIFHGPFKLTFVCPEGGKNSETLYPFC FLPLSLAIKKSRLGVFLV*KGPLSPPL QGNYGVGWVGFFFFSAFVIFIKKLVLS PYKN
1123	15024	A	1130	61	299	IPRVDNYCGYVREHLFSFLFFFKRSLV/ SVTQAGA*WRDLSLLQPLPPGFKQF\SC FNLLKNHCYRDVPLLLNTLCIIFKT
1124	15025	A	1131	2	261	FFFFLVFSFLLRLFLPSPSSPPSPVF FFLPSSFS/CLVSRDLTLTSQTKVQR DLGSLQPLPSRFRKFSCLSLPSS*DYGR TPLW
1125	15026	A	1132	2	381	EFYFFF*SSQMESPISIAQAGVHWRDLG/ SIAPYASWQVILPQPPPGFESFSC RFPSTWDRHAPPRLAKRNKI
1126	15027	A	1133	2	221	PSLLKKLARHSGRCL*SQLLRNLNRNR /CVPAAWTK/GETPPSKKKKNPPKGP GAQTFETPGFGKPKGIKV
1127	15028	A	1134	331	2	RGPPPLKEPSGVFRIFQFKNLESRGGG ERKQSPPLGPPIRRGLSPKPPPEKGL TVFFFFFFRCKDGVSPCCPG/WISRTPG LK*SSCLGLPKCWDYRHEPPHPAPAL
1128	15029	A	1135	3	391	AVNTQMMRK*KSLIADVBEV*VWIEDQ TSHNIPLRQSLVQSKAL/T*RAKPSMKA ERGKEAAKGKLEASRG*FMRFKENN\RL HNKIVQGD TASADVEAASYS*DQAKIT GGCGYTKQIENFTDEAFY
1129	15030	A	1136	107	350	TYSIVATVMRFYFFIIFYFLRWSLAVVI QACCCHPGNWDHGSLLQPLPPGHKFSCL SLLSS*GYRCPPPCQA\IFIFLVEMG
1130	15031	A	1137	35	297	TLMHYTNRVKEKNIIISIEAEKAFDRIQ HPHM/IKYLNLIKAVYNRPASIIISG* NLKAFPLKSVTQGCPLSPLLFNILEV LSTRP
1131	15032	A	1138	378	1	PFTKINLKWIIDLNKHKTIKLEDDIIG ENLDNLGHDYDILDPTPKA*AMKKILIN



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						VALC*NHESFCSSENDTVIRMRK*ATDRK KIFAGDMIKDCYSKC/NEKAEVNNMKKN NPIYKWAKDLNMLL
1132	15033	A	1139	271	361	KW/YWNPIHTISQVCL*GPEIYQHVVYQ MTKQRCQGNM/WAKDSLFNKWC*NKWI FF/C/RI*NLNSYLTPYRKIK*KWIRDQ NITVTTKLLEENMRFSFAFGIGKD
1133	15034	A	1140	28	340	LLYF*YKRGFTMLSRVNSRPPQ/CDPP TSASHTAGIADGSHHARLLFFLEK\BPA FGPPAGRKGANFG*RESPPGFRGIPP/ LPPPGNWD\YGGPPPPKPNFGFF
1134	15035	A	1141	94	128	GSQMPRHLVD*MTRHLATLRES\CYSR\ VYPRFIEFLHFDIQSTGQKSHR
1135	15036	A	1142	85	492	VWVGLLSLEGSPSKFNGFIEFGVLLSSG GFSAWRLFFVYFLRQSL/NSVAQAGVQ QWRDLSSLQPLPPGFK*VLKQRGVCLFV CFETESHSAQAGTQWCDLGSLLQPLSPE FKRFSCLRNSRSLRRDIEPSEGNQC
1136	15037	A	1143	372	3	KMNR*PISIKRIDFIVKNLPK\KFGPDG FTGILY\RHFKEIIQTVCNLFQKTEKE GMLS\IYKASIAQIPKEKDKQTKATD/ YKPSGIEAKIINRILANGIQQYI\HDQV RFTPGMQGWSNIQI
1137	15038	A	1144	56	482	TMKTLLEYWQKNG*VDQWNGIESPEIDPY K\YIQLVFDRAKTCNV/RKDSLNVKWC TYAKKKKTLNLFPTPFTKITSKTYLKNW N/SVNFNLNPLGKTLGDLGFPRDFKFLN TPKAKSLEKH/MDTLNFFKGKICS*KNM VKKNKKT
1138	15039	A	1145	190	482	RQGLALSRLSCSGVITAYRSLKLVGSS DPPTLASQIAGITGIRHCPWPKTFLAS VIMPAHNS*PSLSPVPSF\SLSPPLLA SQSRRSQ
1139	15040	A	1146	138	485	IFFPSV*TIFLLALFFS**MYLIFVKS SLSIYSVYQF/SFLCFWSPISDPKSQRF SLLSFIVCFVFPNRVLLCHPGWSAVV *S*LTAVSNS\LLKQSS
1140	15041	A	1147	101	426	GDWKKFYIYKHSESPLILFEKKKGVL EEYSSFDI**AIKVIYHSRKRK\KNQL ANLTDALKALNKI*HPFMRKTTQQFSNR SFLHLRKGIIYKPTANMIIKEQIIF
1141	15042	A	1148	458	15	VFVCLKICKHRKGTAKKWWYNFMGLPLY MRSVVDQNGTM*KMTIYAPNIGAPKYIE QILMGANREVNSNTILLGDFSIPLSTL/ DKELPELNET*NKTDLTDIYRTFHPMAA KYTYFAGTHGTFSKMCVPGFDIRVILVE FRRSTYGLDW
1142	15043	A	1149	1	507	KGPPAPPPYKKKFQGGPKKFPF*SHPF KRPRGEDP/YKPRNLKPPWAKKNPPFP KKKQRGKGPKNPPPWVKPEKSF*PSPK KTKIWPPPPPGQKKKKPPPPKKKKK KSVSSSPKNI/YRSLFCTNLKKSFT*F *NLMP/TKLPV*EFPPPPYNSF*SAP
1143	15044	A	1150	436	32	NLCMYVVMYLIYVRTYVCIYSIYSLY IDLSLYHHHYSICMCVSIYPIYLSLIY LCISLIYHLFNLCIYISYLIYLS/YVC M/SSI*SMYVCIYLIYVCIFSIYSLYLY IYLSIITIYLYLCMYCLFYLSSTIEF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
1144	15045	A	1151	3	657	QDCKIQNEHKTQNTLFLYTRNAHIKIKF HLHSSKILLAVNLTKHV*NFYAENYTTLM KEKI*IERNKDLHRKQ\NLNPCIWIVKL NIVKIPVI\PHR*RSLTPIIIIPAK\FF GDKEKIIILKFIWKGKIR*LRF*KIRIK GGLNLPN\LRLTVVTVIKIV*YWNKERD RYLNQ\WNKIENS/EKLKPRKYVQLISF VFDTSG
1145	15046	A	1152	430	438	TFWVKKFFLLNLPK*INPGFKKKKNKRG G*KRP/SGSQVLKKLRGKIALTPEGKKG IRDCFCPPPPPLRKKKKPPPIRP*KKKKK KRKRDPFPGNHYSNSVRHTSCYFTLLHL TLQIFFTSRSPVAMSCRINL
1146	15047	A	1153	104	478	ELLLEGSPCLRAESKAGFAGRLVPTLLS WRVQSPGVLCAWEEECPEPPSTGEDAPS LAIRETQIKFITRNHLSPLSMAIFQTNN DN\RTKRK*CWHGCGEIG/T/LLHCWWE /CKLTFP
1147	15048	A	1154	171	476	NSSDYYYFRLRQSFTLVPOAGVQWHDLG SLQVTSDDPDLR*FARLSLPKCWDYRRE P/RMSDSNYFLK*VPVN*KARA*LLFIP SSCQAG/ASAGQTLVS
1148	15049	A	1155	3	562	PDYQTARRRQAPADRCQGPAAITCPR* PKARSSSMNRSNPTVTRTAGP*PSWKTG AASKSQTDGDRKELIPNRTPNN*VST AAIK*QVRPYLTQKVPAG*TFCPHQKLQ GVRPLCRGPP\RPFGSPAVTDNRQAKLK TPTQ/HPADPPEQKRPPARPPVGRHAEV KQPGPPFPAGPRPAPSTDGL
1149	15050	A	1156	67	417	TLSCETQPGQHGEAPS/PTKNA*IALPL SWARPLYFPAPARFTARGGPVFTSKRVP SPPNRRGWRPPP\QFCHAWNPSPKFLAP KIPPT/GPLPPNKEPSKENVNPG/PLCP L
1150	15051	A	1157	446	87	PDCINVISCFITKIYHVFVFFL*RQGLTK LPRLVSNS*AQAILPP/SASQSAGITGV SLHTRPIMYFSSYYIIFGDTVLF\ETQS HPAAQAGVQ*CNLGSLLQPPPPGFKRFSC LGLPSRRMA
1151	15052	A	1158	1	938	FFFFIFATYLFENKGLTGKQRQSD*SIC KHLKGYIYKDKILTASKH/V/KKCPTSL AIREMQILTGIKCC*RCEGNGIFTHYW *ARALAQLLWKNV*QHILKLSMCITYNP TILFLGISNRKVYM/CCPK/DPCSRMSR AAQFVI
1152	15053	A	1159	370	3	AFKAAAEGAAMSVTGGQPVLSNWVVLGG VTTTT/CPTTFIMPDPNTV/RGDILELTR \PLGAQVAMAVHQWLDIPEK*NKHK/LV VTEEDVELMYQKALNMVQNNKKAAGIM YTFNAHAAIDEFHR
1153	15054	A	1160	55	471	SPPPGLPKKIFFWPLSFYVWP*PQRFCP LFAPFKQESNPLKVWPPFGALQNKRSKG CSPSM/SARQES*PLFPKNLETPPFGKG FLKFFFFFF*DGVS LGHPGWSAI/IDSL QPLPPGFKQ/SLCLSLPAS
1154	15055	A	1161	3	467	GYTNQQIFPVDKTAFY*KMPSRFTMARE KMSGFKPSK/DRAGDFKLRSMLIYHSE NPRALKNYPKSTLPVL\KNKAWMKHFCL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QPPVETYCSGKKIPFKILLVIDNVPCHP GALMEMYEINNVNTATNTTSIL*P/VT SGVIS
1155	15056	A	1162	216	464	SSEPGSPGELPYGAQEFVMKAPQGILV IR*T*FFETESHVAEAGVQWCDLSLLQ LPPLRFNQFCLSLP\SWDYRRPERHEAN
1156	15057	A	1163	29	433	AVEFGGDCSPQHPNLPPLGSPQHSPPP LIGICT/REE*GWGGGLFVPCPPALPYP STPSWGGICVCYGRGGVAPP*HPPLT* LGGGSTPTSLAPAGAPRHPGHPLMVLO TLPWGPHTPARKPYINKVLSCVDF
1157	15058	A	1164	486	11	STCLGLPKCWDYRREPFRPALRCFFLN ILLFLKFTLSEINIPTPAFF*LVFAWYI FFSLFSF*P/DLEHYI*SGICVDTM*VG SSCFNPT/WSISSF*LVCLDHLVFFLF FFFLRQSL/DSVAQAGVQGDGLGSLQPP PPWFKRFSCLSRIPAHFEWSRA
1158	15059	A	1165	467	131	NRSLEWAKMYKTYDEIKLVNTLPT/RKS PGLCKITAKFYHIYKDGIVLLNLQEI QVGFHPNS*YQ\IILIPKYSEGTTKKN CRPIFLVNIETKILHEIRAI*VHKQIRT LE
1159	15060	A	1166	455	32	EEGVLKAKRGCKSGLLHQTVNQVNV/AN LEKFLKEIKSDTPVNI*MIRK*NNLTAD KEKVA*IQDQTSNNIPLTQSLIQSRALT LFNSMKTERGEEAGEEKFEASRG*FMGF KEKSHPHKHSASKASADVEAVASYLN S
1160	15061	A	1167	26	418	KIWDYVKQTNL*ITGIPERGGEKVNLE NIFEAI VQ/ESVPSIFKEVD TQEQEIQR ASSSSSS
1161	15062	A	1168	64	313	KWCKGNSYISKDLKELKYLGV/QLK*VQ /DL*SENYQILLKEIKEDLNKWKDIPCS *IRRLNIKMVIFSKLIYRFNAIPKILA A
1162	15063	A	1169	464	36	QQAEEAESL\DPGGRGCSELRSCHCTPA WATEQSINK*SINQSIK*KSKLC/CWEN TLVKHIFHKRLTSRIYKEL\QQLNKKTN NSL*K*EKDVNRYFIKKIYEDI*MANEN IL\IKLVIREIQINLKEWLSWFCCECC FVLVVF
1163	15064	A	1170	290	487	GSLPHHTPKR*PFLF/CVFETGSRSVT* AGVQVHNHGSLOP*PPGLKRSSHLSLPV LIFLFSVEMGV
1164	15065	A	1171	2	413	GKVFI*FSTLH/GCNMK*SRS\LL*ALR FIFLFTARGLTGIVLANSSLHITLHDTY YMGTFHFYVLYIGAEFAIIGGFH*LPL FSGYTLDTQYSKIHYTIIIDINLTFFP HSLGLSGRPRRY*DYPDATTRYILS
1165	15066	A	1172	381	2	PPKLQKNFFFSSTGKFFLGGGRAFSPPP KKGFFSQIPRRFFFLPKKKKIYFCPPP CFGPPPTFFLRAPPPFFFFLLFCSF VGVKFILFL/FYLFIFRDTV*LCYPGWS AVVQSWLTAALTPRP
1166	15067	A	1173	9	405	NLDKKGRNRTPOSWFOANPMASMTFSKK KKKKKKKKGGGALKKKPWGAQKKPGKK KKNFPLKGG\EKKTFRGILEKKPFFGGG KKGPNPPKKKKPLREKKKF*GEKGEKKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						*KFFFKKKFPPPSKKTTP
1167	15068	A	1174	410	0	FSYYPPTTRGGCPSSFPQIFLPPPLLGV FFPFSPLKIFFFPRGFKPFGGVVFFFS PKKKVFFKNPRSVYKNPKKEKK*SLQP PG*VWAPPGIFKR/PPPPFFFIYS
1168	15069	A	1176	319	3	KEARSVFRVEGRG*KNFSASGPPGGGNP GGGRPGRGNFVFLIKKGGPPPGPKG/SP FFDF/GGPPPPPPPSGGSGVNPPPPPF FFFFEMESRSVSQSGVPDADAW
1169	15070	A	1177	385	1	SASFGLPKCWDYRHEPTRPASVSVTVT SRLSGA*ARSGKGTLVFAQMVFK\RIP LTKYSDHSREPSLQLCMQSTPSKAEFT VAKADKRLCCTAKSSTAKSIAQIKCQND AGRSPQESLHVSGRV
1170	15071	A	1178	147	808	KLKEIKKLLLENAGINLYDLRLGSGFLD MTPKAKQQKKENLKWVIRMKNSCASKD TITFYN\YRSDKGLV/SKKYKELNSITE RQPNF*KDLNKDFSK/EQMAKST*KTTE RLFIREMKTKT/ME/YHFLSTRMAKI* KDSNR/RLCRKTGTLIHCW*GTAPANLL KNCQPLFPF*GTVWQFLKRLNLELPDDP AIPPLVICPKEMKT/C/CYTEICTQMFT AA*III
1171	15072	A	1179	1	398	SRSRHCTPAWVRVTLVLKKKEKEKEKEE KKRCPCYIVSHQSL*KPAWQFL/RNVK/ LELPYDPAI/PLLGKCLKBI*KYAYTKT CM*MFIALFIIAKKYQLKRLSTDEWIN KMWYIHAI
1172	15073	A	1180	3	389	GYDRVIPNP*PLTGA\LRALLLTCGLAM *FYLQSMWVLLGLLTDLTIIYHRWSDV ARKSTYQGHHSPPAQKGLRYGIMLYMTS EVLLLGGLF*AFYHS\SLCPTPQLGGHW APTGMTPLDPEVPLLNT
1173	15074	A	1181	354	2	ANSSDACLTDGHRALPLQLPPCGYSIS AAQSSTVPMPLLLIPPHCNRTPSLWHY SPASNPTNPSPY\*TAPSPPPPIPRNNP FS*KFPYVWVYTSLTTCSPVPVSPNF TQPSVL
1174	15075	A	1182	3	384	GANVSG/DL/KLKPVLIIYSSNPR/ALK NYARSILPMLCKQEKKEKKK\AWMTAH LFTAWFT*YFKSTGET/CAKEKIPFKIL VLIDSACSHPRALMEMCKEINVVFMPVN *HSI/LFCMQPMDQALSTYKS
1175	15076	A	1183	1	410	PPLP*KFFSPGGVQS*KGGRFWPPP*VG VLPSSSP/IIFFTPGNWGCSPFSP*KF FFSPKGFICGGVGPFFPPPKRFFSKI PPLVFFSPFFKKKIFFPPPVNFPPPRV FFKRPPSIFFF
1176	15077	A	1184	406	62	PPIINMLCSLAPFFSPPLRGVLPFPF LKNFFFP*GVYFWGGGPHF/SPPPKKG FFPKFPWFNPPPLRKK/YHNFPPGK FGPPRVFFKAPP
1177	15078	A	1185	337	383	RSYISFQK*VKDLNKHFSKDDTQMAN/K HIKRYSTLVIREMKIKPMTRYHFTPTRM AVPF
1178	15079	A	1186	3	471	LAPSDK*ENRLPGNRPL*EVRSPSARQP PHLRSEELRPAATPSGK*GASPPSSHA VREGGGQPPPGQPPRPGGEGRLCPAAP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TGK*GAPLP/EPPLGLGG
1179	15080	A	1187	2	406	FLVETEFVCYVGQAGLELITSRDPPASAS KGAGMTGVSHQVQPQ**S*LWT*/PSSV EAGTSFGLSFLSSSWALSAQEGCLAVPS /SGSRGLLVGALLLWTKPSPQLSPVPAS QRLSSLSLMPPLPQPQHHTHTSIET
1180	15081	A	1188	160	459	NFMTIDMLCSAVVIHFCSGGLDFQL*KL FKSQ*ENNLINKWAKDLNSFTIFS YG*K LAHEKMLNIREIYFTAIMS*YTLTRTV KVKKTDTKCW*GCTATGNLIHCCKNV*P LRNTAWQ\FHKILNIYLPYHPAIPLSDM NSRE*KNI/CHAKMCWIFI
1181	15082	A	1189	232	2	KAPPPFFFFFFF*SGSHSVSWA GI*W/PGV*WHHGSLSQPSPRLK*SSC LSLSSWDYRYVPPHLANLKK
1182	15083	A	1190	2	402	PRVRHAGSPSPPPPPPEGL\SHTSFSQ* VFSWPSY*TPCLSALTASVLSLL*QRS PRTLFTITNKC/DF/PASHSSCRIPAGL* ALGRQGLFSCFFCFETESHSAQAEBVQ WYNLSSAQSSPEFK*FS/CLSLPSS
1183	15084	A	1191	19	390	WCVPAPVATWEAEPRRSR\RSKPLTGRQ SKLSY/NKKKKKKKKKKKKKTGGGP *KKLLGGPKYKGGKKKKFFFKGEKKKS LGGILKKKTFFWGGKKWPTPPKKNKALK GKKKFLGGRGNPP
1184	15085	A	1192	485	112	QRDPDR\SAEAAIKYFLTQATASIILLI AILFNNILSGQ*TITNTNQYSSLIIM ATAIKLGIAPFHF*VPEVTQGTPLTSGL LLLT*QKLAPISIIYQISPSLNV
1185	15086	A	1193	55	385	THAFADAWADAWGLFKGILTENFPNLQK YINIQVQGG*RTSSRFNTKKTNSRDLII ILPKVKDKLSKKKKKN\AENKKILKYRG GPF**KPGGAQFYGGGRKSFFFFFFGG
1186	15087	A	1194	408	3	CQSA\LLGGASQLG\SRGSGVRDPLEEA VCPFSDLQLHAERTTALLKAVRQGHLSL PRLLLSF\VCLCPAPRGGACRGRQASLS CGGLHPVRASRLCLCRKAWAMASVPPP ASLPPCSLISDCCVSNQ*DSTGRV
1187	15088	A	1195	5	371	LFSTNHGDFGPLYLFF\A*AGVLGTDLS LLIRAEGLQPGNLLGNHMYNGIVTAHA FVIIFVIVPIIIGGFN*LVPLIIGAP DVAIPRISNISF*LLPPSLLLLLACAIT EAGAGTG*TVY
1188	15089	A	1196	76	404	PTPLRTHDQSSKVSRYKVNIOKVGAFLY MLSTRTTGI*\IKSTSFPFASPKVKYLT INLTKEVQ/DLWKEKKL/NEIKEDQNK* /NVFFSWIKGNIVN
1189	15090	A	1197	50	334	ILHMVSIPISIIY*HLLPAG*AGTHIG* LPPA*FFWVMG/RDRVLLCHPGWNAVVO S*LVVASNSW/VK*SSHGLSKY*D*RH EPSYPASGTKLN
1190	15091	A	1198	250	1	QYYLVSSNT*SIIDFLQLPQKCIFTVGF SK**CICGFIFKNI*LFF\FCLFESESC SVAQAGVQWQDLSS*QLPPVFKQFS
1191	15092	A	1199	2	402	TDARHHTWLIFFVFLLEMGFHHVGRAGLG LLTSSDPPREAKLNFL*R*GHAVM\CPG WPHE\TCLGLPKCWDYRCE/HTAPKPHH FLFFFFFFSEKNFIPVPRRGGG/WKNLN*

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MEPPPPG*KGFFCPGPPKYWN*KAP
1192	15093	A	1200	50	437	STLYLEREKEQISLSVIVSSPLPSTSTGPTAAQSSISGPSLPLPHNGAGDAPAGLG/YGQGPSGPPWGPS/SGPSPR*ALVCPDPSGAARGGRG\SRGSCCAPAGFAGLGDRHPGGMGEGPAAPPKSS
1193	15094	A	1201	86	313	PPPPGGYPHFSFXXXXXXXXXXXXKSLLPCKGPNPKVGLPPFXXXXVSPKXXXXX*NPSPPPRAPGGPP
1194	15095	A	1202	105	485	VQOTTMARIYVCNKPASTPRFTKQILLDVLK/YIDTQTII LRDFNTP/LNSVMSWRQKTNKDNLNLMLGQLDLIDISRIHVSTR/YIFFSSLHEIYKSGHMLSHKACHNNF*KIEIILIIILLYHC
1195	15096	A	1203	1	476	PHFGPPPPQDPRF*G\GPSTRKGFFPQPPGFFPQAWPRAGQPPGGT/EPVFPPPKHP*RRNPYPKFGSPPLPGKIHQGSFPGSGQFR\PPRWGKKRAQPTFWAHPPIFFFF*GVLLCHPDWGTVARSR\PPQPPPPG
1196	15097	A	1204	1	269	VVEFETYNLGIK/WSKDMKRNFTKEDLMMADEHPRRC\*HHLTPPRTAQVKLELEPNE/WQGCGEAGPATPCWGDAAPVQPLLIQIGRRFLKK
1197	15098	A	1205	459	42	KLKPMLIYHSENPRAFQDYAKSMLSVLYK*KNEAGLRAHLFTAGFTENFKPAVETYCSE*EISLQI*LLI/GHPR/SLMEMYKEMNVVFMANTTSILQSMQDQVALTYEYHYISNILEAIDNTENPLIDLKANAWVPG
1198	15099	A	1206	408	1	EMKTLTEMSSPGMPTEKVSELED/DIN/EMHRKLQCREKR/IKRN/EINVQEL*YHYKRCNHHVMRMEKEQRKEEIFKVI MAENFPNLATNNKSKVKEAQTPERIKTIYIYIYIS*LQKAKEKESILKETCQKTSKPK
1199	15100	A	1207	7	383	LDIGCFWWEDKYSSCYPSLATSGKLKYSFSCLIHCFVLCVCVRAHK\CI*SRAS*CVCVHK\CI*SSAS*CVVCARTNGI*/CQCFLVCVCAQV/CI*SSAS*CVCVCTSGI*/CQCFLVCVCVCVC
1200	15101	A	1208	405	214	AEAGRS LCPGGGGCNE L*SPPCPSAWVT\SETLSQKQNPHHKKKTGQVRGQSSYLPLWEVNR
1201	15102	A	1209	384	2	GVTHH/ARARFFC/LLDTGFHSVFQAAVQ*A\NHGSLQPQPPGLKPSSCLSLPSSRDNK
1202	15103	A	1210	403	2	VPSIQTNCKSLTYDFDFFKQLFKTKLKLDA SFVNVCVNVEPFRFTALSKTQSLCLSLFLLIF*TINCNFCFLRQN/LRSVAQAGVQWRDVGLLQPLPPEFKQFC
1203	15104	A	1211	156	405	ESQMLIQCKSQMLYC*RI*TV/CLCVCVCVCVCVCLTCGTRKVCIVLFIVVLNCK/PLCEPCC*CNRQGWAPWLLPVISTRW
1204	15105	A	1212	70	408	KAFSLPPGVSPGPLCNRRPNFIGGGPKKKPPPPQRVVTQGFNPPPPFFFLWGG*GQD/PPFVAQG*MDPPRPPK\GRGPRHEPPPPAF
1205	15106	A	1213	410	3	KKSMFGFKASKDRMTLLLEAQAGDF\N

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LKPVFI\YHSENPRILKNYAKYT/PVLY KWSNKAWMIANLFIA*FKYFKPTVETC YSDKKIPFKILLILIENAPDHLRALMEMY KEIHAVFMPANTTSILQPMDDQGVILT
1206	15107	A	1214	3	340	KIRVEVNKMYNRKLLLEEIKKIKSLFFEN INKIDQFLPRLRKTROKMQINKIRNEQG GISINIMEIKYSYKEML*AIICKKLNNL HEMNKFL/EHRVPKLTQVEIENLNYIK K
1207	15108	A	1215	1	57	RGLKIQNVNEIKS*CFEKIKIDKFLARQ NFKRKRFKFRD\*KGDIMADITEI*GII RAYY*QL*GNYLENLEEMGKFLVTYNLP KLNH/DIENLKKPVT/REFKSVIKSLP LKKSPLHDSFTAQFYQTFEE*VSVLKR
1208	15109	A	1216	350	1	QSSFFSYYPNFHLLSLFCFKDFLFFYA SVLATNSLPLFFPQISRYFP\PFERERE RERENVVL\CCLGWSAVMQS*LTPALNY W\VRQSSLLSLQAS*SYRCGPPHPANIF HFIFCR
1209	15110	A	1217	139	358	KNTFFVVVEAKRLFVPQAGGQGGNLSFK FPAPP/NLRG*SASSPSSGDYRPTPPCP ANFFFFKKNRISPWGSWG
1210	15111	A	1218	361	50	WGDHGSCLKPQPPLRSKNPPPLASLVTGT Q*LG/HPVAPFPPIQLIFFFFFLRRSL/D SIAQAGAQWCDLSSLQAPPPRFTPLSCL SLKKKGPNPVFVITWMNLEDIMLS
1211	15112	A	1219	1	361	LKQHVSNEKTAIFYWKTQSKTFVARE*K GEILSSNRGECLLQSFKGQPLLLGANAA GDFKVK\PMLLDHSEN/PKALKNYTTS
1212	15113	A	1220	292	362	HIPVVPATQQAEEVGGSLEPRRSRP*PPR LK*SSHLSSLNSWDYRNVLP/RLANFCI FLCFVR\FKLGSNHQNASVSQSARITG VSHHAWPILKLLKLVCLFEMGSHYVAR AGLK/PPGLK*SSRLSLQNCWESRREPP HPDTIH
1213	15114	A	1221	372	3	RLFFLLPPRPKGDFFPTLLIW*RHGFSP PHVFKPPPLNLILGALKKKFFLPS/LPY VKFYFFKRAPLFFF/IFFFRDRVSLCWS *PPGLKQYTHLGLPKHWDYRHEACLAN NHNNNNNTNFFFETE
1214	15115	A	1222	3	291	RSGDQDCPGQHGETLSLLSLTFVNLSLI CNL*TLSLIFVKIQKLAWHGGVRL*SQL /LRLRQENHLNQEG\DCIPAWATEKDS VSKKKKKKKGGPF
1215	15116	A	1223	379	19	HMQILTIMRYTPIRMAKMKKIGYTK/C W*GCAATGYI\WECKMVQSL/WQNTWAD S*KLNTHLSYDIAIQFL/GFYSKETKAY IHTKPC*TMTATLIKSI/MKQYKCL STDKWIKQNRGIYI
1216	15117	A	1224	387	40	KKTLSTP\PEKHPTPLFHPPPQKGGKA PPSFKPPPKHPPPKGISPPPP*IPPP PIYPPPPPAKPPPDFFL*SPPPPPPFSP PPPP*TPPPFFSPPLFFFFFFFFFFLLIR LLV
1217	15118	A	1225	21	477	IVSRLITVRLQKPRLDPRVRPRVRKEN YSSV/SFINIDRNVNLKIL/SSQIQQYI KKLIRHE*FWF/IPGIQGWFNILKSIV TYVNK\QKWKHTIISVDTEKAFDKIH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LALILIKKKKKKKRALPQSFIPGDLFKK PNGGFPGLKMMGRAPGE
1218	15119	A	1226	1	398	ERINHTLFFFLAEAQKRLPTGISGRGRPA IPHNTPOQAPDHAYLPAALAAQHRAGGQ QAPPPG\SSPSSPYDEVKDRGDDVTASH GLRGNWGWSP*ATSLVLNLMYMTAKYG DEVPGPEMENAWNALANNEKW
1219	15120	A	1227	3	238	DAWVAGHDG/RTP*SQLLRKLWEHRFS SGDRVSDP*SCLCITLAWAE*DSSSKKK KGGPFKGTKFNSRGGGRNYFFYGA
1220	15121	A	1228	207	2	NRVSPCCPVQWHDHSSLQ/PRTFGLKGP \SASAF*VAGTTGVHHAQLIFHFFFFY *DRVIQAGVQWRNL
1221	15122	A	1229	15	413	RKSVNVIIHSEILKKNYMIISIDTEK SFDKI*YPPMTKLSEN*DSLNLINNIY/ AKP/VANTILHSKRLNAPPIKQGCLQGC \PPFLFNIIILEVLASTKGRKEIKSLQIR VEEI/KPLSLFADNM/IVYIENPKES
1222	15123	A	1230	363	1	AADPFACRPVSPHPPLYLTSSQSLLTS VSPKKQPPSAGMQLGVGDSLGSWGWGRT KKTRLFFFKTRSLSAAQTRQWCEHRSQ P*PPGLIKRSSHLSLPSS*NHRHMPPHL AN\LCLFV
1223	15124	A	1231	3	402	QANSCIFSRDFGSVQGAGLEPLTPGDPP ASASPRCRDYRC\GPHAQLLTFC*ISI LILV/CIS*MKDYFITCIYFFNYS*QII FYRRASDFFPFLRQGLALSPMDHGSLO PHEPRLN\HPPTSAKGVGT
1224	15125	A	1232	3	396	FLSQHGFLFLFFAGIDKLILKFIWKDN* NNYEKED*RGVITLP/QYKAYSVATVIK MVVHWQSDKHVDQWNREPRNRPNYMSQ *FPL*YVSQRNENLPLHKNPYMNVHNGF ICNSRKQSRYPSTGEWVNKL
1225	15126	A	1233	3	395	LPKCWDYRR*PPHPALF/LFF*KHPKFP KMQVK/WRKH*TENRLVMYFSEKFGD*L KDQHKLYYLDMAFQFIFTTYVMRYSIL FKFNIR*LTLSVVKMAVFLVETGF\TML ARMVLIS*LRDLPTSASQNAGI
1226	15127	A	1234	416	2	KIDKLILTFIWKCKRPLAKIVLKKKNK I*RLPLPSFKTYGKGMV/TK/TKWGWPK NRPIKGTGF*VQKKKTPHIYQQLVFDG ARTITN/WY*DN*IST*KRMKLDLYLTI YKINSKWIKNVRAKTMTFLEENIWI LD
1227	15128	A	1235	384	22	FFQEI*NAIPVNTQMVRQNSHPANIEK VL/VVWIEGQTSNNIPLQSLSQSKALT LFSNMKA/E/RGDKAABEKMETCRGWF RFRERRHVHNKIV*GEARSCGSLAAGS PLKHHLLHNTLIC
1228	15129	A	1236	379	2	SPYTKIHSKCLKGLNVRPLTFKPLEENP G/VMVPDLGPGKKFIS*APKAWATKTKI IQWGYIGLK/AFCPAKEAIPRVKTWSE SEGIPAGHAFYEGFIFQIFKGLQPFHSK KKKDLILKLDLLSADIS
1229	15130	A	1237	1	407	YRVGQAGLKLLTL*SAHLGLPKCWDCCR EPPCLTIAL*SVFSLVLPVLIKLIINF F\CRDGGQTMPLRLVSNVSWPQMIC/LPW PPKVLGLQ



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1230	15131	A	1238	3	380	ELSQRTECCMDIMSYYKAIIVITMAWY*FKDKQRVQONEVESPKTLLIYRLWIYYEGDTTDKG*TF\NKWYWDWI/ST/CKNM*FDYHFTQCIKIN/SQWM
1231	15132	A	1239	1	396	FADDMIVYLENLKSSKKLLELVNQFSKVSGYKSKV/NVHKSVALLYANSNQA/QIKNPTPFTIAAKKQK/YKQKNNLGIY*TKEVKDLYKENYKTSLEKIIDANKWKYIPCSWMGRIDIVKMTILPKAI*RF
1232	15133	A	1240	392	58	SFSMLARLVNSR/PSRVLPASASQSAEIIIGVSHYAWPSKLSF*LTIDQTHLSCNLFIVVFFERRSCSVTQAGGQWYGHSSIQP*TPGLKQSSCFGLPKCWDYRLEALPRLM
1233	15134	A	1241	500	204	SLSLSFS*DGVLCLGWSSTPGLKRFSCLSLRSSWDYRCVPSSQTNF/VFLVEMGFHHVGOAGLELLTSSDNARLGLPKCWDYRVPPRPAAFFLFFK
1234	15135	A	1242	2	397	NFMINNLPKKKALCPVVFTEGFYLPFKEETIP*VIRISLSL/IFSIFQKIETEGILPNSFYEGCIIILISKPYKDI*\ENYRLTSVMHIDARFLDSILANPIQQCIKVIHCHVAFV/SGTQDFWNIQKSM
1235	15136	A	1243	12	362	AGFYHVGQDGLKLLTSSDPASASQSAGIKA*ATVPGLSPLNFCEVRFMESWSWKR P*RTS\VCSALAKCWDNRNASQVVDKLPSEFT/RM*SPCLHPAVSAFCGSASVLPGIIVTTSV
1236	15137	A	1244	183	383	KQAGRGGSCL*/LPRCWDYRRELLHLAFMPG*LKK/FFCKDGLTMWPRLVLNFWP PVILLRPPPKVLG
1237	15138	A	1245	410	2	FSDRVSSCWPGWS/PNS*PQSDQLALKCWDYRCEPLHPAFC*MNFKLVSC*HGTS/DSKY/CQHVSPKNKDISLCNYNIIIIIPKKENIL*YIWFIDFFFETEFCSCCW*D LGSLOPPPPPGFK*FSCPSLPSSWVHRHV
1238	15139	A	1246	440	46	KTEGANINKNTTYQ/NLWDADKAVFRKFRALNAYTRK*ERAQLNLSSTLKRKKEQNKLKADRR/QIMQI**KLGKVENKQTKTIQQIH*TKSWFFEKISKIYEL*QA**RKKGEKTTITNVRNKRYSRVRG
1239	15140	A	1247	266	340	RKCWPGAVAHTCNLXTLGGQGGRT
1240	15141	A	1248	3	391	DAWADAWGSRRAVALFFFWGLGGGLKGTGFYFIQVERRGLNFD*WNPPPPGLRGSSPPT/LPKQWEPGGGPPAPSNFWFFFEKRGFPQVTQAGFKLWN*GDPPAGPSKGVGITGGTPSPHPLFLKKR
1241	15142	A	1249	3	323	MHHHA*LVLVFFCGDKVSLCCPG*S*TPDLKRLSHHGLPKHWDYRC/RATTPGFFSLFFFFFFNPPPEFLLPWAPPSYSLKQNKIFLKRFLPLAPPKGLPLKRAKRI
1242	15143	A	1250	3	405	QPDSPSPQGRLSAPPEQEGGPWLILPHACAPSQICVGPBGASILSYQERKGTQVLSCEGHCKLSSPVGLVGQSFCWQQPDAVQWVFFRRRTQTPTGTVAHACNPSTLGG*GRRTS/RPGVRDQPEQH
1243	15144	A	1251	407	2	PFLKKTKEKLP*GPAIPALGVPSFFEFFFLPYKRKEIKGIRTPPMRIAALFTIAKILNQPKYPSVDI*LHKRHTSNTTLLSRMK

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						H*WIKKT*/HTDMMEYSAIEKNGILSF AATGMSPKDIMLSEICQAQKNRY
1244	15145	A	1252	1	253	VADVRESLDPGD*GCSELRLCHCTPAWA T\SRRTTSQQQLKKQNEENTT*KTYGIQLM NCQIANYSCKLLYFRKMSNLQSNLKKKK K
1245	15146	A	1253	3	372	KKKAQKSGTIVLPCNPSYSGG*VGENA\ WARSQPGLIS*KQQ*QQNQQQTTSKTD PYIYG/YLIHDRGGK\NTQGWDRLLNRW GWGIWLMTQRKIKLELYLTPYTRTNSTW IKDLNVAGCGGSC
1246	15147	A	1254	2	410	KNLTPIVGLKAATN*ESIPFQT/SRKKK KKKKKKKKRGGALKKKFKGGGGGKKNF FKGGKKKKLGGGVKKRGEKKPGGKKKK RFGKKSFFSRGGKKKNRSSSSSSSSSS SSSS
1247	15148	A	1255	61	487	GRPGPTHAFVVIDSFFMGNFARFINHSC DPNCEMQKWSVNGVYRIGLYALKDMPAG TELTIDYNFHSFNVEKQQLCKCGFEKCR GIIGGKSQRVNGLTSSKNSQPMATHKKS GRSY/RE*KKNKKRGGRFKGSQFSSPG MQG
1248	15149	A	1256	118	5	MFIAELFTIA/RRWK*PKCPLTDEWINK M*YSHTM*HY
1249	15150	A	1257	390	1	TQKNTPTPKPKPTSQQHHQKNKPTPPGF FFFSPPGK\GGFFPSPLEFWVPPGFFPPP VFKTRPPEFIFGAP*KKFFFSPPRSLNF FFLRGPPSFFFFFFFFFS*VGKEGSSPSH ENPLFVPTG
1250	15151	A	1258	378	3	GAFFFFFFFFPKGFFFTFFFFFGPGFFF SPFFFIPPPQIFFFGPKKKKKFLPPPPQ KIFFFLRPPPLFFFFFFFFFFFFFFFFF FFFL\DLN*NVLSGTSAPKQELLGMV AYACNPSTLGGRG
1251	15152	A	1259	462	287	RDG\FHHVGDGLHLTS*STRLSLPEC WDYRCDLPCPAIPAVTLYQIYRPLGLE SKA
1252	15153	A	1260	446	34	NVRAET/IKTLEVNTGVNLHDLN*/GKA FLDARPKAQVAKEKSRQPSLHRLR/FC ASKDPIKEVKRQPT/WEKINHVSCKGL EFKIHKELLEKLSNNPI*KWDKDLNGHF SK/ELQIASKHMRCSASLVIRKCNIEIV DPD
1253	15154	A	1261	2	383	GSQRKWFLEMESTPGDNAIDIVEVTTKG FNYYMNLVDKAVAGFERIDSNFERSSSV SKILSNSIACYR*IFCKKKSQLMQ/QTS LWFYFKKLPPPPQPSAATTLISQQLYTL RQDSPPAKRL*FTDGL
1254	15155	A	1262	476	50	FFFFFFFFTGSHSVV*AAVQWHDHDSLQP *PPGP\SDPPTKSSTREF
1255	15156	A	1263	143	472	TGAVPIRPSWN/RPPAMIFF*NAQGILF AEFLASQRAILWEFFEKAYHESVLRKSA KGLAEKCPGKLHQRVLVQYDNALAHFSH QTRTTKSSTRQFR
1256	15157	A	1264	179	489	YIFFFLSLFFFLWPRPEYRGAITVHCSL NLPGSSDPTASASSVAGTKPH*YIFFFL SLF/CFSVAQA*VQGGNHSSLQPPPG K\YPTASASSVAGTKPHPLIFFFF*KKK

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						FL\CFVPOAGGQGHDFG*L*PPPPSLKQGGGLTLRIGDYRGPP
1257	15158	A	1265	1	536	FRGGWGSVRRAPGTASCYLALAGGPPGQCPFAAISCPSPLPWGS*TE/PYVPRRPGDPSAAP/PSW*VPRPGVPRNVPGRRVGDGCGQAQDIQAAASLMADTAPDSPGSA·GSVRALPACVPEISGS/SGLPPGAALP*VAA/RPTPGRHVDTHPRQHSFCGGQEGDIRAFPTLYLEVYPGPP
1258	15159	A	1266	403	2	TSLHPRGYMRLLRQGFTSAPCGYMRLPRGSSLHPRGYMRLLRKTGVHRCPTWVHAPSQTGVHLCTPWEHTPS*RFISAPLGAASHVT/GSLSIQHIYIFVFCLLRQGL/NSVTQAGVQWCNLGSLQPKLPQAQVILTK
1259	15160	A	1267	2	401	FVLNPGGRSCSEPRSLHCTPAWATRAYLQLGKKKKKKKKERGEENKNQGPPLKREVGTPGQKKPL/WGGSNGAGQKQPA/QKKGKKKADHKGQRGN*KRKREGGSGTSKNSRGTGAKA*NPTIWGGGKKI
1260	15161	A	1268	49	416	LRGRALDPRLRECGDLGAPPAPPEVALRAGTCWTR/CTL*APPRGA/DRSPWPPRSPMCKAG/DECQDGIPG\MKAWSCGLRTRQCPWP*PKLECPGPHPAWRT*PLPQTA/CGPGPAAPCAG
1261	15162	A	1269	420	47	GPPGWASFRLNFPKARR*GEWKTPGESGGAFFSPPGKNF\AQON*GRPPNPPPPPGKGKGIQTRGGAGLGKNPFRFWGGFPNPNK*GGGTKKKEGPPPLFFFFLNTDFCNLIKRDRLGVGAHL
1262	15163	A	1270	404	1	AEILELKNVIDILKNVSESLNSRIDQAEERISELEDRLFENTQSEESK*KRI*KNEARQQDLENSFKKANLRVIGLKEEVEREMGVESLFWKIIENS PNLEKHIHIVQEGYRAP\FNSNKKTSRHSINSHTK
1263	15164	A	1271	387	2	KKEKKKEVIIIFVLLPLK*FQNIQVWLVRELEKKFTGKYVV\FA*RKILPKPTQKRCTKNKQKRPRIHAPTAHVAILEDVFPGEIVGRRIRVKWTQQLTRVHSDKAQQNNVERKVQTFSGIDKKLR
1264	15165	A	1272	1	393	FRMGRLPGGGAPHFSDGVAGQRRSSPHRRSRGRAEALLTSQTGRLGRGAPHISDDGRPGRDAP\PS*TGWQPGRGAPHPD\GQPGRGAPHIPDDGRPGRDAPHPFYGVAAGQRLQSRHFGRPRQAAGRWR
1265	15166	A	1273	3	317	SSYETKGVMIASFSSREADNHTAFIRIKTNASDSTEFTILPVEVEVTTG*WKTDEIESCFVFSIAYSGKVKNNC*LFFFP\APGIYSSTEMLDFGTLRTOGKKIF
1266	15167	A	1274	92	368	LCPPGGRAGQGQNLN*GVPSPPGPKGFWGPTYGGGGGKRTTRPGGGKPEKSF/D/GPPGPPGKTKGNPAPKNFFAQKERGPFFQNGGPGNKLF
1267	15168	A	1275	401	3	DMCDWFKKEFSDTTPKA*SIKEKQLTSFIKIKSSCSPS\KNTIKGLTRQEKLGKI·FANHMSDKGLVSRITYEELSKLN\K*KLN·F*KWAKQ*DHLLKKTTH**QICKERYSLGKGKITMRYHSTSIIMCIKTIHS
1268	15169	A	1276	298	426	GATMLVLLF*LAFDLRQSL/NCFPQAGV

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						QWRDLGSLQPSPPWFK
1269	15170	A	1277	421	1	VSEFDQKL*INKENHPKIKKKICNQPL PQIRYMDANKHIKIFSTSLAARETNMKI TT/RILWKTWQFFKKVSIYLPLEPAIS SYLFTQEK*KHIDGSCSPSRVATAKLLA LQWRRPSWNCMHQQRAGSWKQIGAPPFSL L
1270	15171	A	1278	1	218	TRSGVQDQPNQHGSETLSLLKIQKLASYG GVCV*SQLLRELQKNCI\NGPRSHHCT PAWAT\EQNSI*KKKKG
1271	15172	A	1279	88	396	TFLFSSSSFFFGGGVPPCPPGLRPG\PN FASLHPPPPGFGGFPSTSPRA*NWGPR PPPQATLGAFGLEGE*IFPPGRPPPEP*L WGPPPPPPQRGGMWAPFTPL
1272	15173	A	1280	94	399	TDFLFL*TDFFLCLCLSKNKIWNNEFR YGGFSLGVSNTQALPPSQEVNDAIKQMK KHLKLAK/DKISIVRCITKMGGM*LLGYR SSWQVKRITWQLIVLNLAYRAVFGI
1273	15174	A	1281	236	2	TQSRLVFFYMTGPAVYLNHHLRTHQGS HLCFFFCFEMESHSVTQAGW\VWWRDLS SSQPPPPRLKRFSCLSFPSS*DY
1274	15175	A	1282	37	410	KKKTLKKIKKLCPPGVKGEFNPPFYVLS KVFPKKERGLFFKVTFFVSLTPFFKKKNF KIGGGSGFPPLWFFFFFY/RDRVLLCH PGWNAVTRS*LTTSVDSSDPS/CLRLPS SLDY
1275	15176	A	1283	404	232	LSSWDYRCLPPHPANPLYF**RRGFTVL ARMV/GPRDSPASSSQSAGITGMSHCAQ PG
1276	15177	A	1284	3	402	MQIKITMRNYCTPVRMP*KKK\SRTPR C*GGGGTTKILIPCWGDYKIGE/PLW/K SVWQFLIK*NNHLLYDPAIPLIFYTRE MKTYVHTITKYCNHNEK/CMQGFTEALF /TLPKTE/SQPKHSST
1277	15178	A	1285	1	253	LRGKFMTLHS/SILKRG*SQINN*TATL IK*KKKGKIKPK/RSRRKVIIMNRNK*D *KQNNNKFNETRSWFFKNMKKIYKSLVR VT
1278	15179	A	1286	400	105	FNFKKKKKKNREVS*QY*QAKYLKRN FTKNI*VAEKHMKNQAQVIKEMLI*LTM RYYYTPIK\MAKIKLTDNHKCCQLKPSY MVGKEFGKFLIKLNM
1279	15180	A	1287	400	119	TVFHHITGQAGLELLTSSDPPVSASQSAG ITGLSHW\PASSSFHSNHSCVPLEPHQ VAQLDSFGYEKVCFSN*VPGAQDKNDL SEN
1280	15181	A	1288	157	386	NDLQFHPFYCLF/DLFCQSLKKAGMQWH DLGSLQPLLPFRRLCLSLPSSWDGCH VS/PMGP*FCIYTHIYFLVEMGF
1281	15182	A	1289	400	124	FDAPAKGQGGDFGSPPPPPPG/AQKIFP PHFSQ*IG*KEGAPMGQPIFVSFSKTGA PPPGQGGFIPTPCGGPPQNFQIGGAP APGPGGGFF
1282	15183	A	1290	419	3	KNFFFLERGGFFFPGRAGGGF*FPPP FFFQGGKISGPPPPKKRGPAPQKL/R EIFLVLKKGGPPLWPGGFLNPAPKNFA RANFPKRGGSRVGGPPNLFNLGGGW FFRFFFFFVFEFEFRFCPCGWSA

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1283	15184	A	1291	397	39	M WGQVWAKDWIHGLGPKTQGCCPPPLGVFG CP/SLIPPNLFFYGIPGGLKIFVHKNP FPIKKEPANWIATFFPPGVFLFFL/CFF ETRSHSVTQAGVQ*RDVSL*PTSGFKR FSCSLSPSSR
1284	15185	A	1292	399	1	LNFFFLHRQKLCNIGSDDKVPAFSTYP EPRICYVFSLLFEIIFSFDFNKKIRIYK KHVSRIYKDLLKFNNKDNVPKKWAKDLN RHFSKDGIOVKWHIRNC*TLAIK/EMQ NTTMR*HLMNPRMAKIRKTI
1285	15186	A	1293	412	1	ARMVSI SRPLGTP IWRSQKGGNKRVSPP TRENPLFLKNPKKCPKSRD*NKPPLLKK KKKWSGPCPAQ/SCPGQNPHP/SPPKQL PSPSTPPSRPSPTLAFPMAS*LAISPA HTHCCWRELSGTHLSIPCLKPLRGP
1286	15187	A	1294	229	1	FFETESHVSTQAGVQWCPGFKRFS GLSSSWDYRYAPRP\ANF\*FLVETGF YYVAQAGLKLSPGDLPALAS
1287	15188	A	1295	401	2	STLPVH*KWTTKAWMTAHL/FTAWFTEY FKPTVQNYCSEEKIPFKILVLIDNAPGH PQALMGMNKEMSVVFIPV/NTTSILQP\ ADQGVIFTLKSYCIRNLFQHQCTPAWVT QLDSVSKK*INIFQPGMVAHACN
1288	15189	A	1296	1	336	KKTPRRKTHKEHHNGEK\LRAFPRLRS GIKQ/GCAF*P/YILNIVVA/VLAKEYGKE IKASFRKEELKLCFLIDMIIFVEIPENS PQKL\IN*FSKVAG**VSTQNSVAFLEFF FFFF
1289	15190	A	1297	3	384	HTNMQKVLV/VKTEDQPSHNIPLNQILI QNKSLTLFNSIKAERSEBAA*EKCEDSR GWEMRFKKKK/RISITKMQGEAASAVVQ AGTSYPKDLAK/DEGSYTKQQILNVNET VLY*KMI/PTEDFVVRDKSM
1290	15191	A	1298	3	395	SRSVTRAGVQWHDLSLQSPPPGFKQFC LSLLRSWDYRLSPPHQMGIFL/VFLP FFPPGKGVFLGGPQAGGKGNL*WNPP PRGLGEFFGLNPPRGWGFQ/HPPHPQL F/CCFFRGKGGSPRRAGRANP
1291	15192	A	1299	260	4	GFIVSSAVFPLKCLLDILVSSSVLLYC LWNFKIQKSFYFNLSPLVSSFKNSH*N SNI/WPGAVAHACNPSTLGGRGGRITRS GD
1292	15193	A	1300	91	219	LSRLSAWDY*HVPTHVFFVEMGFHRVQ ASLELLS*GDPPALA
1293	15194	A	1301	277	441	TVEF*GVQSMKEET\ELCLFEDDMSVYE ENLKELTKN\LLK*ISNYSKVAGYKVINI *KAI AVLHTSNEQ*NFEIGNTILF/TIS TPKYLGINLTKYAQGLYEENYSNLMNEI KELNTW/RDILCS
1294	15195	A	1302	256	482	YNVYFKICIGPGTVAHACNPSTLG*G*G GRI/TLRSGVRDQQVQHG
1295	15196	A	1303	182	460	VGREFLDMTGKEFIYKFLYIRKIN*SSS KLKTFVLPKLLRD*KAKLQTKRKYL*I TYPVKGLVSRCKKLSKLSKKTTLQKK WAKDMNRHF
1296	15197	A	1304	1	468	FKQFSSLSLLSSWDYRHPTGNFCELPAY KQNPSCSNVFTDNVPVIST*QGLQALS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						PNVNEQSPWRETKKTAVDLCGVIWKPCQ VFLRKKPKTKTGQ/HEQQIFGF/CFFSE TESHSVTQAGVQ*HHLGSL*PLPPPFKR NSTTRTSDYDGP/HVPP/HPA
1297	15198	A	1305	880	1026	EEHCAGLSGSQDAAGVFPAG*GGWAQLW VTRRASLFLDKTHWPVDEQNGLGSLYTIE ATAYGLMQKLELGRYNETHAIAKWLEK QELGGGFRSTQ/SDGDPRETTVVVALEAL TRFREAVPFKGIQDLHVQIRAPKTALNV NWIYIDHSNAYQORSKFLAQDDLEIKAS GNRGRTISILTMYHKSPESREDNCNLYH LNATLHSALEENKKGGETFRLRMETRFQ NN*EATMTIMEVSLLTGFYPNQDDLKQL TSDVERYAFQYKTKTSTDSTVVLYLEK LSHEKNTELGFVRVHMLQAEFLQALVT IYDYEPSSRCSTFYNLPTEQSSL
1298	15199	A	1306	3	726	RTDHYQFQSLKHCLTGGALNPVREKW KRQTGVELYEGYGQSETVVTYKWLSEY DANTYIVK*KTL*TQKEEG\IICANPKG MKIKSVSMVKESLPYVHVVDDEGNVLP PVEERNVTVRIKPTQLLCILNCYLDKCE KTAVS*QGDYFITGDRARMKDGYPWFM GRNDDVINSSSYRIGPVEESALVEHTA VLESTVVSSPYPIMGVKGAYIVLTRAY SSHDT*ALTRVLQEHVIK
1299	15200	A	1307	230	486	NAICPNGSKGSLGLGSCSVTQTGVRW*D HSSLQPRPPLK\YPPTSAS*VA\GPQA GVQWHGLDSLQTPPPG/FKRFSCSLPS SWDY
1300	15201	A	1308	463	440	SAIPVHT*RRRKQTSINADMEKV*VVWI EDQISHNIPLNKSLIQKALTFLNGMKA KRSEEAGEGKFEASRGQVMKFERSHLY NVKVQGEAAGADGEAAASYPEDLAQSTD EGGYTKQQNFSIDV/TTFYWKMMSSRIF IAEFHHTD*GDNGSVP
1301	15202	A	1309	463	59	EVISTLTGMGKILKTKNAK/CWQDCGTK RTFIHCWGYKLVQPLWKR\YTFPYNL AIPLIGIYP*/NMKIYSHKRTCTKMF/I NSLFIISKWKHLRYTFTREWIK/M*YS HTKDYYSAIKRNKLDMFNNHESQKHYG
1302	15203	A	1310	438	29	PGGKGGGGPTAPFPFPFPFPKGVFW* GFPRPFLFKPPPPNKAFFPGAPHFF/SL PPFPRVFKKTFPTKKKFFPPGGGKKKP PPPLQGGKKMGSAKFPSGGKKPWGISP QI
1303	15204	A	1311	2	310	HNQKNEFGPYVTSYVKVEAK*IAKTRK LLEENIGVNIHDIELGSGFLAMMP\EA* AIRLKIEKLDFIKIKNSCASKDTINKVK KTGRPGMVAHAYNPSTLGG
1304	15205	A	1312	19	348	RGQQDVLPG*RGQQDVLPGRTYSEYGL IFSARNPSMEV*SVNHRPFHHHGV/HQ NCSDSGSYFISKECGN/WVSACGIH*CC LVPCLPKAADLGE*WNGDFSLSGKEKKK EFYLIMTFSQ
1305	15206	A	1313	2	424	ENKLTNHGKTGNGGAQSQ/PPECEPRTH LQRGLEGRGGGEPWGGQGPDP/PPSNSSL KNPQAGVPPFSSLKGVKRDERSVSDSG EQREAGTQ*TFVNGKKKKKKKKAKKA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AYSPDSKA/PSSKSSPKES
1306	15207	A	1314	375	3	KKRTLLIPLMNMDAI/MNKILAN*IQQH IKRIIHNDQVQFVPGMQGWFNIQKNINV IPYY*LFY*CYINRIKDQTLIIISIDTE KNDKIQNSFIVKTLRK\IKENFLTILKR IY*KSSNNKKNID
1307	15208	A	1315	403	3	LEGVSFFFRVASQGSILGSCNPPLPRF HHFS/CPHLLSKWGYRFPSPPA\FFFF FLKTGFFFFCKNFALCSFP*KQASPPPP LTVFFFS/HHPFFFFFFFLFFFLRWSFA LVAQAGVQWHDLGSLQPPSLGFKRF
1308	15209	A	1316	38	427	PEXPAPTRPRPSAWQPPRLRSEEPRLP AAAPSEK*GASPPGSHIWEVRSVSARQ PPRPGGRWGVNPPPGQPPRPGGEGRLC PAAPTGK*GAPLPGQPPRPGGRWGGYPP ARSAASYGR*GAPLSSRP
1309	15210	A	1317	43	399	LTFFFFLGEGARPPPPGWPGAHQGITA PLFWGGQGNPPP*PPGEGEPS/QGPPPP GGNVFFWKKGSPRAPGGPWTGGPKGLP RPPPPKGCE*RGNPPPTPKFLGFTTFQ KKGKNSGP
1310	15211	A	1318	437	54	MNEQKGERGLSSLGLPAR*D*GKGNVKE GR/EGVTFSPREPKEESLRWSTPQKEIV GVINHPRGQVRDRQGAGSGCEGFALRAQ TGGPPA*ETRAGEQKAGGGSKGAQTLQ RETRPPRGQRGGGRSASL
1311	15212	A	1319	351	133	GGGWAEPVLTSSQVGRSGRGTPLPDGAA RQRRPPPPRRGSWAEAPTSQTGRPGRGA PHLPDDGRPRDAPHL
1312	15213	A	1320	474	11	KINSFSQKKKKKKQCSSIRKLA*/DQNR HFIEETQIPNKHMKRSSIS/LAIKEMQ IQITKSYCIIIRLCK*LIKNSDSIKCWQ GCREI/GSLIHCWRKLMNSTALQMVYK
1313	15214	A	1321	485	33	CPASRVAGITGAHHHAWLIFVFLVEMGF HHVGQAGLE/LPVSWNGGHL/RLCLLF GYCGQCCYKPS*RRFFCVSYIRA*K*G FVCLFV*MVSCCVTRLEFVVTHRCNHSK LQP*IPGLKCS\PASGF*VARTTGLYHG VWHVSNSTALTSGLQ
1314	15215	A	1322	451	145	THPFGRPRGGVFKVRKLNPPWLKKENPL FIKKKKKPGPGGGPFIPTPSEG*/GKK KGFNPEKEASNKPKFAPSNPQTGLGKKK KPPSLKKKKKKKVYSLIF
1315	15216	A	1323	470	151	GKAEERHDPGRACSEPRSCHWTPAWAT \SETPFKKKKKKLCISWPGTVESCFSVR T**I*LRQYVLYLFLFQPKNVIYLFICL HDKANVMVFLDFKYYFCFLFLD
1316	15217	A	1324	64	367	TWEGEGSWLTSQDRRTAPLHPSLDNRVK LRLKKKKSVMGFLSPSILLAKNQIKKPAP FTMA/SK/RIKYLGINLTKDVKDLYNEN Y*TLMKNLKGGAMCSFTSL
1317	15218	A	1325	193	381	AQLFKTSMGNSETLSLQKKKKKES*LTL PSSWDYRHPPRPVNF*\FLGEMGFRRV AQAGLEL
1318	15219	A	1326	410	7	GFFPY*LPK/SLRC*GKDFYNQSGGQA RWLPPVIPPPEAQAGGSP*GRSLRPTW PAWSNPFLKKPTPLFLKFS*GRRIALT PKAKVSVNWDSPALQPGGPKTFPPKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKLRITIGPGVVAHACNPNTLGD
1319	15220	A	1327	295	3	VCHFGIYFCVCSLYFTCLYFPFLIFL*V TLTFLVIFYFDFTVLFIIISL*YFNDCSR CNIHM*LLSLPVLIFHCCC\FVFRDRVS LCHPGWSALASSLL
1320	15221	A	1328	2	392	RQASRPP*SAPPAPAGKEGSGE*PPSPK /PPPPPPKVVPFRGFPPFPAGPPPPPP KKSPPPKTNPPPPP/IKPPPPPPPPPP PFFFFSPPPF
1321	15222	A	1329	378	7	TDDLILKFT*ERYKPNQF*KRTKLKDSL PDFENYYKAKVVKTRW**YKE\KHIDQW NRIESR*QIFNIASII/HIEKEYLCNKW CYRTTKMEEKNMNLKPLP*TIKFNSK*I TDLNIKTITITWLKL
1322	15223	A	1330	403	2	VTGFRHVGCAGLELLTSGDLPTLASQC WDYKHEPLRLGELRSLTAAWAMQQDPVS PNK*IKIK*I/P*SEQSGI*SIHNVVQ NRHFYDPDTHFHHSKVPLTHYVVSPPHS FLSPTPGNHQCLLSVSMDFSIL
1323	15224	A	1331	1	389	KMKSQAIDLEKIFTKHISDKGLGYGLYK ELL*FN/R/RCQTTQLKMGER*TNSSM GMSFEWMVSKHMKRCSAFPSLVTREMQ VH/TTSLFVERYHYTPTRVAVIKQSDQV \W*ECGIRTLIHC*WECKMIAT
1324	15225	A	1332	392	3	NNFMPSSA/PPPPPPFFFGGPRVFSPPP FFKPPPPFFFGPQKKKIFSPPPPLKFF FFLRPPPPFFFGFFFFQKNLKGKGF F*PRPEKKKPPPGGVFFSLFFLRCSV ALSPRLECSGAISAHCNLCI
1325	15226	A	1333	394	1	SQVVGPTAIHYCAWLVPKFLGHFSKTTI SAPLLK*TSTRAETSKSFS\CPRKMERA EGRRMFLGKSLKQIVLLF/LISGSCVT AS*FL/CFQTESHSVAQARVQ*HDLGS LQPLSSRLKRFSCFSLPSRTRG
1326	15227	A	1334	416	1	LTLPLKPTPYNTRKENYRPISLINIDAK IL/NILAGKIPQYIKVHN\NMGLTPEMQ GLENI*K/RKSVNVIChINRKEEKILL INA*IVFDKNPTMI*KNSWQ\GEYKEIY SNILLNGKMLKACHL\KTRIN*GCQLSP DAW
1327	15228	A	1335	391	57	WQRCVNDKNLYQKEKQDNVREK/WAT DLIINFTHEEMQSVNNLQKDTHPHSLVI REMQIKTTSY/HLLAKILNSDNSSYW*G CGMGTL*CCWVVSKEIHALWEIVWFIY SK
1328	15229	A	1336	285	2	IFFFPWRGEII*HLSLINKGSRQNERAH \KNGDFSQIISKLLMYKYKILNQTTI KYMFFPKKHRTSIIKIEHILGSKGSLNNC QRISVLQTRV
1329	15230	A	1337	34	391	AKIASLYSSIGNRANSVSKQNKTKNQ LKN/IKTAGGLGVVAHSCSPSTLGGLH\ DPGV*GCREL*WCRCTPAWASG\ETLSQ K*INKGKERKKMKNCWWMNNSLIQLTS FSFTKTDWSS
1330	15231	A	1338	292	1	GGGISKTPGGEGAINPKKPPALPPGGKK EAFSPQKKKGERA*RDISEDI*MAN KHKMSCPPLMIREMQIKSTMRYRFIPI RME\ILKKQKNS



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1331	15232	A	1339	369	16	DPWQNEQLSRVTCPPRRASMFRT*YK VIIAALMAYSVGPRAVSCIRALWTTYG\ IMDNYKRHERRFLKPL*WPGMVAHACNP STLGGHGRHERVGRVRSIPDCVVRVAAG VKASI
1332	15233	A	1340	394	1	TQSGVQRHDAGSLQPQPPRLKQSPHPSL PSSQDHRVPPPCPARPCSSHDSYVLREG PCGRW/HESRGRVFLVLFSS**LSLMRS GGFKKGFFCTSSL/SLPPST*DVTCS SLPSAMNVGELQPHIFMHGF
1333	15234	A	1341	400	161	KIGPNLPCFSTKRPWKIDKIQFWPPGKV F*/SPPPPKKILFFPPPPSGPFF\PPPLP PLPKSFFPPKPNLPPSFGFDIPPP
1334	15235	A	1342	377	3	NRHFPKAE TLKASKHLKRHLPLLVIREV QIKTTNICHNIATRLAKM*KADNTKCWE SCEPVLTFY\C*WEYKLVQPL*KMVWQK PKVCVPYYLAILLLQHIPEGTCAS/CY* DIHKRLLTAMLFAM
1335	15236	A	1343	170	369	RCNENKITKEVYFGEIFVRLDNKEKNTS FFYFYFLFY/CWR*GLALLPRLVLNS*A QVVLPPWPKML
1336	15237	A	1344	385	2	SDLRRSTHLGLPKCWDYRC/RATVPGR LFIPLMVSLKHKSFKF*RPIYLFLLSSI MLLVSYLRNH*LIQGHKDLLPMFSSKSF MILVLTSSILSLLFCFLFFVLRQGL/N SVTQAGVQRHNHGSLOQP
1337	15238	A	1345	1	281	HMATKHMKRC*/SEMCTLKQLNTTTPD HQNG*N*K*LVNFKGWQ*FGAVWNLIHC W*DCKLAQPFWKIDLSIKAKISMSYSHV VRKIFKLKKN
1338	15239	A	1346	176	1	SVIWNIKEP*IAKIIKKKTIVGGLTVP DFKTYKAMVI/KTV*SWLKDRQRNQWY RED
1339	15240	A	1347	398	2	PRPPGPVRRRCPS/LTATSGSSSPSSP FYLGPQGFPLPAVLNRGPGILFWGPHK KNITLPARGR*IGSS*TAPFFF/SLFS FLLFSFLLFDTGSYSVPQAQVQWFNHGS LKPQPPGLKLSSQLLRLGW
1340	15241	A	1348	9	395	GLQNPCVGLVSGFFFFFFFFFFPKKGLGV PKKK/RGPNPNPVGFEFLATGPFFWTG PLKKNPAPPRALFWGPPPPPPWG*NPP PFLARGSPFFKKFFGGPDFFFYRTNPRG PNKRGPPLKLGWNP
1341	15242	A	1349	119	1	ENVFRNM/WPGMMAHTCNTSTLGGQGEW ITRSGV*DQPGQ
1342	15243	A	1350	58	396	GIRVGKVCFIIFFFGFFFGKGVSLPP GRETGGPPL/LIKPPPGVKGIFLPPPP GGGG\CGPPPPPRVIFVF*GKGFP*GP GGF*PPAPKGSAPPPPLWKNWGNRIFG GR
1343	15244	A	1351	396	1	GPTKGPFPFLDGQGFPPPTLKQNFPPFA LFFPPPLGKRLILGGF\PKPGGLQPPT* KPLRFKPGGESDCFPKFF*GRIVCFQOS LCFFPPPKKKKTAFGRFKKKTLLFFFF SDGVSLCHPGWSTVAQCRL
1344	15245	A	1352	1	250	RRL*SQLLGRRLRRQNGVNLGSGACSERS \CSERRSRHCTPAWATKRDSVSKTKCR RHQHVGS�TVRLRPYWRHCGCHWWP

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1345	15246	A	1353	249	3	CGATLCPRKYMKITPSFFVEIDN/AILKFIWKFPGPRIAKTTLK*KQG*RTHTPHFHNILQKAIIVKTMWY*YKHRQSPGRVAH
1346	15247	A	1354	15	416	LLTLSSSLKITIHTNKGRT*SFIRENIIIFIATTNLLGLLPH*FTPTTQLFINLAMAIPL*AGAVIIGFRSKIKNALHSLPQGTPTPLIPIILVIEITISLLIQPIALA\ARLTANITAGHLLMPLIGSATLTI
1347	15248	A	1355	2	416	IKYLNVRPETLKL*/ENIE*NPHNIGLGSDDFFNLTSNSQGIKEKIDESDYFKLKSCTESD'TNRIQLKNERKCLQITCDKGLIF*KKLK*LY/KQKTNNH*K/WSKRLKYFSRKDIHMAKRY/MKKCSTSIRENKP K
1348	15249	A	1356	426	85	HARLVL*FVF/LFETAYLSVAQA/GGAMAQSAHFSLELPSSSDTATSTSQVCYHRNT/RLLF*IFCGYG/RLCCLGWSRTPRLKQSSHLSLPKCWDYRWEPLYARPYLSCFPENARLG
1349	15250	A	1357	2	301	GGLLEVQVQDQLGQHNKTPSL/IKIYILPIYTQKN*KNLTRHGMCL*SQLLARLR*ED*SSPGI*GCREP*WRHWPVWTIQQDSKSRGEKKQVIFTHYT
1350	15251	A	1358	2	389	FLHVGQSGCELPTSVDLPASASQNAGITGVSHRSWLKFSLLDVPSLTP/VSSAVPLISYLATGWRQAAIAASPIFLHQLARPAQPARAAADS*LPADSAFPKQWTC**MFTGALFKKKKKPCFVAKK
1351	15252	A	1359	309	3	KWDHIKLNFTAK*TINKVQRQPMEW*K/IFVNPVDKGLITRIYKELKQLYRKKKSNLIFKMSKS\SSLAIREMQIKTMR YHLLTPVRLVYVLPKRARS
1352	15253	A	1360	300	2	KRAFH*KKMPSTFTAREGKSMPCFK/ASGWATPVI PAL*EAKVGESLEPRSSRPAWATRDSCLE*K**INK*KLTLGANAAGNLTLKMLICHKS
1353	15254	A	1361	396	60	HKVTRKSDGMLCHSGFCSINQLAFCCLEFQPGGPRGTPLP/PYKPPQKTPKKTGPGGGGLYSPFPGGGGRNPFPPGAQGGFF*PPSPPPPPPPGGRKKIFLPKKKKKSLLEFF
1354	15255	A	1362	37	385	ALFSFSFFFGFFWGKKIFFFGQGGGRAGGHSNLPEPPPPGGGAPPRPNLSGGGE*RGPPIS\GEIFGLKKTGVPPGGRGWFKPPAPKEPPPPAPPRGGISGQDPLPPVLPWGKKN
1355	15256	A	1363	12	421	EPWEPQTLGICTHLQTLFHDYQVLMKMLVVTVRYHLTPVKMPFIRKTFDTAGM*KKKGCCYQGSKKGGMLI/HPPWGAL*MSIVKKKTWGTFFKKIQKELPWPDAIPWLGMPKEGNSVFQRGMGLPSVIGTLFPPIAG
1356	15257	A	1364	278	3	CCTGEKLETFLLR*ATRQGCPLFDNVM EVLANAVRYEKEIKGIQNGKKKVKT\SLFPGDEIV/YAENPHKS*PKNSL/KLKSDCSKVNIQKPIAF
1357	15258	A	1365	265	330	WPGAXAHACNPSTLGGRGERIT
1358	15259	A	1366	379	1	KRKLMYCWNECK*IQPGWKTVWHFLKKLKLELPYDSVILLLYTFLKES/PVYARDI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CTPKFIATLFIIA\RCSLTHD*TKKMWYLSIMEYYSAIKNE/YLPFATTQMNLEDNIFSEESQA*KHGVFIFP
1359	15260	A	1367	1	376	HLPGAESQPPPV/DNSWDRPAGRTQLLWTPA/DPHSYG*GGAGPHPCPSQPGCCAPVQSCS*APSEAQSLGAADS\GPAATLPA RQLITKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKDDSGKG
1360	15261	A	1368	2	409	EEAMPKAKMG*RPFAPNSQILNAKKLLKEIKSVTPVNI*MIRK*NSLIADMKEV*VIWIEDQTSNIPLSQSQIQSKVRMLFS SMKAERREEASEEKLEVSR/GWKSAGFM RFKERSNLHNIKVGGEATSTDGEGA
1361	15262	A	1369	220	416	PQPLFDWQMYTYTLHNDILVNDGRLSPGGQGCSELSLCHCTPI*MT\SETLSQKKKKKMQARGLS
1362	15263	A	1370	310	289	AFR*AFHSKGSK**H*EKKVN/WNFTKT*NFCTAKDIKRMKRQPTKWEVIFANHIYLTGILIS\KIYKELRTQ*PETQSLK
1363	15264	A	1371	3	322	HASERTHRRGKSTETTPAWATERGSVSQKTKNKKTNK/RNTGSSIHMVSDFEKQVTQTF*SSMQMSNKPLKRYLTSVIE MN IKPEYHFTPIRMAI IKKTDNTKC
1364	15265	A	1372	3	332	GKEVS*EDIMMLHVYAPNNRASKHMKQNL IEMQGEI/DE/HPVIIGDFS/TPLSI I DRSGQKI IKDIV/ELE/STVKQLDLI/D IYRTLYLKRVEYVF\FTSLSKTFATINC ILGHKV
1365	15266	A	1373	381	2	CSVAQAGVKWCNHSLSQP*TPGVK*SSC FSLPSHSDYRHE\PALFFKFFVQMGST ML*FS*ESCIKGSRQPCSYYTLHSPPIF SSLFPLAPESIKRQEPSFFFEEMESCSV TQAGVQWRHLSSLQA
1366	15267	A	1374	1	385	YKKGINAKIFNKI**V\ESAISHDQVGI VLVLQGFSLI/RNKSISVTHVNR LKN/HMLI*IDAEKAFDKIQSSHGKIGIKGN FFDLLKSIYRKPMANVILNSEKMKCLPC KC\KTSQGCQLSPLFFLFFF
1367	15268	A	1375	1	357	CSGVISPHCGLKFLGSNDLPALASRVAG IIGMTP\HAQLIKNFCCCWWR*CLAFGG *RFKTMCRPIVK*NKSINK*NRTVCMSCGDS/RQLLGRLRWSPGLRNVQGCSEP* WHHCTSACL
1368	15269	A	1376	1	375	HRPKFKSISLLEENMGESFHDGLG/GSD LLDMAPIVQSIRDKTSDFLEIKKSCSSK GTV*IMKKQATDWE/RTFVKHTSNKGS I MYEEL*NL*KL*NNPI*KWAREFSRHL/ EDTQMATKHM/KCSTAL
1369	15270	A	1377	260	400	KRGLGKTVPFPWPKKNGPFFFFPKTTSK GRKTLMVNPE*PKYYSVKKKKKKKGGL PFPCKIFFPNLT IQTTFWPKTNPLTLK KRKKPPKKTPTFWGHFFFERGTTKQTGG KKNPFFKKGWEKLFLLGQKKKMAPFFFF QKPPQR/WRKTLMVNPEP*NLLKKNM
1370	15271	A	1378	403	1	TGVSQALSLFFFKYFKPRMVEFLVEPSR *KGPSVYGLQIFFSIPKVPFPFCFWAF/ SLV*SSPPCLSLHLLPAFGVLPKRSLPR PMLQSFSPMFFARIG*FQILLNFQSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						S*FFFFFFGDRVSLCRPGWSAVAP
1371	15272	A	1379	195	381	AERYQTSRSTADRISCLFI*SAEI/VFP DSGKKTGGNNNNNNNNNNNNNNNNK ISLSLKP
1372	15273	A	1380	361	39	PPVKETAKDVNRRFPKQPMNTNST*SDA* VDEVVCL*FQLIGRLK*SRRIA*AQEFK AS/HGQHSETLSLKNYLKKKRFSTLLFL REMQIKTTTRYHFTPIRMAKK/SHHTKC *QGLAMLPRLALNSWAQAILLHLHFSLP I SWNYRHTTSTQASLHVLFVIGCLGNRL LTSFAVSFTGG
1373	15274	A	1381	400	90	LPSSWDYRCAPPLLANFCVF/M*SQGFT RLVSNS*PQDPPTSASQSAGITGVSHHA WPAFFIMWFSSSYSR/TMH**QHPHV*K LHICPN**KS\LSCPQVPTIIV
1374	15275	A	1382	1	431	DNIPKKSAYVYWTILFKKG*DNVEDEAY SGTLAISIC/ENIHLVCSLSDEEQRST AQTIANITIDITVGLAYTILTAKSKLNKL CT**MPKLSYPLF*KIL*KNKTKNIV\P NQLQIKAEIPVEILHNCQDPETWLG GV AHTYN
1375	15276	A	1383	2	432	ELSADVSTFFFTITPLSGVL*QNWGIAAF IPIELRSPTEVTFSFDVGNPFEISLQS PTHFSDHQHHVRVERNMEASL/QVDQ LTPNTQPAPADGHVLLQLNSHLFVGGTA TTQRGFLGCIRAL/RMNGMTLDLEERAQ VTPEVQ
1376	15277	A	1384	1	421	NPPALASQRAGIADICHCAWPLRLSKP QFSNL*SKKFALGDV*SSNIL*YIYIFF EMESRSVTQAGVQRHDLGSLQP\LPPKL SLPPKLSLPPK\SASCLRLAGSWNYM HVPFRPANFCIFSGDGVSPCWPRTRTP G
1377	15278	A	1385	2	416	IFSVDETALYWKMMPSRTWYL/RKEKSM SGFRDSEERLTLFL\GLNAPGELELEIL LI*HPEILGPLNYVKFTLSVFY*WINEA LITAHMFTAWLTECFKPSVETCYLGEEM PFNILLIGNAPGYPRAPMEIQEINIIV
1378	15279	A	1386	170	1	DGVFLIFGGQNEKLNKNKG/DLTKLPR LA*NSWARQSSCLAFSKCDWYQREPPCL A
1379	15280	A	1387	47	418	FWGFFFFFLKKKKAALGPWTPPPPGQGG PPPPPPRPGKGGPNPPRQTIYGFWGQR GPPPGGGGEPGPPPPGEP\PAGPPQTGG PQNWPPAPGP*KGFGASKGAP*KGVD P GGERSQVNRGA
1380	15281	A	1388	58	503	RPTRPGNYIMIKEFIFQKDRTI*NVYAP KNIALKYIKQLINLKGKRDKLTITVAN ISTCP*VTDITSR*KICKGTEELF*QPA \DLIDIYRTLYPTAA*YTFSSAYNYSK IGNSIGHKTFN/CKRNDNIQWLFSDHN GIK*EINII
1381	15282	A	1389	2	401	LVSQVVNSKNRILKKIKNSTPVHT/RQM IRKQNNLIADMETVLVWIEDQTSJNI\ SQSMTQSKALTLFNSVKAERGEAA\EA GRGWFTFRKERRQL*NLQVESEPPS\AD VEAVASYPEDVAKIIDKGYTKQR
1382	15283	A	1390	294	3	KIVIFDFNDVKNCS*KIVIFDFNDVKN

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						CSSKTVIEGKVS DCKKIFSKHISDKYLI SIYKELSNLNNNQPN*KWAKDL/NNM SSKHKRKCISISFGKMQIKTQIRNHYIPT DAW
1383	15284	A	1391	3	422	PLFKKEEGTNFPFPFWRFFPGGKSFS PFFFPFPPIKGGPKVQKGRFFFFF F*DGVS LCRPGWILFPQVTEALLRGFL ALSSLCFRLDKFFFFF*R*GHLLSRWDY RHEPPLRIS*RKTKE\KGLIMLTRLV
1384	15285	A	1392	3	400	FLYIYKDIYR*YKTFQNNKGLKIYFK* EKDLSKLF TKDVQMTNMHI*MGSTSLII KQM QIKTMMKHSSLP ECLHFNANITC WKRLGPAGTLILRW*ECKSVKPL/WETF *QLIQLSMQENYH/DPATPLIG
1385	15286	A	1393	409	2	IVRHFSKEDIHSTNEHMKKGFSLVKEV QIETTMGHHHITVRRVKIKTDIFASA\N TKC*GYGKTRTLINS/YWECKIVQPL/ WKNILAVAYKIKHTFFPRIHLSGSQKS HPSIYSKEMKTLRQHKDIFMATLSQN
1386	15287	A	1394	409	24	KSPFFFFEKGFPSPPPGGAQWGGFPPE PPPPVVK*FSPPTPPNKGWRPPPSW/P G*LFFFCSPGGFPPLPNWFLTPPLR*SY PPGLPKRWGFKQKPMGRG*RAFFCDBPKI SKKLWSGKKKKKGRPLAI
1387	15288	A	1395	83	411	QRDSVSKTKQKKINNKSRDTLNRHPTKE DRWM/ANKHLKRYST*LVIREVQIKTTM RYYYISIKKSKINKPDHTNCWQCGRPG TLIYC*WE/CKMVPSLK*TFW*FLKRLN
1388	15289	A	1396	308	14	NFFFFYSWSNIIYCQKGTFTPI SDKID FN*KIISROK*QYMLIKSGIKN/DITII NTYTSNNSSPKYIKQTLTGLKGEIAPST IVVGVFNTLSIIK
1389	15290	A	1397	321	1	KQ*CSIEYS/FKYTR***SKL/WPGAVA HAYSPSTLGGRGGRIT*GOEFKTSLA
1390	15291	A	1398	183	48	KWPGAVNHACNPSTLGGGGRI/TLRSG V*DQHGQHGESP SLVGRVR
1391	15292	A	1399	18	422	KAGMAILDKVDFRTKNIITE*/EKHFI ITKGSVREENISVLNV/WPHYRASKHMK Q/ILIELHVELGEHTIIVG/DFNISFSV LNRIDKESARRR*NI*NNINHQLNLVDI Y*KTNTTNGRTTFFPSAHKLFTIIHI
1392	15293	A	1400	28	339	YSCDHNSVQPQTPGLKQSLCQPPE*IAG ITDARHHIWP IFF\LKRSFVFIAQAGTQ WRGLL*KKKKVGGFKKGSCLTLPGRGDY RRFREEKILIPGRGFCNELI
1393	15294	A	1401	390	1	FGLGKHLVHMTSKAQSIKEKTD*LDFLK IKNFNFSDTIKGMKRQARNGEKIFPRH QS/DDFF*WAILDTFPKEDKVMANKHIK RCLRLLLL\SMRYHYH*NKKT DHTKC*R ERG\ELELLCCW*EYKMQ
1394	15295	A	1402	149	402	RFWIHLRYKRVPPLNPNVITWKEKRGF VFVFVF*DRVLLCHPGWSAVPWS*LTAA STSWA\K*SSHLSPSY*DHQHASPCLC N
1395	15296	A	1403	1	403	KRKSVPELIC/APRC*APCSYRPNLPSS PGPHLDVPGPTPTPSPPRPGPARGPAA RPKEPAEPGKEERRGL\PAPEG
1396	15297	A	1404	342	3	KEDNLIDKGGSPKQQIFKVN*ATALY/YT

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						ALYSKKIPPTLIAGKEKLMPGFKASKNR/TLLLGANAAG\DFKLRLPIDHSEL*/RPKSTLPVL*KKA*LRAHLFIALFTKHFKPTVE
1397	15298	A	1405	498	66	KNYAKSTLPML*KWNSKALMTAHLFTAWFTK\FFMPTVETCYCEKKRF/SFKMLLLIDNAHSHPRALMEIYKEINIAFMSAKTASTLKPMQ\KVILAYKSSYLRLNI\FHKTAAALSSDSSDASGQSFK*IKWGFTRTRGRTRGSAR
1398	15299	A	1406	3	411	VSPCLCLGRSQTPEIK*SSPLGLPKCVDYRHEPLYLASMGVLNCPISNLGQCIPP*A AWWSLLLGC\PILMLNLVQTPDLPVQLPRAPGPR\HPPVSAS*VAGTLGTHHYAWLSMLLGSTL*DVFPFLSPSLIPSEE
1399	15300	A	1407	361	2	IRVPQKKKIKSPGRGHKIFSF*RGPPFFSFFFFLQKESHVSQTQAREQWHDHGSLSRLPGPK*FSH\PPPHPPVTGTTPLEIYYYYYFLRQSL/DSVALAGVQWHDLGLS LHPVRVRPV
1400	15301	A	1408	393	2	PGFNISVLKKASGGLFFFFSPLGKKGFFSQFFFFGSPRVFPPPPFFNPPPPFFFCCL*KIFFSPPGLKFFFKRAPPFFFFFFFFFPDRVSL\CCPGWSAMVQSRFSATSTLRAQAIL
1401	15302	A	1409	393	60	LNVNPNL*SYLDKHRGMLYHILQSKEFLSKTSKAQAKEVTLCWYDYNKLMFCTAKKTL/IKVKR*STE*KKIFVKY/STK/G*TYRIFNKLNNKNNTQFKNRAETSRSKMAE
1402	15303	A	1410	422	2	VNDRKMDGWMNGWKEGR*TQKKKGRRRKREKERSMFLEGRKEGREKEREKESQKERQKRGKARKEQRQEARQGG/EREKERERERERERERGERGRKSSS*TGSKVVKIILLAVKMLVHLKSLHLQKVCVFSFSRS
1403	15304	A	1411	398	64	PGFFFFKLFVENFFGPHFQFFFPKPKGNPL*PPQRGPG*\RFPGVFPPLKKGSKKKFPPPPRGTPRWGKKPLLPKRPGFFFGPRVSFFCLIEIGWFFWAQVPKKKKKK
1404	15305	A	1412	391	125	EPAPFFFFFPKRGFFP\PP*FGYPPGFSPPPFLKTPPGNFFLGPKKKKFFFPFGKICFL*RAPPHFFFFFWPPRQAICFIIE
1405	15306	A	1413	3	387	TPDLK*LTRLSLPK*WDYRRATTG\LF FFKPFASLGSISM*YHSPVCLASKLRILFDSSFSPSATAKHPLTSFAAAWLSPFALIQHSSSESSLYSSYCPVPILF/IYLFIFLRQSL/DSVAQAEVQWRD
1406	15307	A	1414	409	1	KRSGFFVF/SPPFKKGSFAKPFPLGSPVFFPPSSPP\GFFFFSPPPKRGFPNPFFWGAGFFPPPLF*NPPDFFFWGPKKKNFPPPRGKKFFFKGPPPLFFFFF FFFFFFFFYKIISIKGEIGRSSVVR
1407	15308	A	1415	3	385	HRPPFVMGLSPRPAAGVPGPPAVLAHQHHAQFLARP*LPPHGAGLRTCSPPCLS LPNPPWAPVWPEPP*ALPPAP/AVGPIN
1408	15309	A	1416	2	238	PGGRGCSELLPRHCTPAWVT\SKTFSQK

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						RKKREKPGSL*EKTLEFCQTLVFGPKKK NGPPLLGRVWAKRKGGFHPPLKN
1409	15310	A	1417	3	394	NKHLKRCSTSSVIREMQIKTTNRCHFSE *KHW/I INMCW*ECGQTELSALLIRC*\
1410	15311	A	1418	307	357	WDSEMVQPLWERKEYLKEITAESSWDPA IPLLDI\YPKRNEASC
1411	15312	A	1419	341	3	LETTRKTAEKIKRRAGFEK*NLETNKNNGN TISQNLRDVAKEVRREKFIAMNA*\SKK KEKP*INNLMLSLKELEKDEQTKPKVRR KKKILNIRAEIIRD*KNSGKD*KKSWF
1412	15313	A	1420	405	1	IFVFLVGRGFPPPLTRMVLIFWPHDPPPL PP*VIEGLFH/LPAFRPGAFLRKMVPPY *KNKIPPRKNTFFFLKPPPPFFFF*DR VLLCHPGWRAVAQSWLATASTSQAPAIL PPR
1413	15314	A	1421	1	399	WGEELVPSGRVHELFSALRSDRTDSV CSCGGQCHCPGAIPGAALKAACRGDPAS RVGVETGSTMGNNGFFSFFIFKPYFFRD RVLPCHA\AMAS*LTAAST*\VKSSF CLSLRSSWDYRCVSPHLANFKTF
1414	15315	A	1422	168	414	OPTLLTELGLRPVPPHPATMNILY**IN TILHYSYKNYFLFLRQGLQPLQAGVQ WQNHGSLQL*TPGVSLSSWDHPNPANF FIIFFLERQGLTLLPRQVLNS*AQ/CNT PASAFQSAGIIGMSHCWPKYN
1415	15316	A	1423	369	1	EWREKAGESLEPG\GGGCSELRLCHCTP AWVTEQDSSYKKKKKTPGGGKGVF/C*K LGGGINF*KRVFCFGKGTPTKKKTGGEA
1416	15317	A	1424	403	1	EHFCKSQDRDSVPKKKIYIYPMVSFMP INLTNWIKFLERQKLS*QIEBAIENLNS IY*/PNESEFII*SLPITKAPGPYGFTE FYYSFKGEAMQILHLFQKRG*RHSFSN VIKTLKSKPEK
1417	15318	A	1425	401	3	KNTEHSKRYSTIPQRYCGSSREFHFLV HMKVMFPLFKCAIALCLKQVYTVFFETE SCSVTR*/EVQQQDHGQQQPQPPRFQ/H PPTSASQIAETTAILENFRKICIVFLRQ SL/HSATQA*VQWRNHGSPQAPPG
1418	15319	A	1426	386	27	FFFFFKKNFPFFFQVEGKGRKLG*QPFP PG\LNKFSAPPLPGGNG*R\PPFARLF FFFL*KRGFSPLNQGLGSPFFSPP\R APKNVGFQGITPPPGNFFFFFSEAES RSVTQAGVQWREPGS\QPLPPGF
1419	15320	A	1427	398	2	CRINGVLILC*CECKMAQTL*I*FGNFL QKKLDLTCDSTIPLGIYPRDMKTYVH\ KKTCT*MFTAALLIITKSWEKLLRPSEG EWINSRHPYDRIVLSNYETHNVNKIQRH YAEAKKTV
1420	15321	A	1428	401	70	GLQVHATTKFFKFFVETGSCYIAQAGLE LLVSSNPPG/SSFPKCWDYRCETRWWPF LFKFSLPFVF*LNHLFCLHLLPLFILK LNLPCFMYLFIIPALYSLSLALFRND CDLSPIHLEVKKYFSKKDRL
1421	15322	A	1429	388	131	HHAQLRCFFNSFVEVGVSLCCPGWSQTP GLKRSSHNLNFSKCWDYKR/AITLPSFF *IALF*ENPPNCHSLPTPLSPPKLAALG NSCLHPWLPQPPVKGLSDSFVCMHPGS RGGGCLQRH\RGFKQENWFNPGGRSS*

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						PRSMYCPFAWGAQGGSLSQKKKKKKKKKS KNYQKILSTQKTQKSRVTVWSKHCTRH CEK
1422	15323	A	1430	184	413	VSEFLDFYFLFF*RW/RSHSVTQAAVQ* CDCGSLQPPFILFYFLRQSL/NSVAQAG/ VGSLOPLPPGFKQFSCLSLSIWD
1423	15324	A	1431	76	533	SCKRTTGRQFPDLPTRPPTRPQGFAVLA HAGG*WRDLRSLQPPPPGFKRFSCISSV LWCTKAFNDFQEIYSFSS*I*GFDSFE VNFFFLFMGVSL\FARAGLKLGLSGKLP ASASE/SGGIIGVCHWAQLL
1424	15325	A	1432	373	29	RQGFPPMGRVVLDSLKKKKFQIPNSKIF PGGGAPLVIPPSREGEAGKFF*P\GGKG AIKQNYC/HCPPTWGKEGNFVSKKKKKK EKKMHQK*RCVKDQQ*T*MLFPSPKSI YYFK
1425	15326	A	1433	389	73	TDCPAIGRNHRDPVRPLLSPPHRI/YA NLYYYIIVRILTLIQSTDL*ISPVLV LTRVCVCVCVCVCVCIILPS/CYFVCRF MYPTTTVKVQNISIGQEKQKTKT
1426	15327	A	1434	402	39	QAGLQLLASSDLPALASQSAGITGVSHC ASPSISL*APLGLDTFSDPFCFNDLDSF EEHWSGML/SECP*TGI*DLSEFS*VYW GYGFLEDHRGKVPFFITSYQSYTPPTQL IIADVKFEQLV
1427	15328	A	1435	105	387	EFSKVAGYKINTYKSIVILYNSNE*FEN \KKIIPFIIASKRIKYLKI/QFAKAVQD FYAENYKTW*RIIKEDLNK*KNVLC*WI GRL/NI/LKMVLLP
1428	15329	A	1436	242	2	FGGGFFWVGTPNKMGPFPQIIKNLF/TR PPENF*KPP/LPPIAFFSLGFLGVFFFF *DIVSLCCPGWSA*AQSLAALTSFG
1429	15330	A	1437	411	0	LLFVAQECLKWFSA LGPGVPCS\LPAN QQPSVWVP*QS\EHVTVLQRFCLWPVLG PAYGQIWEVPVSTLK/PPPPGFK*FS*V SLLSAWDCRCTP/PTDPANFCIFSRDAV
1430	15331	A	1438	41	412	FFCTD*GSLCCSSWTQTSGLKRSFHLSE PNCWNYGH/RASVLGLIFFFLRKKT/C P*KKFL*NEDLLCCQLGLELLAPRDS LGPQSVGTANVTTPRW/LLFL*TQNYLN SSRVRFSPAPLKYKEV
1431	15332	A	1439	1	406	HAYNIV\NPSPVSLTGALSSLLMTYGLT MGCHFLSITLLILGLLNTLTLYH*WRD VTRESTYQGHHTPPGQ*GPRYGIILFIT SQVIFFTTRFF*AFYHSSLSPTPQLRRHW PPTGITPLNPLEVPLLNLCVLLR
1432	15333	A	1440	3	422	MEKVSVVWIDQTSNIPLSQSLIQNSAL SLFSSMKTE*GEEAAEEKFEASRAWLMR /FEERCHHNKVGQ\EAASGDREATGSY PDDLAKI IDDSGYPKLHIFNIC*KPTDT DIVDETALC*KKPSTYFLFFFLKQSLAL PP
1433	15334	A	1441	375	2	KVSSPRAENVILYNCPPLFFFLCQD/CH SVTQAARQWRHSSLQ* TGL\ASQVAG TAGAHLPSQNLIGRGIRSLA/SVAQTG VQWRNIGSQPLPVRIKGFSSLSLKSSW EYRCPPPCPD\LFIFL
1434	15335	A	1442	397	122	GQASLELPTSGDPPASASQSVRITGMSH



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						CARPLGSCISLFPAYPFCFLKCFLE/CCREVILL*CSGWS*TPGLQSSGLSLPKCWDYRCEPP
1435	15336	A	1443	3	299	WEKMFAMILYLSD*ATVSRPYR*LLQLNKT KYKLKLSQS/MNRHFTRGDVAMANKHTK RKSTSLVIREIKTMRYHYLLKRMABEQK /SVKWCQECG*GGGKCG
1436	15337	A	1444	10	410	CTLFSLISPDASAGGICTMLLFQNTLNPK ISLALGVSDKCFNSFLIMTIVRNVFYIH GKKCILYCSPGCAHTMHMTLMHTHIHLK QFFLRRLGLTLLPRLECSGAITAHCSLDL LGSDSPP*EMFYIYMV\EMFYILFPRV CTHTYAHTDAHTHTPETIFFETGSHSVA QAGVQWRNYCSLQPRPGLRFSSYLSLP GS*NHRHVPP
1437	15338	A	1445	431	9	GPAQSLDSSVSPGLGTISSTVKWRHNAYL AGLSGGI/PCDCFLGPRVPWGSIGQWH WAVSPTLS\PTVRPPLFRETLYFT*V*V PELETCPO*HISHCRCVINWCEDHTPK KHLVCVHACVCVCVCVCVCVCLGRSRQS EH
1438	15339	A	1446	85	416	PGCLSLPKIWDYRCEPPRPFFHFFSSI QGPLTDFFLTPLEQVQISPTAKGFLKKI PFFFF*RRGVPILARVFKS*PHDLAA SASQKFGITGVSPHVHPIFLY/CSSIQG PLTDFFLTPLEQVQISPTAKGFLKKIPF FFFLRQGLT\RQWSTHLGLPKCWD*GCE P/PMPGLHCEFFKG
1439	15340	A	1447	376	3	IKSEIITETESRKPIEKIS/RAQSCFCGM VYEIDKLLARLDRKKMKTLNINRN*RD EINTDFTDIKRIIRENYQDYGTGFNNL DETDIFLERHQLPKLTQEEKDNLNSPIT IKDIEIIV*NLSTG
1440	15341	A	1448	2	192	SKWIKNLNLKELKP*DS*KKPEGNLHDIR FGNDFLDVTPKN/MATKGKIDN*TLPKF KMLMRIWRN
1441	15342	A	1449	411	3	VFLPPLPPFCFLNFF*GKGGFFFKIFF* KKKGVEGPQLGPPPPGPFKKKFF*IF LKAPLFVPTLKLPL/CPPKKKNWENNP PPFFFCFFVKKTQFYFFFFFLRNRVLL CHPRWSVMV*SCLAVASTSWAQATCP
1442	15343	A	1450	413	1	EA*TGWCNPPGGGACHEPR*PPCPPWA TERGFVSKKRRQEK/SRIMECFQDNLP GFFQIFSVMKNKQEGR*FWTK/VKMTKY NA*NVNGS*YWKRENEECYDVVKKLF QSILS*YVKAR*KPGCWLMAAIPALW
1443	15344	A	1451	4	384	DPAIFLLGTYPREMKTVHIKTCTQMFA AVLFTVAETSKRPKCPTE/VNKI*CTY I/MTYYSAMKRDE
1444	15345	A	1452	3	390	LPDHPGSSVSTPRGVIITGRGFLLFPW VSFFFFFFFLKRISLLPNWRGGGQNL NKSPPPRGF*NFLA*PPQGGKKKGP PGAPGDKNP/QPFFFGKKKIFNPPTG GEKKKPPSPFKWGGGPN
1445	15346	A	1453	37	381	LILYINVCVCVYIYTHQTQMGSHIVAE AGVQWCNLGMW*P*TPGLK*/FLSSGD YRLTLPHLANLYIFFFFFEQRG\FFLL KLIV*NSGPKATLPRVGITGLTHTPRPYR

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						GDLFF
1446	15347	A	1454	3	400	TEMVLHTEMVLHISVWDPDLLDRPGRGVT WLMLTAEFLYGGTEAFSSSFVDV*GPCS ETVECFSD/L*A*GPP*NT*SPIYRFAS FLLAFCIYLLETRSP\SVTQSGGK/WQD LTSLQPLPRLK*SSCLSLPSSWE
1447	15348	A	1455	77	398	RAEIVPLYSSLGNRVRPPSQKMYIYYEQ LHAHTFGNLAEMDKLVERYKVLSKFT*E EI\NSPVS IKEREF\AVISLPQKETLG PDSFTGGFYIFKEELMPILQRLFW
1448	15349	A	1456	397	69	CPPGLSGLEPVA*AVPP/RRPAPPPPPP AGIDAGLGDDPLQQTTHA/PPAAAGSAP AGCAAGPARGAPRGRSPRRGSSAGAAPP PWPPAAAAASSAGGSSAPCASSPAAPPT
1449	15350	A	1457	400	2	ALFFWAPKKKKNFSPPGKKFFFFKGGP PLFFFFFFFFFFFFFFFFFFFFFFFFFFFF FF*RRPIFILFYFLNQKNIPRDFFFFFFF FLRDRVSFCQPGWTAMV*SQLTAA\*TP GLKQSSHLSPSS*DYRWVPPC
1450	15351	A	1458	343	11	QGVHSRKYKEISKLS*KNPNTRKWAKD TNRHFTKDNIQMENKNMKDVQARCSGS* F*KN*NFKSYAL*PKCSEI/KKSVTGTN WRNSQIYDKLSTLQNN*WIFSRSLYNFE
1451	15352	A	1459	109	401	QNYRQLGQWDRIESTVIDPCKYGLIFD QSAKATEWRKDS*NHQTS/WWKESFTRV KALEEITKRKVNLSLISVKTVDHVIKV *LKKKKKKRGRFKE
1452	15353	A	1460	42	424	CPAN*NSFSRDR/SLPMLPRLILNSWPQ VVLL/PWPPKVMGLQ
1453	15354	A	1461	419	69	IFPLKKKKRGGGVGPPPLYPPLGAKRGG SP*KQNLKPPRPHKENSPPFYKKKKKGG RGGAPFFPPLGGKTKKFFLPK/IKVS FNPNLFP PPPPGGKKKFFFPKKKKKKK SRNTVWF
1454	15355	A	1462	1	277	CHTNFLCMSFPPAISHHPLMPPHPVSRS VAQAGV*WCDLGRG/CELSRCHCTPAW MTERDSISQLIRKKKKLIKIKKKKNKNK SVIFLGGGS
1455	15356	A	1463	382	3	KAGGSINQNSPPPPPPGKKKKPPPKKK KKKKNPFWGGPRILPHNPPPFER*R*KI FLGPKFLTPLGPKIKPLFFFFLKKKKKK RMTY/HSVAQGPLLNKDTLQAG\LSKA* RSPPKSKSMQSFHRN
1456	15357	A	1464	561	86	NDPILSLKAEKTFGKIQDSFLIVSSSL\ NKPGEIGNLLS**KASTKQNPIMNLRV\ LNVFPLRS*TRQVCLLSPLLNFIVLEIL AHIISQEKIKKIQI*YKEEKLPFLTSS SLFI*VKNLMEFAKKLLELINEYNKVER YKINIKNILLAKNTWTLKF
1457	15358	A	1465	3	221	RFHRVSQDGLDLLTS*STRGLPKC/WD YRLEPPCPAKTCLILNGSC*VFLCYLSC FKAQERPSQNSWGAFTL
1458	15359	A	1466	2	396	WWPAWHTPGLKQTSRFSLPECWDYRRE PP\PGLVKFLL/IQYRVVTQHVLGDWV QDHHPIEICLHKSVI*NGIVFAYNLRT SSLTLFYLRRLG/SAPQAGVQRHKLSSL LEPLPPSFKRSS\CSSLSSWDYR
1459	15360	A	1467	349	413	RLGL*PRKIDTD/HVSLRKDTG/WPGAV

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						AHACNHSTMAGHRRQIPRSGV*GQPGQ
1460	15361	A	1468	403	2	LPVEWKGIGFSGFHPPLRLKKFFSPTPKS*D/YRGGPPPPGYFFFFFLKRGFSPFGRVIFKFPFPGVPPPPPPQNFGFKGRS/HPSRALFFFFKRVFF*IYFFFFFEMEPRSVPOAGVQWHDLSGLQALPPRFM
1461	15362	A	1469	423	3	IEFSFFAPSKDKGAILGPSTLPLPRFNNFFCPPFPINKDIRRGPPPRPNFFFFRKRGGFPHWAGMFLSFLNLQEGPPPPSPQ/SVGF*GRN/HPRAQFFFFFKFFF*CYFFF FFFEMEPRSVPOAGVQWHDLSGLQALPPRFM
1462	15363	A	1470	13	427	RTRGLVFDKTEFKPPKIKKKKKA\GPFLRGNRSILKKKATFPKNLFAPNPGPPKFIKKVLSDLQKLNPPPRMGGNFTPSLLK*NKSSKQQTTRDFRDLTSPLDQGD*KIYKTFYPKTTEYTFSSAPHGFY/S*FDHKI
1463	15364	A	1471	378	1	FVRPPFFFFSSSRPFKVVGGPLPPAPQFFFKTPRGNPPLLRG*KPPPTPVGGAKGSPPW/VPPGFPPKGGGVFFFQQL*KISPPGPAPP*LVWGGESPPFKKKKSRPGVV AHACNLALWEAKAG
1464	15365	A	1472	412	53	SRLSFFLSSEPHGPPSPLGPATNKVAF C*/PPPPF*PSPPPKFFFF*GPKSVIYFYQR*PPTSRIFFPKGGAGPP/PPFWGFVNPKKK\LKPFSPKSPPAAKFKNPEGTKLGFFKKKKKKL
1465	15366	A	1473	116	34	DWNKPVLI SNVMTGLMSMIITLLQLFLL*LFFFK/WELTFFGKFHQRVDPFSQGS LGRGQFFLLTKTEYHIFFLIKVFNSKTEGAGLAT*IK
1466	15367	A	1474	42	428	EIIMESINRFDVITF*NFCL*CYLSKINRQASSW/ENV*NQYVGEKILIFLIYKECIQINKK\KLRPKIDTQVKDKQISEEGMQMANQHMIQC\QPSLVLNKMQIEIAEGH HLPYQINKDSKMMVEERRQ
1467	15368	A	1475	87	433	PQSSPFS DHCSYQRLFLHLVKVSTYRLQKIRKIHKSPGNNEYFGGFFLFFSFLFFETGFNFVPQAGVQGD LG*LQPLPLGFGFS/CPQPPRTFFFFFPLRVWGF IQKKKFLFV
1468	15369	A	1476	212	430	SLILMTSNGIHFIYFLFLLLFFFF*DRVSACHPGWRAMS*SYFT*ALTSQVK\QSYLSLSSS*NYRHTAIMP
1469	15370	A	1477	493	2	PGAAAHACNPSTLGSQGGWITRSKIPHPG\TLWNPRSY*KTMCGLLEAP
1470	15371	A	1478	454	492	HRVGEEF/CLFETESHSLTQDRVQWHD LGSLQPPPPRFKQFSWYHI*PHAW
1471	15372	A	1479	2	213	IDQERERLMEGDRERDTETDAEKDMGRE/RNRYRERERLRG\RRERRKRDRMT*M PRERERENLSLYRETYRDFETEWVMDRERQLKRRL*AVIVPSHSSLSGSRKTP FQKKR*REGERKSEFLIQDI
1472	15373	A	1480	77	453	SFGDSLTLSPRLAVQWVYLGSL*PPPELK\YSPTSASQVIHYLLFFFFFGKKVS FCPQGGGEGPPFGLLEIFAPGLMPFFCLNPPKGVVWR/RPPTMPKLFFVFFIKRGF SPGEPRGVSFPEPGT

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1473	15374	A	1481	398	96	KRPVVCFSPPPKGGFFPLIFVGRFF SPPPVFK/SPPPFLFFPP*KKKLFSP PRKLIFF*KPPPPFFFFFFFFFFF FFFFFFFFFVFILLLS
1474	15375	A	1482	484	64	QKRQMANKYMKICSPLVIREMQTNTTI RYDDIPTRVAKNKTNK*KSNSTKYCQBC ESARP*IYCWWKYKMVQPLWK/S/VWQY LLKLN*LPYDPIPLLSMYPSTQIKTCI PTKTCAQMYLVTLFIITKNQKLAHSARV G
1475	15376	A	1483	2	400	YNKKGQGVAPRYDVTANFPKELAKII DEGGYTKQQSFNIDYALYWKTPCKSY SWR*IH/SLASKDRLT\LLVGNVVGDFK LKPVLHCSKNPRVFENYTKSTLPVLCK WNSKAWITAHFLTAWVAEYFEPT
1476	15377	A	1484	459	65	GGPPPPHKTIDFFFFFFFRGESPPPPKK KKKKKKG*DNAEQAQSRPPPSI*EKI MHLICALTEEY**LTAEIIASNIHISTG SAYIILTEMLELSKLST*WVPKLFYPNQ LRT/RAEL*MVILNK*DQQF
1477	15378	A	1485	2	518	PPPPQRFGLRGGAFFFFKKKG*DNAED EAQSRPHPSI*EKIMHLICALTEEY** LTAEIIANNIHIHISTGSAYIILTEMLELS KLST*WVPKLFYPNQLRT/RAELSMVIL NK*TSDF
1478	15379	A	1486	122	501	PRDPPALALQAGITGLKQSYFLSLSS WDYKHKPPCAGYLK\VFLEN*YLALY VF**SYQGTSLVTQPPSLIPRHSSPGVS VQLFQKK/DLQHGCLLTPSISGYSVTWD GVQWRDHGSL*P*PPRF
1479	15380	A	1487	491	425	IPKNDI*AEP*RINKR/CAKRMVVRKGF EASTICKALRYEEIVCSRNTFVHGWL *ENRGQIMKGFNGSVEKLEHN*KFYEG* LLYRFE*LAAGFIVFQQ*VSKEIVKAWP GTVAHACNPSTLGGRGWITRSGDRDHP G*HA
1480	15381	A	1488	441	17	KKTNIYDQLIFNKGAKSTKLKNSLFNK WCQDKIS/IQKMKVDPYLISNI\NLKW LKDLNVTAKTIKLLKENTGAILHDLGFC NAFLDGKPKAQTTKKKQVK*TSSKFKSR CQWLIPITLWETEAGGSPELRSSKPA WPT
1481	15382	A	1489	413	1	LEWKEMVFLFWPGRVGNPGPK\GWLRLR PPPF*FSFQPFWGPVGLLEPKNFYY*P PGAHGPNPPPPGGKG*GPPRVGGGKFN *PKFGPCPPGWATKQKPVFQKKKPKNKI KNRTVKVPKVTKFIIYYVPLNGVSN
1482	15383	A	1490	359	407	RHRMITFFT*IVTQNFYPL*KKMDIQIQ ED*RTPN/RDQHKHTPRHIIKLSNSQ\ NSKRILKTRKK*LVVY*GTHIRLSTYFW PKS
1483	15384	A	1491	397	39	RKFRGRSFAKTLFSGPGQG/PKGNPGLI PEGPPPPFFWPAEDGGFFPPGQLPPQG PIRGPGPFLGFPVPPPEGEGPPPTGP*K PGQKRPKRGWSPQKKGPKKKTLEFFFF CQMESRSVT
1484	15385	A	1492	378	1	FGVFWFLAPRRKGGFFPSHLIWVPPGFS PPPGV/SNPGGIKFGGPIKKIFPCPR

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						GKKFGPFGKAPPFFFFFFFPQDGVCSVAQ AGVLQ*AEIVP\FPPT*ATEQDPVSKK PTRPPTRPPTRPPTRP
1485	15386	A	1493	3	428	TKSP*PDRFLAEFYQTFKELVPILLKRF HKI/EEGTLPS*FYE/ACVTLLPKPGKD TTK
1486	15387	A	1494	3	417	ILNNARLKPFLLR*TTROGILLSLLFN KI*VLEFLAGAISQEKIKVIQVRNEEM SKTLFSQTT*S*GRNPFIKIPLPKMSVV N/NFIKVTEYKVSII
1487	15388	A	1495	429	4	PFCLGSKRFPFFFNPPRGKGF*KKKKIF GPFRGGPPLFPPLWAPKGGGPPRAGGSG PPPPKGGNPLFINPKN/PPPPGGAIQ SRFLGGVNPKIFLFPGGKFLTDPGFPPS LPPGGKKKKPRFQKKKKRKRKVKEKKY FL
1488	15389	A	1496	3	433	FSKEDTPMVNKHMKD/CCTSLVIREVQI KTTTRYHLMPTRMAMCIYIFNYILFLK/ SKNNKC*RYREIGTLIH/AQWKYKMLQ LLW/KTIWQLLRMLNTKLSKDQE\IPLL GI*KKKKKKKKRGRFGKINFDPGVE RINFYNSAPK
1489	15390	A	1497	3	326	WPACL*AVAAVALLVPEATRLTMGNLNT VCTPHSIAELLSSKG/DLWLTDNR/LLK YQALLLE\DLQLRTFTCLNPATF/VP TGEPEHDCWVVVQTGKRNNKDHCLYSL
1490	15391	A	1498	345	22	KSKWLDLHGKCKTLKR*YRKPTK*\LG HGNDFLDTSNAWFI/RKIDKLDFIINK NVCSGKVTVKRMKR*TTRDKISSKGIS DKRLCKIYIKILTTOQ
1491	15392	A	1499	194	432	PVVCVCVCVYVCMCVFETQS/HVARAGM Q*HNHSSLQL*TPGLKQVSCNLSSWD YRHTPN*FFFF/CNFYLERGGVS
1492	15393	A	1500	2	417	RD*FMRFK\EKSYSCNTKIQREAAANV ETMASY*EDLAKIINEGSYTK\SQIFNV DEVAL\KKMPTRTFIVRERKSI PGFKAS KDRLLFLG/ANAPGNIKWKPVLIYHST NPRAFKNDAKSILLVLYKLNSKAWRIAH LF
1493	15394	A	1501	414	0	SSSSSSSSSSSPKWTGALQP/LLSRTP LKDSSEESSQ*AEL*AVHLVVHFAWKE KWPDMLYTDSLAVASGLAGWSGT\WKK HDWKICDK/DWGRGMWNL
1494	15395	A	1502	3	125	RLGLPKC*DYR/RAATTPGLH*F*SWKE QRPQ*LALGRKPVNRNKNTQKYIHIYTY TH/PIPTNVYICITYHIHTPV*YTHIY I IYLFKVLVFGFLRRSLT/SVAQAGVPW RDHSSMQPRPPYKQLTCH**LASQSARI TGGSHHTWPALILKLERTEAPVISFRTE TSK
1495	15396	A	1503	406	172	DIILDR*RQQRLLRLRQKQRETETE/RR DRGRERQRYRQVQRRRQRRRLRHR Q*QRQIDRLRQRQ/RAERDRGRDRDR GRDRGRDRERQRLRQRQ*RERQRHRQR /RERDRQRQRDRGRRRDRRETDRGLDR G*DRGIDRGRCSDRGDRDRGLDIGSDR DR
1496	15397	A	1504	3	420	ITGVSHRAWLPS*FLKFFVVVEMESHV

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						AQAGLK/PSGLKRSSHLDLPKCWDYRHEP\PHLAFFQFF
1497	15398	A	1505	407	1	PISIIYHSDPGSLKSYTKSTLPVF*KCN NKTWLTAYLFTAWFPKFKPTVETYC/S RKKSPPFKMLLLIANAPSHPRALMEMHKE IPVVFMSAVTSILQPMQGVVLTFSYY LRNTFCKAIAAIDNDSSGGSGQIQ
1498	15399	A	1506	1	408	PPGFKPFCLSLPSSWNYRHPPP/RPG*F FVFLGGTRFHHVGYTASQHLTSRETHAY ALQ
1499	15400	A	1507	2	416	EPRSHHCTPAWQLSKTSLQKKKKKKRKR MVFTGRKKGLFFGN/LKNLGTLRSREYPL GPGIKNRLAQKRKPLFYKKRF*NINPGG GAHPGGPKSWERGGGRKI*TPVGKYASN PEYHICIPGKRNQNPFLQKKKKRRAD
1500	15401	A	1508	276	14	SPPPYFLLIR*GRKGRGQF*LRLFFII NLRQCL/DSVSQAGFQWHNHSSLPQRT GPK*PSFLSLPSSWDYSHAPQLLAFYGA NCFN
1501	15402	A	1509	1	391	NIFKEIMSENFPSLMSENFPSLGKEIES QIQEAQRTPNKMNPKRSTPKQVIKF*V RE/MLKTAREK*IVICKGTLRPAVDFT AETLQIRRE*DDTFKTLKGKKKKKTL AKLTFPSILVFKKTRGGR
1502	15403	A	1510	2	419	PRVRSRATNVISKYQHKKKNTSK*IKD LNVKPEPIKLL\EKTTGEKLLDIELGND FLDS/TPKTRAPKANLTP*NYFKLKSFL TAKETFN\KTPTKRGANHISDRGLISKI YKELTIQ*QKNNLISK*AKDLKRHFSKE DV
1503	15404	A	1511	392	122	SVSLCVSLQSSGMFRC/LPTMPLRR*RQ ENPLTSAGGGCSEMRSHPCTPAWVTQD SVSKK*INK*IK*/Q*LRQNVKIKPSPI FCEQGKRRK
1504	15405	A	1512	2	281	GGCSELRSCHCTPAWTT\SETLSQKKKK RKKICIECNTLKSH/ILSFVCGKYHSP VSCTCL*WSLGRSLKRSLEHQQNLNDP YPIFQNETNIH
1505	15406	A	1513	242	382	QGPNLG*LHPPPGGLKGFSPLTLLRSWK NRLPPQHPFYFCFRKNKV
1506	15407	A	1514	1	388	RTRGTERDT/RFRERRERDRGREGYRW RYRERERHRERES*V*RDRVRDGRVID RERERQSERERLR/RERDWERDITYIVRE TETERETEGERDIBRERDVRDRYM/RD RDRDILRE*ERDRETALDSEK
1507	15408	A	1515	4	285	TRXQICNGDKTALY*KEMPSRMFPARVE LMPGFKASKDTLTLRLRPNAVGVNLKP MMIYYSENPRALKNYDKTQLCLYSTNGN KAWMTDYRFT
1508	15409	A	1516	415	2	MGDRESLPPSRVFLFFLAPCPKGILFHP V*FGSVRSFSIERCYR*QORNEFWGPVI RVKASSRAG*VVFSSSTAPPLFF/CFE TESCSVAQAGGQ*CDFSSLRPLPPKFKG FLCPSLPDAW
1509	15410	A	1517	1	324	PTRPEMGRHAAPAGLELLSSSDLPSTSA SQSGGITGVSHRTWPILASNNY/SMDKL CAI/CERFILFLLKNILLWILILFIYI FCLIK*CITINFQSNSLLPHSIHLYI

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1510	15411	A	1518	2	163	ACRYPWLNFVLLVEMGL\TMLASDLERS G*PQ/CDLPASASQSAGITAESHHGWP
1511	15412	A	1519	425	52	VLRGAQFLFQEARLKWDFGPGGMAPP CNPEPLGV*KGPLPKG\GGPNPPGPPRGNP VFSKKPKITPPGGGAPEVPPPWGGGAEK FFYPGGPRVQGT/RKTTPPPPGRQKGT PLPQKQKKKKPWSL
1512	15413	A	1520	3	404	THASGKSNIRGLTLPVFRTYYKAAVIR/ TVWP/WLRANTNRQNR/DGPEVDPYKC SQMIFDKGAKAIQ*RTDNLLNKKW*/ES *TSTCQKKKKKNQFR/DPAFLIYTKFNS NGRKNLRVIGKT*KVLKKNIKQNWGDLG
1513	15414	A	1521	332	39	TSRETGNFQDLDTAFLENVGVLFWRKG KGKIDIGIGTKEMP*FPI*LLMFSYIVI ERERKPE/LSLSPSLECSGMILAHKKNS LPGSSSDSHDPASRVAG
1514	15415	A	1522	482	0	RARTSGVLLCSPGWS*TPDLR*SLCLSF PKRWDIRT*ATVPGLLYSLYSRFP/DE LKGCEKSRTPA
1515	15416	A	1523	1	417	NKC**RCEEKGMPPVYVWYBECK*GQPFWK TKERFFKKNL/NIELPYNTAIALLNMRP Q*I*SQ*RKVCSCMLCAT\PTPNK*IKT MW*VCLVEYSSPLKKN\LLFSTTWINLE DISSNK/LRHRKSSISRHLLL
1516	15417	A	1524	1	397	RDSTYQGHHTPPVQ*GLRYGVILFITSE VFFFAGFL/WSAFTRSSLAPTPQLGHW PRTGITRLNRLEVPLLNTFVLLASGVSI T*AHSLIESNNRIIOALLITILGLY FTLLQASEYFESPCTISDGIY
1517	15418	A	1525	2	376	LKAKTGQKGLLHQTVSKFVNAKEKFWK ELL\KSATPVDI*MIRKRTSLITDMETV *VV*KEDQTSHPILPS*SLTQSKALNLF KAMKTDGKGAVE*KSEANRGWFMQFKE RSC/RFCNIKVVQ
1518	15419	A	1526	3	386	ESMLKAKTGQKGLLHQTVSKFVNAKEK FWKELL\KSATPVDI*MIRKRTSLITDM ETV*VV*KEDQTSHPILPS*SLTQSKAL NLFKAMKTDGKGAVE*KSEANRGWFMQ FKERSR/RFCNIKVVQ
1519	15420	A	1527	127	388	KRKSQINNLLQFKELEK/QEETKPKAS RRNKKKKIRVDLLKIKKGKPLEGVKKKG GFF*RTNKRDKPLLKPKKKGGGRIKTF HKTS
1520	15421	A	1528	3	402	HENHMKICSTSYVIRELQIKTTMK*YYT PVRTTAIQNTDHTKCWQG*REQ/GSLIY CW*QCKMVQ/PLWKRVMQFP TKLKHSLN I*SAVLLGIYP\KSGKFNVTCTCT*M FLAK*PQCSSVDEERKKM/WMYGFE
1521	15422	A	1529	2	365	IEKLYRSKAKFFCRDRVSLCCPWSRTI GLKQSSCFGFPKCWDYR/R*AALSGRL LTSSH/REQIEQETHYPEKSAKLFMQ DGPPRRK/HPPTRPQASNIQNKFSFFLR QSL/NSLAQAG
1522	15423	A	1530	1	418	GTDTE*ACDKIQKPFDPKRLNKL/IRK KHLQLDKYL/WKNPIASILKSRRLKSV RLRPGDGRQGCSPFPAWLFNIILEGLARA IR*EKQKQKQGQ\QIGKKEVNLSLFIED IMLYIENLKESTKKPIIINEFSRKEDF

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						RP
1523	15424	A	1531	381	3	ILQGFVIRKKSIFQKACHTSDLTWLTNLSCLHMKGLPPHRLYSSCTVLLFLRKPVMRKTTLSCCFLT*DFFLPLPPCFFR*FILLIF*LYFCKDKVSLCCPSWSKLLP\QSSCLSLPKYQDYKA
1524	15425	A	1532	38	479	DEACGPQDPYLTPYVKTQWIKD*TRNKG IQFLEENGKN\FDIGFSSDLLDMTPKTR ATKVKL\NDIRLRNFCASKDTINLSLLC R\KR*PVEWEKISANHISDKGLISGIYR QPPLNSKTSHLI*K*ARDFNRHFSEEDI QSALYRWVL
1525	15426	A	1533	105	447	LIFCRVFEYLHSLHLPQEICLSLALFSR FTFCV IICEVDVWSVIFKVPFCSKRNKV AVHTMLYIQIFVSLFI*PQNWKPCKPA TVERINKMWYIHIV/EYYSANKR
1526	15427	A	1534	76	471	VWVCLLSLEGSQSKFGNSIEFGVLLSSG GFSAWRLFFVYFLRQSL/NSVAQAGVQ QWRDLSSLQPLPPGFK*VLKQRGVCLFV CFETESHIAQAGTQWCDLGSLLQPLSPE FKRFSCL\SLSPWPSPG
1527	15428	A	1535	45	338	SNNEPFLDWIVM*RKVD FIRQPAMTSSV VGERRRSKALPKAKLAPKKVMVTIWWSS ARLIHCSFLNASETIASEECTQQIDDMH *KLQRLQAALINRK
1528	15429	A	1536	425	1	FFNITFHSVSFSPLSQKCILTL*ILLKS IVKNNMRNFQSLVRK*AKDMNRHFTDD HVQMAS/XHMKRCSLVIGEMQIKN\TVS YHYPPIRMIKVRNSSNTKCW*GCGQTGS LMRCWW/NK*NQLLWKTGIPPHGLVSTR SRVF
1529	15430	A	1537	4	443	ETFVDHYQCGGIRPFSDQLQHAGRTTAL FKA VRQGHLSLQRLLLSF\VCLCPAPRG GAYRGRQVSLSCGGLHPVRASWLLCLPK *AWTMEGTSTPASLPCLISDCCASNQ RDSVGIGPSEPGAENLLVPRFLSPSEK RSIWVG
1530	15431	A	1538	487	3	TQNGGVLLSAPRSVFSPTTLR/CTLQAQ C*AFWWGGTQQAASSTAAMAAMKPLGIW AGGAAGILPKLGFQD/LPLSAEADPAGK ELSIGRQRAWREQPDQSAEPPFSQAPRP GYPFSPQPLSMRRGPGANPLARPLRGP VRVRLRRASSERQKRSGGSGPLG
1531	15432	A	1539	394	489	IYLFIFETESRSVAHAGMQWRDLDSLQPSPTG
1532	15433	A	1540	475	202	PGGGWFSPPDNFSLKENSQGGPPVSHPP PPPGNGEGGKTPGAGHSGI*NPPPLKI N/LEKGGRGGPPGPLNPPFPKEKPRGG KKKKKKKR
1533	15434	A	1541	14	468	LSMWWNSRLKARRLVLSQVVNA\KERF LKEIKSVIPMNTLMVRENRSLIVAVEKV LVA*VKEQTSNIPLCQSLVQS KALTL LHSVKAKRG*EAAEEKLEAGKHWF LRFKG KSRLHNKIVQGEATSTDGELQQVTY PDL VKIVGEGDYPKQ
1534	15435	A	1542	479	141	RKTDSWDLIK\SFSTAK* AINEADGQTT EWEKTFANYASDKGLISRKELKQINKKK ANSPIKK*AKDTKKQPTNMKKCRTSLII



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REMQIKTTMRYHLTTESF*LLIKSQGRAL
1535	15436	A	1543	17	474	NPKKKKKKKIDLLDYYTYLPK/AEYTF SSEIHKNWLYIN*LRANLNKFIN*KIKT ILSDHNRQPEINKCNKTKR/RVT/TQK FKNLILSNYVWKGELOQTQIAEFLKRNVN KNTIYLNT*NTIKVLNSGGST/ALNTYI DKNFKKRVPS
1536	15437	A	1544	89	481	ICLKVISLRQENATSVACTVSCLESGSR ASENLVLHNASPNSCGLGIAFTCLCNV SSGNKITDCYD*LSSS/WLGFFFFFLK KSFLFVAQAGGQGGNLG*PKPLPPLKQ FLPPPRANFCFLEKTGFFLF
1537	15438	A	1545	1	300	PPPPAPXXCRPY*XPWXXPVYHSSWRHG SGAAQGAVALAGFGGVGRQGPGAASVIP LCPENQGCREFPGPSHAVPAPSALPSLRS LTGGQIGGTTRAAQAVG
1538	15439	A	1546	2	436	GAPETIKSIKGYND/RLCTTKFYNLDEM DKFLVRHKLEKLI*E*IDNLNRWITSQE TDW*I*QQSSSSSSSSSS/PSSSSRPN GFTTESYQSFEKLIPIICKLLKKIDKE \GHFPLQL*GITQIPKPDYH/IENYRP ISLM
1539	15440	A	1547	54	419	PATWEDHLSQGGDCSEPRLLHCTPAWV RE*DPTSKKKKEK/NDQ*LLIP*S*RRL *RSSHQTSHLMDWNSEAGR*EATFLRSY SKL\KEELELLLLILDNDHNSD*YLL SIYSIPGTVLS
1540	15441	A	1548	37	339	KRWKCLRA*LLMRPRHAD*LNPDGVGYS EL*SRHCTPAWVTEQDLVSI STNRKNBR HTLEYSHQHYSG*P*TG/ESEYPSAL* QREIIDYSFIQGMTDQL
1541	15442	A	1549	477	1	PGSHDLGSYT*PQ/VVSSPEVTSRDAPS HPSAPKFCSNPCRGRNLTSSKQPKLRLT SAVPGAPGARGTFHALGAGAAEAGGHS SRPEAALCRPLPPLPMTLTSHPLLSGPG RLAWGCNGRR*IKGGG
1542	15443	A	1550	430	8	CWPGSSGTPDLK*STRPGLPTCWDYRHE PLCPASKTFLSPQIETPYPLNNAHSPR RPALVNYSLLSVMDLPIL\AFHTNGIT GYVASPAPPVRWGSHSVAQAGVPWNLG SL*PPPPRLK*SSRLSLLSSWDYSHMTP LN
1543	15444	A	1551	2	419	ETSPSLQGWLGVLFPKRGAKTSRFLIIR PQGGSFKDGDFFNPPGEIKTPPAKKKKK KDSARSPPARLQA*GAGLWDARASFRP FOAPVPLSAQPPRAQPLAVGTSRDGSSG PTPGQESAV\PWREKHPQPPPPQG
1544	15445	A	1552	2	387	FRHVAQAGLELLG\SSDPSVSASQSTGI RGMTYRAQPGL*LFNSKNSILSGPKV/L QDYMW
1545	15446	A	1553	393	2	KNPIFFFLKQGFPPFP*LEGRGKFLGPC HLCFPGSKKG\LPHPPQLIGAPGPPSP GFFFLKRGFS/LFCPGGSFSLRRKGPPP PALPKF\GFLRVTPLAGPNPSFFFFF RDGVSLCHPGWSAVAASRLTA
1546	15447	A	1554	1	427	LLLLILYAVEAVT*TEGAGYPPPLPGSY SHRGASGHRAIFALHLTGCCCI*GAMHC

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						ITTMIDIEPPAITQYHTPLLA*SGLIT*GL\LVLSLPVLDAGITILTDRLITTLFNPDDGGGDPILYQHLL*VFGHPEVYIRILPR
1547	15448	A	1555	3	382	TLYLLFAA*AGGL/GSALSLLIQAEIGQPGNLLGNDHIYNVIGTAHALVILFIVTPIIIGGFGN*LDTLIFAAPDMALSRLNNISL*LLHTSVLLLLASAIVEAVA*TG*TGYLCLAGNYSHP*ASV
1548	15449	A	1556	380	3	EVSPCCPGWS*TPGFKQFACGLPRCWSYSREPAPPAKACFLDI*VK*WFC*GSPÉVNSRPGLYLFIYLIKQKGVK**PARYLVLFCCFFVFFVFF*HRIS\SVAQGQVQWCDLGSQPPP
1549	15450	A	1557	100	254	IPTVPTY*TPIKSFHARISSGPGYSWPVDSAK*VPLAVVSLDSR\RDSGNLVHPLMRVTN*MKRHLVTLTQS\CYS
1550	15451	A	1558	2	289	APGVSSSTMEDEMGGLPEQRRGCSKQRS HHCIPAWATE*DCLKFNKNKKNYLLISLRTQSYLYF/C*VNSY*LKLSIKLAGGTGEKEH*SQKRKSK
1551	15452	A	1559	24	354	PLPSASPGPEGATPVPTS/ACPNKIKLYHLKKKKKKKKKKKKKKKKKKKKKKKKTKKKNKKRQQLNE*ETG
1552	15453	A	1560	376	2	AARGSGVRDPLEEAVCLFSDLQLRAGRTALLKALFK\RQGHLSLQRLLSF\VCLCPAPRGGAYRRRQASLSCGGLHPVRASRLCLPKQAWAMAGAPPASLPCCSWISDCCASNQ*DSVGVG
1553	15454	A	1561	3	408	AASTVFLPFLERKIDFGFLFFFFGEKKFPFLAPGGAPGGLFSFPEASSPGLNPPFWPNPPEK*KKGGPPPPGFFFF*KKRGFPGG\PGGAPFPDPKIGPPGPPKGGEFRGGPPPPGPNFFFFFLKGGGGGPP
1554	15455	A	1562	355	161	FKPGDGGCSEPRWCHCTPIWVIMRDSVSKPKQSKTKRNVFT/C*D*VF*NNNINYNCF*S*RALYILYEKQFM
1555	15456	A	1563	410	1	TPPPPPKNFLGTPLFPKNKAGKGLFPPPLGFPPKGGQWPIPPQRFPLFSPPKRRAD*KKKPPPALKIRGNPNPVFPKGFCGFSFFPPPPFPRGGGLIFFLPP/TK*SGG*KKPKKKKKKEKCPKKQRGGIDQLTSNLGV
1556	15457	A	1564	2	374	ADRNLTNTFFDPAG/GVGDPILYQHIF*FFGHPEGYILILPGFGIISHIVTYYSGBKEPFGYIGMV*AMISIGFLGFIV*AHHIFTVGIDVDTRAYFTSATIIIIAIPGVKVF*S*LATLHGSNMK
1557	15458	A	1565	396	0	IIFLIFLRHGFVVAQAGMQWCGLGSLQLFPFGFRLFS/CLLSSWDYR*RQG*TMALARLVLS*PQAI\SASPSQSPGITDVSHCA
1558	15459	A	1566	186	452	KQKCNFKTLNTKYQLPFFFFLERNFCFCPPGGGEGADFTFLEPLPSGAKGFF\CLTLQRM/WE*RVSPPTPLNFGFLVKKGFSLCGSTGF
1559	15460	A	1567	453	37	KTALYWKTPSSTSTARBEKSVPGFKGQAHFLFRGKHKFKLVSKLIYHFENP/R/ALKNYAKSIL/PYKWNKAWMTAHLFSP\W

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						FIKYFRPTVEM*CSYNKILVLIDTGLDHPRLIETIK\FINLHVCVLENTTPIVQPLPR
1560	15461	A	1568	453	39	TALYWKKTPTSRTSIAREEKSVPFGKGOAHFLFRGKHKFKLVSKLIDHFENP/R/ALKNYAKS/TLAYKWNKAWMTAHLFSP\WFIKYFRPTVEM*CSYNKILVLIDTGLDHPRTLIETIK\FINLHVCVLENTTPIVQPMFRAQ
1561	15462	A	1569	1	352	FGTRRRERERERERERERERERERERGRGGAHQIPISIEGQHKIVGAIY\CREC\GEKISGSTSYIKVWDIRDSAKCIRTLTSSGQGISGDACAATFTRAITSAQGEH*INQIALRPSGT
1562	15463	A	1570	394	3	TLDWFPQSRGGSTGKPVPSVCCCCCCCCCFNFCQEAENNAEGLHNNQAGRTKDGSFAPSHDH*A/PRGTEV/DLLESTLQTSIKQVESKPR\EQARTGAGGQKEKATQNPESVLTSMYTKSQSGSEGRLPENR
1563	15464	A	1571	399	2	KHQLPVFWQYNKKAWTTRTLFLDWLHCCFVFEVRKYLASKGLPFKVVLIIDNAPGHPPTPT*VQY\KGIEVIYLPNTMSLI*FLDQGVIRTYR/SHYTQYSMQRTISAMQENSNKENTIKVWKDSTTDDAIVA
1564	15465	A	1572	37	400	RGTITGEAASADQETADKLSDAINKIMEKKG\Y*LEPQVFNLDSTLFWG\KKKPQRTLLSKEKKRAPGFKTGKDRITLLFC/ANAVKLIIRTALTYKAENPQALKENVKHQLPVFCLTTRGL
1565	15466	A	1573	84	485	AGHKDSPRPHQTQEPSSLHLWDPAAGLQVELPASP\GRALALLSPWVVDGTGRPGA GGGTRRGSGSGPTGAHGAGGRMLMHGGLQVPSPAPREGS*GPARYQAQRMWARTAGGPSTPSAGASRVSPSPHCPGP
1566	15467	A	1574	3	463	TPAQGLRDPNMRKHAYCGCCV/CITLCVGAQNKNAVCGLYSTCPRLCVYEHEHICVNE*VCEHVCERESVRVCESTH/LPLCA*TCGPITFGCMSEKHVFSYTPCVHRVCVCVHLGCCVC/VCVCVCVCVCVCVCV
1567	15468	A	1575	1	383	FLSFGFAPQAGGQGHNHG*GPP*P/PKAKGIFPPHPPEKREQRVHATPPGKFLDFFFFWKKGGLNLGPKKNLPGGKKNLLVSPPKGGGKKKETPGPGGVFFWGGIFFFFPPPCSPG*PLSLLKKPKGG
1568	15469	A	1576	35	469	RIPRCHQPVGPLGCREGAKPQGPDPDAA DSHPPASPAH*/P*SLHRDPIPGFRGPRRNAGAGPRAHTAGICAPQPN*SRHHPWAAAPAGDDSPPTSLGSHVPVGRKSSDGCRQRALCTPGSPAPSEAEVGGSPELRSLRPAWA
1569	15470	A	1577	473	62	SLEINPYISGQLIFNQHAKTNH*SMRKE\SFFNKWCLDN*ISTGRRMKLDPYLKPHIKLNSK/LKDLNIRDITMINLHDLGFGNGF*TM*TK*AIKEKIN/WDFIKI*NFCA SNDIIKKVKRPNVTAITCNPSTLEGPR
1570	15471	A	1578	59	426	LERRSFAPLSPFFAPQFEMKKGFSGP*KFFFSFKALNFGGGVVPFFPPPKKRFFSKNPQEGFI PPPLKKKKTSQPP/YKFGP

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						PKESFKRAPFFFFFKGPPFFPLVSNQWT GKRLPPPPPKETQNPSSFQIGGQKKGK GGPQSFSFPIKKKKKKGGHSRSRTSPRV
1571	15472	A	1579	2	419	KANKTKNAYFEGINKMDKPQVILKKKY/ REKT*IPSIGEEKGIMSP\NSEDTRRII KECFKQTYAHRFYSLKE/MDILLESKHL PKLTQ/EETDSLNSPV
1572	15473	A	1580	129	403	YMFFIPINCQDHPK*KKKKKKKKKKRGG /RPFKKTLRGPKLNRAENKFF*KGSI KKKCLEILKKKLFFGGERCKNPPKKKK PSREKKKF
1573	15474	A	1581	317	76	PRFFFFFFPPPKGFFSPFFFFFFSPRFFP PPFFLKPPPRFFFGPFFKNFF\PPRP LIFFFF*APPPFFFFFFFVF
1574	15475	A	1582	259	377	PREMKTYLPTKKLGYEISHYH*WWGCKM VQPVWKTWQFLKGLNLIKLP*DSAVPLV GM*PREMKTYLPTKKLGYE/MFTLSLLI IANK*KQPKCPRMNKW
1575	15476	A	1583	1	415	PTRPITSSICLRQSYLKALIAYSISHI ALGV\TAILNPTP*SFTGAGILIIA\HG LTCSLLFCLANSNYERTRRIIILSQGH QTLPLIAF*LLARLANALPPTINLL GELSELRTTFS*SNITLLTGLNLT
1576	15477	A	1584	216	406	LNLLPLVLGGSSCLPPPCGN*KPPPPP G\LFLEKKGFSPCGPAG*PPALRGPPP PPLPRGLI
1577	15478	A	1585	383	3	KKFGYPFYWIG*KILK*FPG*K*SLPHR KSPFFFFFF*GRVLLCPPGWRGTTKGHS QVT\LPAAAMTFQV\K*SSPLRLPSR*G YRQASPSWGNFFF/CLVESLSMLPLIL NYWAIAIKPSGPPKVLG
1578	15479	A	1586	126	413	NPTLKK*KMKENRMKKNEQSLRDL*DTI KLTNRCILGIPKEERKKAEGIFGEIMV GNSSNLIR\ENINLNIEVAQ*TLSRIN* KRATLRHVIMKM
1579	15480	A	1587	242	409	GWMIFRFNFFFLRGSTLTQTQAG*GG DFG/SLRPPPPGLKRFSLTLPRSWDYR H
1580	15481	A	1588	2	338	EIEKKKGKGGKRRG*RSNKKKRGGRLEGQ KY*SPPCPRLSFFLVDEKGPEVLQDSL GWWKTP/SGCEMTDSSQPY/YRAFYVL KN/QRVGFSVDVGEIEKDQDVEKNQDPS CPRL
1581	15482	A	1589	360	0	NNFLEQLKFPPKKKITDTSYKAPRFFFF FPPSQKGVFPPTLFFGFPPGFPFPPFLN PPPGFF/CFWAPLKKFFFPYPGG*TWVS LKGPP/L/RFFFFFF*DGVSLSLCHGWSS SAQS
1582	15483	A	1590	75	412	VEGQHCNFCAAQETINRVKRQHTLELET FANWSPDKGLIPRTYKELKHLNRKHSY *KWADDLDRHFSKETYPKTYSTQYC *P/SITTIEN*KLKTSNIKTRLQGGHKRL ER
1583	15484	A	1591	309	1	FSTQGAHMQVCYMDTFHDAEIWTSIEPV TQIVNMLPNR*FFNCPHFFPPPPFCSP/ LVSFLLLRDRVSLCCPGQSRVSGFK*S TCLGLPKRWYDKCEPHVA
1584	15485	A	1592	2	415	LSLSLSIFSFLP\FSLFLPSLSLSLFLS

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						FFLFLSFFPPSFFFFHFRASLCHLGWSA MA*SWLTAVSTSQ\VKQSSHL
1585	15486	A	1593	3	396	HSAFLFFL*DRVSLCHLSWKAVAQSQLT ATSTLL/VLKQSSHLNLP
1586	15487	A	1594	300	62	KMTGVLKSSCGKSPKQVGWLCVVCVF/ SFKRQGLAS/VAQTGMQWDHSSLQPPA PGLR*SSCISLISSWDYRRVRPRAPG
1587	15488	A	1595	1	412	FDRPAADQKAASALKASGVQAQMAKGT YHDWSLQDWKVLWMTH*VS\QQEQDPTNL YISNLPLCMDELQLENMLKPFQVISTR ILRDYSGTFRGDGFARMESTDKCDAVIE HYNVLLIMTPPGVSAPTEPLLCKFAE
1588	15489	A	1596	428	2	QSESREPENFLLPTSTSSLLLVHCLSR TCVNSTLSCVPHFHLTFNSHLLTSQP RRVHFC*LSLSSIISWKLNTLPGVPIR \ASEIFGLRTIRNPFPLSHSVLPFSL ESHVTTQQGVQWHELGLSLQPLPHGCQWL SCL
1589	15490	A	1597	2	442	QGSLL*PHPPMLK*SLTSAF\NYRHVSPH LANYFLFFF*KQGLAVLLGLALN*AQ/C HLPALASQSAGITGVSHGAWLFFFLLNQ CYLI*FLILIF\ERRNSPVAHVLVNGGD LGLLKPPPPGLMGFSCNLNLRSGKYKPP ATSPGYIFC
1590	15491	A	1598	419	121	NLGYPRVSPPPFFLNPPPEFYRGPPKKK FY/PPPPPAQKIDPP*TPPPFFFFGTG SHYVAQAGLELLASSDLPASALQSTGIT KHEPPHLAETIFLVFL
1591	15492	A	1599	45	397	DRVSLCYPGWSAVV\*S*LTAASNSW\V K*SACFSLLSRGDYMCMTHIANIKKNF LGRVRGSHL*SYHLKLCCLK*RTKEGFL SFFWKGKRHFLGQKNILNPRKVFVFLPG PPKGLGY
1592	15493	A	1600	3	397	SRPGRFSLMLTSLWHS*VCRAALAARE EQWSGCFKSHF*LEVNFVWSGIDREV/C GY/LKTVLGEDLNDYVSTQI*D*LMKPR CPEKQDESLLKEFGGGA*RLNVVHRPGA VAHACNPNALGAKGRRIPRSG
1593	15494	A	1601	244	2	KTKTSFHSLLIDSCGYLLSYSNFQI*KKM IFK/YLHLRAVPRHVIVRFTNLERQEKV LRAAREKG*VMHKGKPIRLTADLSA
1594	15495	A	1602	435	2	PQEAITYPTQHPTYGAICRIARIHGSRD Q/SVEMKWHPQLTITPSGP/LGKSLLP PVALCFADLEVFIKGGMLSPGVTTISL NWKLRPLPWVILQ*RTPLARVIPPDIQR EIRLLLNNERKKSYPVWNTDRPLGHLVVL PCPMVIK
1595	15496	A	1603	288	8	EFPLIREMQIKPTMYRLTPV*MD\R*W *GCGKRGTLVHCWW*CKLVQSVCSRSSK NTIELPCDPAVLILGMHTKERKLPCG WTRGVGPGYC
1596	15497	A	1604	411	236	LIPSEHFFFSG*F*AFDRSSLAPTQLR RHRPPTGLLPLSLQGP\LLTPSVLLS* GGREKGNFTPPGGQGGKIFFMGPPKSNP GPGV
1597	15498	A	1605	2	437	KCLRISPCAGPRRPWCPSFEPRVCVWFL GVPOVG/PEGP*GEG\GFEGGDVRLWQ GKKKKKNTLGGKRGWPFPEKRGFSLTP

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						WFGPQGLWEPCLNPGGGLFLIGGFQKGP KVLIGKGTGPKKKNNRPRKRGSGLGPP GKDDFPL
1598	15499	A	1606	31	467	EFFGRRFRGGGCSELRLRVCTPAWTEG DSISNNI*LVNEN/HTVNSWKCSDS
1599	15500	A	1607	418	32	VGQVGLELLTSSDPPASAYPK*WDYKR\ DPRAQPNPNILKAQSNRSPRRQR*PASS FSNQNSCMHRCISLP*VLFLIFFKNRP* NNSFGYNSSGWWSGLNILNSC*FWFLFG NSDTEIRICRSFHRGREV
1600	15501	A	1608	379	3	FPILSPSYNPSSTELP***SLQSPLEFP YDFFSVNMFSLFFNLKSHTVAQAGVQW RNHGSLSQPRSFQLK\HPPASASAGTTGM CHHAW/LIYLCVYLFLEMRSHCVSQD*V QWHNHSSLOPETPTK
1601	15502	A	1609	456	99	PFPTFPFPPHSNWGLGLGCGL/EPTMT SGLGLKGSPP*SPPAHLRSLGAQLCPVLR APVLGPSQMPGRKKKPTARGSPWRKGV FVMSGQSDPLGPSSCQELGPRQSTQGT PGA
1602	15503	A	1610	1	420	FRFSDGAAGQKCSSPPRPGRGRAEVLLT SQTGRQGRGAPHISDNGQFGRDAP\PS* M*WRPGRGAP\PS*VGWRPGGDAPHF/Q TGQPPRGGAPHIPDDGRPRDAPHFPDGV GAGQRLQTRHFGRPATAAANKVKVVTSLR
1603	15504	A	1611	426	3	KNPFLLEAKVSFNPKWPPALPPGEQRDS VSQKKKNLLIHKKAHSH*FFICRE\C ESALLLHQNIHAGGKSYVCNK*GRGFRN KSHFTYQRTSHSGKKAFL*KBCG*DFL*K AILTAYQKTHSGKKSFVCKEGR*DFIQK TK
1604	15505	A	1612	428	273	HHA*LI FKIF/CVETRVSLLCPGWS*TP ELK*SSLLGCPKCWDYRREPPIRPTT
1605	15506	A	1613	311	4	ANKFKNLNLEIKFPEANLPEKFTQEGGLN NPVSLY*KN*TYSLRLFP\KKKSGPDD FTGEFN*TSKEEVPSLHKLQKI*ERNT LPNLFHKARVTQVSKSEM
1606	15507	A	1614	338	88	PNPPPPSKGK\GFPPPTPGRKKKTRPPP PPGKFLGF*KKRGFPFPERGGP\NPAPG GPPPPNPPKGGGTKEGPPSPGEGVFFFF
1607	15508	A	1615	2	162	KHGCTCLYSLLLGRRLRHESCLNLGGGC RE/PE/SHCIPAWATE*DSVSEKKYL
1608	15509	A	1616	3	399	PEVREYLTSGRLPFKVLILDNAGHSE PQRFNTEGINVFYLLPNPRSLIQTLDQG VTRTFKSHYTWYSTERIANAMEENPDRT S*KSRIMTPL/IDAIVMTEKAMEAIMP KTIISCWKLCPDVVHDFTRFT
1609	15510	A	1617	390	1	KRNCFGPFLTTPPGQRLGGFKFLK\HFF YYRGERGGFFSPFNKGFPFPPPPFWGFF LGALKF*RGVPPSKPPPGPGKFKLKP FPPRKS YGGCFKFLGFPFPEGPPPPQK KKKKNF TAARDLEPNW
1610	15511	A	1618	468	0	MKLVNIWLLLLVALL*GKKHLGDRLEKK SFEKAPCPGCSHLTLKVEFSSTVAEY EYIVAFNGYFTAKARNSFISRALKSSEVHN WRIIPRNPSSDYPT*WP/VALKKKKKK AGV/LPLENYSIITRV
1611	15512	A	1619	421	2	SSRLSLPKCWDYRREPPRPAQPRILKKI

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						S**EPFFLLILKCI*LRTQGLGRGHKGKLNSTYVLHKFMD**LGQLMNGLNMLDESSFCNVLKHTKQ\WRDYFVCLFVCFVRQSL/NPVSQAGVQRRDHGSLRAPPPGFAPFS
1612	15513	A	1620	406	2	GTKKASSNGFINGPGAAKKKSQTFAFLAKPGAFPSILLDEKNRPQIKPPACFP/SIRESQTSYPVFFFWSPSCGFFFFFWGKPEP LLLKEAGKVPLFLFLFGL*DGVSQCPQGWNAVLRSQSLTAESNPASAHAS
1613	15514	A	1621	411	0	PPPPKKKPSGPPPP/PSSSSSPSPPRKFLGCPRVFFPPPPFKPPPKNFWGPPKKKKFPPPPGGKKFFF*RAPPP
1614	15515	A	1622	2	403	TARCGLNFFCSSLPIFIAS*VAGTTGTHHHAQLILLIFCGDELSM\CPGWS/PNSHLGLPKCWDYR
1615	15516	A	1623	298	411	LIINVCWPGLVAHACNPSTLGG*GGRI/TMRSGVRDQP
1616	15517	A	1624	263	2	DSVSKKKKNFKE*LIPVLLKLFQNTBEEGILPNSLYKAGV\LIPKPKDT*RKEIYRPISLINIDAKIVSKILANKIQ*FIKKITDAW
1617	15518	A	1625	3	281	PFSCLSLPSCWDYRRPPPRPANFF/VYFYKKNTRTQCFTVKHGFVLTRLVLIS*PCDPPSLASQSAGITGVSHRTQPHTVFFLNNPALPKLQT
1618	15519	A	1626	300	20	NPGPRGFPPPPGPPKRLDFRGGAPRPGF*YFLKNFLGFFWFQKNFLVFFLGKTFPPPQFFFFFF/RDRMSLCHPGWSEVAQAWLKAAALTSQTPAI
1619	15520	A	1627	394	40	PQFAAASLFSPLFFFFPPVFSPPPPFKTPPRIFFFWPP*KNFFF,PPPAFFFFFFLGAPPPPPPPPPPPPPPP*DRVSLCRPGWSAVAQS*LTAAALNSQT
1620	15521	A	1628	386	3	IFPTRCTHLHLGTNKLPTCSFFDQAKNPFCS\HHSRGVGLRARLFCERLTIEGAGTPACPAP*FPGEPTRP/EGRVRLTPAIPALWEAETGS*YVARTGLELLVSSNPPLSASQSARITGVSHRTWP
1621	15522	A	1629	401	93	ARGVLPPLNPPPWGGRRGGSP*GKNSKPPRERGENPPPLKPKQLPPPGGGPPPLFLGGS*SKKTPPPPKGGAPINQKPPPGLP PGKKGAPFPKKKKKKDKNIIRTKKKARRSGSLQSQHPGRPR/RGGPPLTKNPPLASPPQEKRGPPFQKKKKKTKI
1622	15523	A	1630	417	47	PPPGTISSPNP/QKNLKKGPGPGGNPRNPPPIGGQRG/RGLWAKKSRRPGPPRGNP PLFKKKKINGGGGPPPVVPPPRGARAGKSLYPGGGPPQ*PQMGPPPPPPGAKKGGFPKKKKKKPKKPRKT
1623	15524	A	1631	416	54	EYWCGR*IDQWNRM*FKMDQHLHSQFI FN*ATKAIQWGKESLFNRLCLKNWLTIR DK\IYLDACLTYY\*KINSSWHSGAFL* SQILERLRQEASLSPGI*VQPRQHSKTP SLKKFFFKFFS
1624	15525	A	1632	2	373	LVFLDNMLKLLRHSALASACFPEDLAKIMDEGGYTKGQIFKVHGTAFCKWKMPRSRT FVVREQSVPGFK/ATD*LLLGANAAGN\

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KLKPMPIYHSENPRVFKNYVKPILPALY TWSKA/QMAAPLF
1625	15526	A	1633	3	383	NIWN*KAWMTVHL/FIT*FTEYFKSTVE NC*EKKKILFKI/LLLIIDNTFGHPKALM EIYKEINVIFMPANTISIL*PMDQGVIA TLNSYYLRNTFHKTIAFINYDSSDRCGQ SQLKNFWKGFSLDAIR
1626	15527	A	1634	2	182	GACTQLIGRLRQENRLN/SGDRGCSEPT LHLCTPPWATE*DPVSKKKKKNPCPKLK KGPPP
1627	15528	A	1635	331	1	LFPPPPVLKSGPGPN*N*PPLKGKSGFP LKKKFFFFFF\FRDWVLLYCLGWSQTS LKRSSCWDYRCEPPHLPNF/SYF/CRD SVSL*PRLEGGSI IALCSLKLDDSSP H
1628	15529	A	1636	80	381	KLKCHAHHSRGFYKYSFLQLGASQFPQ VLRITHPHKGSWAAPRS*G*SQC/SHFF SFFFETKSHFVVQAGGYGRNFT*LQPPP PGLKRFSHLSLPSSWDYS
1629	15530	A	1637	381	38	SKRQGFHHVGQAGLELLSSDLPTMALH PTCPLQKCWDYRC/DATAPLSSSTFFMQ EKCLAF\PLFSSAPHSL**PKAVIEKD CPGL*IW**VARSQRMVNFNIK
1630	15531	A	1638	3	295	PGPDGFTAEPNQTFKE*LIPIVLKLF*K IQEVR\FKKFSITLTPKSNKD
1631	15532	A	1639	48	380	ILGKAISFTIE*KGLKYLGIYLTKEAKG LHTENYKMLLXELKKDNTIWKIGILCQ/W TRRLNMVKISV
1632	15533	A	1640	343	23	SWLTAT/FCPLGSSDSPASAGVELLTSG DLPALAS*TAGITGVSHRTPALSINTS TLLCSSPYCPPHLQSLQGTTPVPFLKA QRTGCLLQGVILTSQAENFCNKH
1633	15534	A	1641	3	397	LELFSSAHCCPSLTVMQYYP\RPSTHD CQREKSPHRTKKKKPLEGVFLG*KIKTN LENPPPLPFFGGGPPPKGGGPFKIV*GG WPWPWGLKIPTLPKGPTRPPWGPGLGTF GGEGKPLRAFPLORFRRPE
1634	15535	A	1642	2	308	NKWR*GNWISVKIDNFNFPYLMPTNLS* IRDDLNAKATTIKLVGENIGENLGIGKN F*ERTLKA\LRGKKMDKLDFITIGNFCF SKDRIKNKNKARRGGSRL
1635	15536	A	1643	16	386	EKKKLSLFTENGIPYL*NPKESAKRLLS LINDFSKV*GYKNN\DEKSVAFNTNK
1636	15537	A	1644	533	3	PLSLSLSSLSLFFL*DRACFVAQAGVQ WDLGSLQPPPPGIK*FS/CGGNVAVTP RLSPLTLPAMTEVRLPSSKIQTNKEKNT VMSEIYQSLM*MGWG/M*VRMCVKFKP WVDN**VSMGCLLPSFLPSFLSFLS PSLSLFFPYFFETESCFVAEAGAQLDL G*LQPPPPAVP
1637	15538	A	1645	341	19	GIGGRPP*FQLGLRLKOEK/HLERGKGF NEPKSRPCISAWATKGDCFKKKKIHT LQQIQPKQSWKTDISQFRDYKTIIKT VGHGIWIDIFINGIELSENINQCS
1638	15539	A	1646	279	3	TFYHNEKDNKCLWTI\GKI*MLTGCIY ECKMVQLPWKTAWQFL/R/DVNI*LPYD LAITLLSIYTRKRKTYVYTKTCIQMFLA VLFTTAKRWQP



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1639	15540	A	1647	392	1	QKLEIMLREEGMLKAKTGQKLGLLCQAV THLVNAKEKFLKLNVLQGTHKW*ESET AKSLILFNSMKAKEGE*AAEEKFAASRG WFM/RFKERNCLHLLKVQGEAASAVVEA VANYIEDLVKKIDKGGCIN
1640	15541	A	1648	425	148	SQSLI*SKALTLCNSMT/ERAEEVAGK KLEASNF\LKFKKRSCV\RVNMQGKVA SLDGEAAASSPEDLVNFIDEGGYTKQOI FN*DKTSFFF
1641	15542	A	1649	271	462	RRQKKRHKRCILSPLLFDIVLEVPARTI *QEKKIKGIQIGKKEV/KIISLFADDDV LYL
1642	15543	A	1650	70	398	RPEASLRHMCINAGQLLSKRAKLGALSL SFFFWKKS LAFAPQPGQGNGL**KPP LPGLRGFSGLTLLRN/WE*RWVPPPT\ NFGPLIKTGFFPLVGQAGFDLRTLGLALR
1643	15544	A	1651	425	3	FEFGPKVGFPLGPRFPRVPPFGTLP PKRGPRCFPPQPGAPPKIWTTPGALPQ GVGPALPG/ALQKFGPKNPGGFFSGPPQ MAP\GGFPGGP*RPFRGGAPFFFLRQG FPVAQARVHLPGSSDPPISAPQVAGTTD VC
1644	15545	A	1652	385	2	KGNPNPSPPETKFFFFFF*KGLLPLPQGG GQWGYFRSLQPPPSRLKLFSCPNLPSNW EYRGP*\RL*LTGRGTSGSKTKVPTP CGPFNLNLGLGTQARNFS/RLVFFFFFFE TESPFVAQAGIQLRDLHS
1645	15546	A	1653	242	3	KNKNFGINRGFFFTFKVPGFFFLGKVK LFFFFFFRNLFLLKAKPP*\VFFPIGPSF FFFFFFFLDRVLLCCPGWNVVQSL
1646	15547	A	1654	3	285	HFIITYTKDLNRRFSKEDI*IIIKHV/KK CSPSLAVREMQIKT*VRPGTVAGTCNPN TLGGQGRRIQDQLKQSKTSSLOKKIL FRLARHGGTCP
1647	15548	A	1655	1	373	KVSLFFFEQGLLCCPGWSAVVSSLQPPQ CPRVKQFSHVS/LPSN*EYSCPTNTFSL QVCVSIHKYI*YIYIYIFKFF/CR/DRT LARLHRLVSNWSQAILPPWPPKVLGLQ
1648	15549	A	1656	189	2	VQPGQQRNSISKTKNKTQKLPKTKSP GPD*FKEELIPILHKL/F/HKIEDKGTL HNSFYVVTI
1649	15550	A	1657	385	13	GGPPPWGARSPPKL*NPPPPRKKPPGPP PPPGGAPPLGGFFLFFPPPGGPPPGGK /SFSPRFFFFFFFLGGGQIFLSPGGG PRGVFSPPAPPLVPKPAFFSKKKRGSS GGEKPEADGYFIK
1650	15551	A	1658	352	2	HLSLLSNWDSIRAPP/RPCVIFKNVPLN IFFL*RGVTMLPRLVLNDPPISASQVAR IIDVSHWAKLRRSV/CYVFETGSGLSQ AGVQRYNHGVSQPPSRVS*SSHSLWK YRYPPRR
1651	15552	A	1659	265	3	HSGQRDEGRMRCGEWLESHGVVRARSCM TLKTSFLFTMAKI*NQKCLFMDEWIKK MWHIHTMEYSAIKR/DEIPSFVATWME LEVIM
1652	15553	A	1660	1	163	NQQNENRKTIEKIIGTKT*LFKKIKKFD KPLARWT/RGKKNIQITNIRN*RRDVI
1653	15554	A	1661	56	320	KFFMYSAGESTKIRCLF/SCLFLFLR/Q

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ESRSVSQDGG*SEPRSCYCTPAWATE*D SVSKKQKNKPKKNLNLKCFASSLLITLP PARHKA
1654	15555	A	1662	3	421	GIITDTFPNLEKGINIQVKV/RPPSR FNPKKTTSRDIIKLPKIDKGS*KQKE KTSKSARLPQPHGLLGLGLKSASSPIK KERKQ\QITYSGAPIFLVTD FSVETLQV RREWHDVFKVLKEK/DFYPRIVLVKIS F
1655	15556	A	1663	362	2	VIFADEAQILKKEDKLDIFIKMKTSVHOK TLSTEYKDNHREKIFVSQISDKELISRV YKGLLKLNTDKNLILFYF*RLGHSVTQ GRVQWCNHSLSHPQTPGLK\NPPTSAS* AAGNTGVHL
1656	15557	A	1664	79	355	IHLPSLIGDFNLFTGISLLICLVLFVFI FETGSCSVAQ/S/GVQWHNHGLLQPRPS GLRQSSHLSPSSWNHRHGP*FIYF/C VEIRAHVHP
1657	15558	A	1665	47	384	KEKASGPLINFFFFPKLCKLAPFFFLPF FLWGGGGGKFSRNPQKHFP*KRVFVNF FFFFFLLRHCLTVSLSHCHPGWSAVA*S QLTAGSNFW\VKQSSHL/LPSSWDHRH APP
1658	15559	A	1666	163	601	IFCKGGVLPCCPGLADLHFTSNISISFY YSSGGLRMTNKTETPMSTIPKGVGVAWR FGNSECIFQELPLTLHLLSTMLASFIH SHEASANALVGRSLTVGWGCRGVGVSD PAAWLWRDLKGC*DKSHSVTQSGGQWC NLSSLQ*APRLKRSCILSLPRSWDHHW VPPFLANF*IFCKGGVLP\FAQGW
1659	15560	A	1667	418	3	SVCGLGPKCWDTGKPLCPAPSPFFY/EG SITLIPKSEMHLPRNENYRSGFLN/M/ DAKILNRILANCISN*I*NH*\*KVKFT PGKKDWFNKRKPTDIIYPH*QNREEKSL VSSTDMAKVFNKIQPVRLRELTIEIKGNF LNL
1660	15561	A	1668	411	1	LRLHVGRTTT\LFKAVSQGHLSLQRFLL PSVEICPAPRGVYRGRQASLSCGGLHR VRASQLLWFLTQASAMAGPPPPVLLPPC SLI*DCCANNKGGF IGVGPFEPVGYNL LVSHLLRPSEKPSIRVGVT*FSRC
1661	15562	A	1669	151	1	PLEKEABITGP*PHAWLIF/CFF*TESR YIAQARMKWHNLGSLQPTPPGFK
1662	15563	A	1670	1	389	TFF*KLKMINLSEEGMLKAKISQKLGLC \TVSQVNSKEKFLKEIKSATPEST*MI RK*NSSVANTENV*ERSRTSHNIFLS*S SIQNKDLTFFNSLKAWRGQEVAAEKSEA SSGWFMRFKERSHLHTIK
1663	15564	A	1671	1	363	ECTGPKIAKILEKKNVGGLP/PNFK I*YKAPVI*FWLKVPVIPSSSAILMKT *Y\YFKDRNQDEWYRLRVWKINSHIYGQ LI\PSKGTCTIQW*KSLFNK*CWNWLF TCKRMKD
1664	15565	A	1672	203	2	ALNKRDMPS**IRRCNII/KCLFSPKM N*VFNVIT/IQCPSGHFFTTEDKSILKF IWKSK*PRLAKRTL
1665	15566	A	1673	15	378	NYHHNQNEHMYHSLPNFFFFFFFGKGAP PG\PKGGRG*REP*IPGGKGNPPL*PP

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						KEGGPPGGTTPPGKPGKTIWDFWEKGGFP LSPGGAGTPGPKGDGPPWPKGGGKPGG TKQPGPKKFF
1666	15567	A	1674	2	349	LFLTVALARLVNS*PQ/CDPPALASQSA EITGMSHRAQPRGIR*I*CGSYTTCHPL LLLT\YLFYFSTESHVQAGVQWHD GSLQSQLRRLT/CILTLPSWD*PHVT PG*FCLF
1667	15568	A	1675	348	78	LGPWVPPVIPAPLGG*GGRSPRPGFLT NPGPKGKPRVFLKIQNLPGV/RGRPLFP /GSPGSGGPKSP*PLGPSFPLT*NFSPP FWGPPGGPK
1668	15569	A	1676	2	385	TSRRDYRP\GHHNQLIF*/SFCRDGASL CCPCWSQTPGIKKSSCLVPRCWDYRCE PGL*I*MGKNPT\LFSNGL*CDCIPLIH SIADIRKKPHS*LQGL*LCHQONSQTES CSVTOAGVQ*CDLGLSLQ
1669	15570	A	1677	386	1	KSTRPVLYKWNKA*MTEHLFTA*FTEY FKATIEFTFCSEK*IPLKILLILCNVPSH PRALMGMYKEINVVSMPDITCILQPM DQGVISTFKSYLRNTFDKAIAT/DS DSSDGSKNLLKTFWKGFTI
1670	15571	A	1678	2	193	EGGRIFFFNSFFEVILTLLI/PKPKKV VERK*SYHPISIMNGDVKILAQTLLN QIQY LKRIIHYDS
1671	15572	A	1679	561	830	TLLLGT\NAVVDFFKLKPLTY\HS\ENS RGL*KSWINLGLTVFYKWTNNAWGDD RHHLVYRHGFTGIF*GSQLKTYCSEN IPFKILLFIDN
1672	15573	A	1680	415	2	TSCAWLSLYPVLYRSSLPRFIFCHFK HLWYKNITKKAEEINTNFCCYINRVLL C HLGS/ATVVSS*LTVTSKLLGSRD PHTLSLPSS*EGRCITPRLGDLNLF SRDGGGIRGTSTLPRQVLNAWPQAIL LVRT
1673	15574	A	1681	1	78	RPRIRHEVGQAGLKLLTSGQTPASVP *CWDYRPEPPCPALHISYK*NHAMC GLKCL AVSA*RHVLGFIRG\WHVECC FPFCS*AGLKLLTSGQTPASVP
1674	15575	A	1682	414	162	GGPGGPIPGA/AGLRPPPPPLGNPPPP *KAKICPGGGAPPVFPGS*KGGGES P*PPRGRGPFIGVQLPFGLGHKRG LFPKKKKI
1675	15576	A	1683	378	129	QFFGPRNFYQIFNFPG/PPV*HSPL FGPKFPFPSPGGGQWGLGNRP PPGAKGGSTLRGPRTGGSRGPPG PGKFFFLKQSLAL
1676	15577	A	1684	3	374	GISVLPGIGAPGNKPELFEEVKLYN NAREKDYDNMAELF/AVVKTMQALE KAYIKDCVSPSEYTAACSRLLVQY KAVFRRVQGSSEISSIDEFCRKFR LDCLAMERIKEDRPITIKDD*GNSLS
1677	15578	A	1685	2	373	PFIRPETIKLLEEIPGGKLLDLGL GNDL LARTPNAKINTWDHIKLSFCT IKETINTMKQPTDCEKIFSRLLSDK GLM/SQMC KELVQLN*KK/TDDSVK GWAEDLDRHFSKKDIKMANRPGKVL
1678	15579	A	1686	378	201	HATCLANF\CSYG*DRVSFPCPGWS *TPBLKRSTRGLPKCWDYRCLGRS LLFPGA

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1679	15580	A	1687	1	404	PPDH MCVNPGGGACSEPRSCHCTPAWVTERDS V*KTNKKKKVKRRKKIFHANS/KLKRVM AVLISDKIYKLLKVRDKEYI IKGSTY QEDISITNTYTLNT*APKYMKDTLTBLK EEDIIYAIIVGDFNTLLIICRG
1680	15581	A	1688	307	33	DEGSCHDAHAGLKLDDSSGLPASASQSA GILGVSHGARPLISSYNGTSHGGLGPAL VTSFNLSHLFKDLLSLQI/HVTF*GMGL GFAGAKLSL
1681	15582	A	1689	11	394	IFILEARTRISSRTFFKS*INHAPYNS AI*LIGIFPREKK/STCPYIYTQMFAS LEVTAQTRKQKCPSTGE\WSKNLWN
1682	15583	A	1690	20	391	SEGKGWYSCTKWQSMKLGGITFFFFFP PKNPPPKKSGP/QKGPFF*GKGPWPBK KRGHKN\RGFPKQARPPKPVFFLIPGK RGFLLGPKGG*NPGEKRNPPWP*KGGK NPGNPKGGPHLTL
1683	15584	A	1691	72	392	IKMIGSLFFGFAGFFFGKKTFFFPQPK R\GGKP*IT*TPPPGN*RNSGSPPPQKV GIKAPPLPK\NF*FFGKNGVTPFPFGG FEPPTPKEPSPPVSPKGGKTNAP
1684	15585	A	1692	389	161	HGCACLRSQLGLRREDCLNQQG*GCS EPTPAWVTE*D/SSQKNQSKIKKSGL DNSFSIG*GILGLSTCDYS
1685	15586	A	1693	286	363	DGISL*PRPGLRQSPQS\LLSNWGR STPLCLAGFFVVFETGFLHVAQACLRQG FTMVAQS/ASQKIHIT*GAFETIQVLFY WGGVGFQWRFFFFFETESHVSTQAGVR GCSLSSLQVPPPG
1686	15587	A	1694	1	356	ELLEPRGRGCSERRPCHCPPVRVAEQDS VSKKKRERKYLFLRFNWRSLRIFYFC */HPLQHNIQNISFTLQNSFGFFSRQYC PSPLEIIFLTPLTENLLGLFMKGIIQNW FFGVGLF
1687	15588	A	1695	3	298	KYFETNENKNIQYQNL\AVKLVFRENLT VVNACVKKEERFQVNNIALYPKN*EKSM LNPKGKIIKVRSEKNDIE*KNDEENQ*N *SWYFEKITWQTLTD
1688	15589	A	1696	3	405	RLWCGWRNRHLGS*NRVENPETGLHRYA QLIFLTQVQKQVGEQPFNK*CGGTWAP TGKT/MEQPPKASSSSSSSSSSSSSSC KM*NIVFFKMGENLWDH*AKSYEVRTKA *TIKGKVDKLDIFIKIKHFCYGKN
1689	15590	A	1697	6	392	LQRTLLVGLFNAAGNLKLPMLICHSEN PRALKNYAKSTLPVFYKWKIAWMTV*T VAAWLTEYFKPIFENYCS/EKKIPKFL LLTNAPGHPTGLMEMYKTTNVGSLPAN TTSVLQPMGQRVISTFES
1690	15591	A	1698	390	3	AIIESDFLTSREVAKLRVHPFVWLWV LEPIGKVKVKNKWP*KLNK/NKKNHCI EVSSSLFLCNEPFLDGIVTCDEKWILY HNW*SAQWLNREVAPK\HFLQPNLHQK KVTIVVWWSAAGLIQNEH
1691	15592	A	1699	1	245	GGGGEYSKIIAIAKTALKNTTYLGIYLIK \DVPDLYTKNYGTMLREIKYLEK*RARP CS*TERFKIVKMSI/LPNLIYRFNTI
1692	15593	A	1700	2	324	GTSGTSGTSGTSQTCRISRVSTSSWTS

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						GRHLQCHVSKAESSWFVLSASSCSTGSP ISLSSG/GSSLSNSSKNLTLPCLFSSLL S*P*ANPVDSAFKIYPGLSSVGSCL
1693	15594	A	1701	183	372	PGVLLCWPGWSAVTVHQCDHSALQPRTP RLK*SP\STWDYRYTPLCPA
1694	15595	A	1702	29	382	GKRFPCSWEPKFPLTQGGFPPLHPGQKK KPGSKKKDKSKCW*G/CREA/GTLTHY RQELMVQSFWK/TVWQVLRKLNVELPY DPAFLGLHPTSTQKR\DTMFMA/AITL /ISERWKQPRCTS
1695	15596	A	1703	1	382	KKVKIIGEAAVEFPDTIKKIEEKEYLP L*VY\NADESGLFWKKLQRTFISKEEK \SMDRLTLIILCKCSWVYEQDGP*ALKE KGEHQLPVF*L*NKKAWTVRTLFLD*FH QCFVPEVRKYVASKRL
1696	15597	A	1704	2	330	KLNNLLLNNS*VNTETKAEVSSSLEIN EYEDTTYQNLWDAAKAVLKGKHVAPRHF LQEVKK/RLKRFQINNLTLYLKE/LKE HINLKASGRK*MTKIGDLFGLYFVLNG
1697	15598	A	1705	100	342	APKWSIVCPVLVGSWSH*/PSRMKPWTL TRQGFMTLARLVLS*RRDLPALASQSP GITGMSHRTQPLLINLMEIFTEILS
1698	15599	A	1706	600	211	SCSVARLEFSDVIKAHCHL/RTPLKQKS SHLSHLS\WD*GRVPHDLANF*IFCRD RVLPRLLQAGLEL\LASSDPPS*ASEKC WNYRHEPTVPRQNLGLLKTTYGWVFLKK YILTVSVFSLMCLDHCLLM
1699	15600	A	1707	409	1	RGPFFFSPPGKAFLLKGSNSFFPIKTRA PKKPIFSPVSP/LNFPPKTGFPPVFPQ MGGFFF/CFPSFLFFLPPLPPPPFFSFP PPPPPPPPPPPLFFF*DRVSLCHPG WSAVALSQLTAALTSMDSNSPTCV
1700	15601	A	1708	154	2	IGKPLAGLTK/RKRENT*INKIRNEKGD MTADNTEIQSIIRDVFS*RTAHQ
1701	15602	A	1709	263	37	SAQLHPLNIQNHRQSTLLHDFFLKKQD/ G/WPGAGAHACNPSTLGGQGGWITRSGD QDHPG*HISV
1702	15603	A	1710	390	42	YAGGFRAIFFFPLPREGAKNPNFPVGGP PFGGPPFFFPAPSQKKEPGFFGKKGVF* GGAKGFPNARGPFFF/G*KKKKGPKNKT PGFFL/MGPPNPGGPPPRGEGGKIGAKK KKKSIRL
1703	15604	A	1711	3	167	YTCVFVCLCLCDCMC/CVCACMYICVCV CTRVC*VCVCMCVRVCVQALTVLCKSV
1704	15605	A	1712	116	391	KRNFFFGPQGGEGPKFN*RGPPPPGVK GIFPPSPPEG/GKKKGAPPPPGIIFWFF KKKGVPFCGPGGV*TPDPGGPPPGPPK GGAPRQGPL
1705	15606	A	1713	401	47	HHYATKPFTHAHTCTCIQDTCNTCMQHT QVHT/HTDTHHTTRKVSVCVLMAEQE RPCPHC*GGEAGAECEGVCWGLSS*TW RNRKGAHTVRVVGQEQSAGCAHGLVFP RSYLWT
1706	15607	A	1714	1	400	CVESCEVDIEMVSCCV/CSG*SAVCSGT ASAHCSLPFGSRDSPASACQVAGTTGM PH/LYPGVPLKPREGLQFTELPSCGLEI QPTCENKR*HVPCAL*VQLTDIRPN*RY QFRVAAVNVHGTRRFTAPSKHFCS

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1707	15608	A	1715	413	3	LNTFEPQRSFPFIVNSSEMILLVECLFVT SGWIYHERFLNPGREIDWATCYSETGPC PVTQDGVQWSNHGSL*PQTPRLK\HPTT SVFPVA/RQGL/NSVAQAGVQWHDLGSL *CRLPSLKGSSHPRLPSSWNRYAPPCC I
1708	15609	A	1716	421	144	RLECSGGITAYCSLNLPGPSSSPASAS* VAETTGLLHWKKKIVETGSHFIVQTAFK FLDSSDLPALAC/SWDYRSELLCPACFY NFCLEFINIPC
1709	15610	A	1717	3	384	YSACVCVCVWVDVSVHRCMSISGH/ARI IRVGPAHKAQSSCRPVAGCCTSAQTTP WCSAATADPPPR*GESLEGPYSGSHSTC CPGCCLDW*HSLPSTEPAACRAGAPGGG H*AWLGCGGRAGGRPG
1710	15611	A	1719	3	615	PVGSWARSSGAGWPPGSPQSVSDGEAGH SIPAPRGQCSRHRAEGRTARVCLSHCSF SGFRPGLVPIR*SLGRPDVAQAIVPDSQ EGRKTGIHAEAVMFPLGPGKGVKGCAGG RLCPSSPPSRCLDLGRRGMPSSSGPAGP RPSGVGSDLRPGAGAAATSSSSSSSSSS SSSSSSSSSSRDGEGP\TGSVEAPGSL GPWLPSQPS
1711	15612	A	1720	320	3	GLKWLNLKDNSLYLILAKVDDCLDEK* YADKMLQYTKSVWVSRRGCQGVGEKK QATEAAQEWELRK\RLYWRKECDALRAA REEQKELRDVRKAKKVVCVRV
1712	15613	A	1721	44	373	KAMGQTLWKTWQFLTKEEIGPM*QSCP T/DLALVFLGICTIDLKAYIHTETCTQM IITLLIIAKNRKKASCSSVGE/WNKKL YYIRTMESYSSLR*NELSSYKHHWGGGS
1713	15614	A	1722	135	396	AQGLFCTSVKLASEQPLRILFQLDKRNK \FEIYGTSG*L*SIICQNNLQSKFQMY HHKIMSSLGAVAHACNPSTLGGQGGQIT RSGD
1714	15615	A	1723	4	383	LNLRAKAIKLEENIGIHLPLDGLDLDL LDITPKSQATK/AKIGN*GFIKLKHFCA AKNIIKKMKRQYKEWKIFGNHVSDDKL VFRIYK*HLPLIIKNSSS
1715	15616	A	1724	2	405	NSRTSLILNQNL/IKLSEKGTWKAKTG *KLGLLQK\ISKIANAKEKLLKEVKSA TSMNM*MMRK*NNFIPMQKVLVW/I* NI/PLCQSLIQNKALTLFNSIKAERGEE A\KLEATKRWFMRFKESCLHNKVQDEG
1716	15617	A	1725	90	400	SQLLRRLKQNSLNPRESSSKTTTRTKVS HWHKNRNVNQ/YNKIENSGINLHIYG*L TLNKGDEASQYSS/DILFNKWCWQKKKK \YLDPYLTPCTKISSTWTISGFL
1717	15618	A	1726	390	1	TFFPKI\KKIL*FTWGPRRPKIANVFP *QNKPKIEGIPLPGFKIYYRALVTKTAW F*HKNPPIGQRNKVENSETNFHPPSELN FFFF\YRGAKNIHWGEDSLFNKWCWENW ISI*RRMKLGPNLTPYTK
1718	15619	A	1727	3	365	HASAKSNLRWIKLNLRAKTIKLEENM GENLWDELSRGFLDRT/PKLYSIKLKL RK/WNFIKIKNFCFSRDT*KS*MAGKNI LSGKDLYSEYLKK*CNLIIRQSKTST*M FIAALFTIAKH

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1719	15620	A	1728	368	2	RNCLNSEGGGCSEPRSRHCTPAWATEPD SVSKMK*KKKINK*IMPLY\EQQSETEY FKLPLTLA/SRNMKFLGINLSKGVQDLE TENYKILLQEIEEDLNK*RNKTY*WIKL NTVKMKSILSKR
1720	15621	A	1729	326	30	NPFGGPKKGGSGGREIKPPLPPMGKPLF F*KTKNKWVGGAAPPVIPP/SGVLSQKK TFTLEGGGPNKLNSPPALE/ARGPKKNF FQKKKKKTKQNPSQREE
1721	15622	A	1730	1	374	IFNADKIA\FWKKF*KPQGTSVGREEKQ APGFKAGRNLTTI/L/GASAVGMIRA ALICKAANPQVLKGRDKHQLPVFRLLYN KKAWTTRTLEFLDCHFQCFVPEVRKYLAS KGLVFKVLLLDNGPC
1722	15623	A	1731	389	1	FPPKIFFFSTLEFFFFRFPFPPF*P/ SPPIYFF/CAPKKKNFFPPPGKNFFFF KTPPPFFFFF*D*VCLCCPGWSAVAQ SWLTTTSVFRVPVI
1723	15624	A	1732	118	422	DIITHLFKWLKFKK*EKGLNIFTKEDM QMEKNLKRCLT*FVVKELQIKMRYHYPP IQMAKI*KN/STISIAWQGYRTIGTLF/ HC*EQPFW*FLSKLNMILPYNPA\IML LSIYPNALKKHVHTKTCM*MFIAALFII TKNWKEPRCPSICEW
1724	15625	A	1733	407	1	NIKGPFRGPLIQWGLLIWPKDSFPILGY PPFPSPKISFFFLARSCGAPNHFPLPN QSPCFPQPSFFLGEEKKEFLPGYSLAFP FN/RFGGS*RVRKGNNGGPIMPGESFLFF F*DRVLLCCPGWSAVA*SRLTATC
1725	15626	A	1734	322	362	TAIYIYII*LFTDNI PSHPTWIEIYKE INIFVPANTIPVQHRNQVICTFRKTI TVTDCDPANGSGQSKLTKWKGFTILDAV KN/IRDSWEKVIG/TIN/GVRKLIPSL KNDFKRPKT
1726	15627	A	1735	49	395	RGGPGFFFFFSSKKSQILPPGWKGRG EPRVNGTPPFRGKGNPPAQPPEGGKTG PPHKPG*FLCFLKKKGQKGG*GGPQ/A PGPKGAPRPGPPKGGEKREGPPGPTRPN LYYAH
1727	15628	A	1736	417	2	FLFFFFFLFFFFSFASGPEILFTCL*HT HIHFLFFYSKST*PPVFAGGMFQDPQW LPETKMVPNFKKKRTTLT/YIP**KLCE CDLSNFFCFF*DRLLLCRPGWSAVA*SR LTATSTFQAQANRTRG
1728	15629	A	1737	316	338	FFFLSFYFETESYLHHP*GFIVKLSKVK DIEN\LKKTARGNYQVTYKGASIRLAAD FSAEISQAWREWDNMFVKLKEKTNWQPR IYKTLFVPHF
1729	15630	A	1738	197	379	QKRAQIDKAFICRDIAL/P*FQ/MYYW ATVTKTAW*WYKNRHIEQWNRWS\PEI KSQSYSHL
1730	15631	A	1739	4	401	RGYRHAPPSLANFCTFSKD/MGFTVVLN S*PQ/CNLPASTS*SAGITGISHCTRPO MATFLIGHKIIIPWSVLWPNL
1731	15632	A	1740	94	117	KDRPMVPPVGAGEDQADEPCRGHASLWS QLVSAPTTPIPLPGRDVPSRATPFAAL AAQPP*ASPYPLPPLGAGHASASPVT VPFSPISESTGS*ESAL/PAPRPGSG

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1732	15633	A	1741	3	390	VDQFLISHDL SKL TEDEVHNLNSSTTIG \EVEFKVKKL\ *KKSSGPDGITGKFY* TVREEVTPIL/SYLF/HEIEKEETLVNS FYEARIL/ LPKPDKNKP*TNIDAKTTS KVLPNRIWQYVKII IQHN*VG FV
1733	15634	A	1742	3	442	DLHSRVEPRVRPSVRKQ*VVLKVLICA SKDTLKRAKRP I GWEKIFVNHMPDKDL IPEYKINMQKSGVFLFTNNSYSSTTDND INKWAKDLSRHFSEEDIQMANHKM\KR* SVSLVIREIKIKTTGR* LFTPKCWQG*G EITLVH
1734	15635	A	1743	411	2	LEPFKHPPEITILGAPKKKITLPPPRPK KCISLKGPPFFFCRYRVLCCPGWFST PGLKQSSHLGLPKWWDYRHEPYCTQSSF SLSFFLKQTGR*WFDLSNFFFY/CYCFI YFSRDRGLTLPELVLSWPAAILL
1735	15636	A	1744	1	393	RPGGPPKGRSREQGREGRSRRRRPRAP WARSHMWGARVFSVPRSFDRPQEKCVQ SSKYQQLPARARDGTGNLIRGAPLFFF* DGVLLCRPGWSAGFKQFSRLSLPSR*DY RRTPPHPANF*ML/CLRRSLT
1736	15637	A	1745	395	0	PSAPSFSTRL*LGEPGFP PPPFLKPP PRN/SIFGAPKKKFFLPPERGKKFVSLK GPPLFFF* DGVLLCCPGWSAGFKQFSHL SLPS*DYRRTPPHPDNF*MF/CLRRSL T
1737	15638	A	1746	397	1	CGNFLKREKNFEARRFLQK*AARFRNIR *VTPEITAFCP L*HVASFLVFLTPNFPT IPQLYCLEPLGEMGGSGSKLPPFPSTKT PNPLISVNLCPF\AIKENFFFF* DGVLL LHPGWSAVAQSRPTATSTS
1738	15639	A	1747	392	2	FTKKGGRGGLSP/LPPQKIF*KKKTLK KPFFWQRVWFSP LFFEQKGQGPFFFKK PFF*KRPPDTPQPPPSFIFFLLFFFR /HLVAQAGMQWRHLGSPQFP PPGLTQSS QLELPHTPPHPDNFCIFGRDR
1739	15640	A	1749	33	403	IKGFKKKRGKGGAPQKKGGTGAKPPPPP PQGF*K*QKRKNGSPPNVFFPNPGGPPP PPPFWGDKRGGPPRGGGAPPPRGKREN PFFPTLA/HGKKEKKK
1740	15641	A	1750	3	396	KRQTTNWEKVFA*KN\ADGLISLIRKRC LKVKK/W*R/DMNTQFTDKGILMTNKH M KRSSTSLIMEMQHKAGVIFHPSDWQKC* STDNTQS*QGHEMYTIKHSW*TFDYQQ PF/SESNL
1741	15642	A	1752	30	419	NEGIGAGHEVSFAANKCRSMRKNVEVLA LNRRLDGLLSGLTSTQALPGWAYLHLL SHHAVRPLFLCFKRGWVLLCHPGWSAVA QSQ\FELLGQVILRPHLSS*DYRSIPP CLANFKNFFRERARYACR
1742	15643	A	1753	16	410	VGPKKSLQVWAAVQATLPLESYDLAHP IILKVS LADRAI*NLWQIPIVAS*YIP LGF/YSKAMPSSVDIYSSFEEKKTHFFL TGGGGPPLYSNYLGRLGGANHLTPGVKN QPGQFGKPPPLQKVQTLARG
1743	15644	A	1754	2	17	NSSLIKHRRHTGERPQCSECGRVFNQ NSHLIQHKVHTR*RMVI*SR/CGKDFT QKSTLI*H



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1744	15645	A	1755	138	380	XPXXXSPXPPPCPXPLSSLFLTKCSAY*TPAHRPPPPGPFVPPPKPCPPPPPLRPWPPLPLLTPNPIPPPTLSFHPGPALS
1745	15646	A	1756	194	3	WLCIPIRHTEQQPGFPF/LTIWSQFYSPLFCLFVF*DTVSLCGPGWNAVQSGLTAASTSQAPSL
1746	15647	A	1757	2	403	RVLFSPTLAYTYLLFLYGATILMGVNIWKQPNCPK/GQQKIKLQYIYRMEYYSALKKK*ILLFAIR*VNLGDI MLSEVSQ\SRKKNIVLSHMW
1747	15648	A	1758	398	65	FFFFFFFFFP*TKGLGCIHRCDHGSEFPQRIH\GSSNAPSLAS*VGGTTGAFHHARFTLIQSSSVHVSTHTLHPYPSLP
1748	15649	A	1759	456	31	FAKRITDKLLSLIYLAT*KGEITKALIKQ*\LKAQAKNSLKRHTIVLNHMKL/CLILLIIKEMQIK/STLRVHFFFITLAK\I*KLGNTEFCWQGL*GTLIHCWWECK*HNSYVGGIWQ/FSNKLYVQI*YNSAISNLDGRVGRPG
1749	15650	A	1760	3	378	QFQFYFYNGSVIKAVWYWSKNRK\IDQ*NRTESPDKNLHKHMQLFDPKGTNPQWRKDDLKFKWCWNN*TSCTQKKKKKGGGP*KEQNLTPPGWEDIIFLFGAPKNMPGAGVKTRWGGKPNPGFPQ
1750	15651	A	1761	69	384	YTSASWGGARYTASAGWKTLLLLFLFI*DRVLLCHPRWSALTQPRIIAASTFQ\VKQSFWMHIGDWDYRRCMPPCRANFENFLCKKKKTLRRQEVNQTPALVRV
1751	15652	A	1762	390	1	KFSTPGNKNLFFLKAPPPFFFCRGRVLLCCPDWYSTFGLKQSP/CFSLPKCWYRRESPPQAFFVFFGLPSLPFSPPPAPSLSQSSSFFF*MEFHSFAQAGVKWLN\LFGSLQPPPPGLK*FSCLSLPPTRP
1752	15653	A	1763	2	390	PRVRGFFMRKFVDSYLVPTYKSNLKWITDLHVRKAINLLN*NVRHLYDRELNGFLEMIIKTKAAATTTKLDFIKKNFCAQQMSS/MKVKRQSTKWKKKCSYHISDKGLVSRKYVKAYNSSIRTQSH
1753	15654	A	1764	334	3	WSKRSGPPLSKNQTKKNATKQPOT*KNWINEIGPII/NTSPSKEKTGSNGFTD*FY*TLKEELLSILLKLFQKTEKSVIFPKSFYVKDHSSCLSGIHPKDANMEQHMQINQC
1754	15655	A	1765	259	1	KSTFLMKKYWKGSFLKKHFFLETRSLSD/SPG/GVQWRDHSSLQPRTPGLKQSPHLSLLSSWDHR*APPCPANFRFRLKTRIGRDV
1755	15656	A	1766	402	386	FKKKSRLRKI/KVQDEAASTPDLAKTI/DYEGHYTKQQIFHVDERAFYWKMP/RTFIARKKKSMPPGFRASKDKLTVLSGANAAGDLKLPVLTYS/ENPRALK/HYAKSTLPELYKWNTKAWMKIQKFPS*FT*IFM
1756	15657 -	A	1767	2	406	PRVRPRVRKLITLLNVSQRWSSEKKKKKKKTKKKKKKKKRGGRL*KKKKKKPRRGVNLFFWGPKKSTPPRVFKHRGGEK/PPPPPKKPREKPSLGVGSTWHGISPIKHSKKTSTK
1757	15658	A	1768	14	409	IASGFLFFIYFGVIGRPPKRGGVFFPFGGGGAPHPQGGC*KKKRGGGGPPFFFP

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						SLGGLGRPRPMSKIKTPPSAGGKPP/PFLRNQN*TGCGGPPQ*PPLFEGGPGGKNFSPRRGGGGGGPKTPPPPPPGGE
1758	15659	A	1769	305	1	TKTGPFPSNRAKKKKIVFQKKKKKKKINCFVTAPFKGIKTEATD*EKIFAKHLSVKG/LVYL*YI*ISKIYKELLKLNNEKTTIPIKK*AKDLSRHFTRYTD
1759	15660	A	1770	148	402	FSPVSLG*GRGNIYAGMSNV*EVPPPIDFQHEVKRALQTSFQVKLVKIIFFKSTI*KSLAK/WLAVVAHACNPSTLGG*GGWITRSGVKSEPGQHGE
1760	15661	A	1771	250	2	KKKKKKKIIICFVTDTFKGIKTEATD*EKIFAKHLSVKG/LVYL*YI*ISKIYKELLKLNNEKTTIPIKK*AKDLSRHFTRYTD
1761	15662	A	1772	407	1	KKIRRGGGQPLFLPLIGGGREKKFFPGKRGFY*TKAGPFPSWAKKKKFVFKKKKKEKKIIICFVTATFKGIKTEASD*EKIFA KHL SVKG/LVYL*YI*ISKIYKELLKLNNEKTTIPIKK*AKDLSRHFTRYTD
1762	15663	A	1773	1	406	KKKKKKKPTTFPGLPFFFSLSLPPRVPGA RGPSSFPSPKPLGCG*TKSGVSPAPKK KKPRKTNPKNFPNPNKGGGKFFNLPT HPPGGTTPPF*RRRENPPGFAPQKG/EV FSPGGRNSRGEPRGGPKKKKKGG
1763	15664	A	1774	2	378	AAGEWLHQSLQSLPPGLKQSAPLGVSK W*NPWHDPPPAPRFVVVVGVVLRWS FFLGAQAGIFFFF*IEGSHYVAQAGLE /PRLQSS*LNLPSSWDYRPVP
1764	15665	A	1775	1	431	QQMRDKRNLFEHNK*GIRGIYLNIIKAR HEKPTVDTILSGESFSSKIKTMLISPF FNTVLGVLA*ARKRKDI*VGK*EVKSYM FTNDMT\LDNPKDSTPKKKKTGYFMGGP GSKPPQRRGGAFLSLTRDPLERFPKTA LFTLGQKKIKGPKFFS
1765	15666	A	1776	334	402	KGGGGVGG*QGPWRLAHTDK\KEERKR ERERKRQRKKERKKERKKEKKE*MKNNK KKNK
1766	15667	A	1777	406	3	SPSSSSSSLSFPPPPFWGGPRF/SPPPP VFKPPPPFFFLGPPKKKFFPPPPAV*FF FF\LGPPPPFFFWFWEAGFPFFSPG* GP/SGPMAGFRSLPPPGNSLSKKKKSEG LGEGGNSVLTRVLLISSYQIPGNPR
1767	15668	A	1778	70	409	LISFLVSSLIVRLYRPLLCFLPDPSKGH CIPCLLPFLWILLHIFLFMHSFIYCLIN DRVLLCLPGWCAVVRPRLTAASATQ\IK RSGSHLSLPSSK*\WDHRCPGFFFFFF FF
1768	15669	A	1779	390	31	SHLSLPKCWDY/RL*ATTPSQKILVFTH G*VLSLLSLSFLIPD*TF*KMSLMRPS LTQKSSIIQHDLLDKVPITIFLRQSL/D. S/VTQARMQWHDLSLQPPGLKLSSQ PQAL\SSWDYR
1769	15670	A	1780	357	1	LTLFWGAQYLPKKGKGPFFLLSLSPSPV WGPLPQKKKSPPLCFYFLNRVLLCHPG WIAVVQSWHSSAHFSL/VLTRFK*SSCL SLLSSWNYRCTLHPPNFLNFWYRQNA VLPKLV
1770	15671	A	1781	122	254	RKNE\WSGAVAHACNPSTLPGPGGQIMR

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						SGDQDEPG*HEPPRPDTSFFLYPSH
1771	15672	A	1782	45	387	TOTPKLRRFFHFSLLKSWHYRCSPL\ PQ HNGYFLTNLDIATSMFFFKDRVSL\ LAQ AGEQWCDPSSLHPQTPGLRR\ PPASASQ EGETTGAAHHHTWRNLIYFFYYTYKF*GT YEMA
1772	15673	A	1783	1	401	FATLARLVSNS*PE/CDLPASASQSAGI TVSPAHLAISPSFPAMPSSGLGLSYPAY HPGLGLRCHLPVLTSPWTSDTGPSSVLP DAGALHCPPEPQHICPL\LSGWLQTP
1773	15674	A	1784	432	1	FLFLFFFIKKKT*PFFGAKPNRGF*KPP EFFQIF/S/CPVFLGRFPKPKQKEFFFP REMGFFFLFSPQGGGPARGFPPPLNQG EAPRAGHKKKGNLGGRTFFFFFEMES \FSVTQAGVQWHDLGSLOPLPPPFKRFS CLTHAS
1774	15675	A	1785	15	434	RLSLSCCGREEHSTLPGAPWRCTEIAWA DSPDPAPSPPSALPSLLPFHVYRDVCPV LCLRGWP**MVERGRLGISPTWLLGWPF PGGA/PHIKPE*YFLFAYTILRSVPNKL GGVLALLLSILILAIIPILHISKQQSII F
1775	15676	A	1786	1	258	CWPETPVLK*SHLDLTKRGEDRREPVAWA ASTTIFFFETGL/NSGAQAGVRWVHLGS LEPLPPIPSLFMT*GPCPGLGSSWPLR EF
1776	15677	A	1787	399	63	SLHNQVVKSTPTLKTSKKISHI*STWPG VVAHACNSNTLGHHGGRT*/RSGVODQ PGHHSETSSQRLRNPIKRCIKYLAHESK CCINDSFTVSVTSRKLIGKREVSPNNIT FR
1777	15678	A	1788	3	474	MSISPVRWNSKEAGRAANRQFSPSPWK DSDRDASPPEPASPTIG\PIRRLAESSW TWGSPCAEHPRARAGRKAATDCPWAAG SQWRGPAGQGAPRSCLFPGSRTAARAQH PRVAPPPPPAPLNTRASALRSQLPNPL *VMTPRPPAAAPRSPVGP
1778	15679	A	1789	66	395	LVQPLFDFIWHSRSLSLWGGRDLLWSGKE TMNPNCLNHSIGVLQEWQSDVKRRRLM ESLTGPAADVIRILKSNNAITTAECLEK ALEQVFGSVDSRDAQIKFLNTYQNP
1779	15680	A	1790	413	1	PSFRALITDYS*EEGPRFWQV\EKKGQP LKPHPGGLGSPHQESPRVGGPKRGGYNPF *KKRAKFFAPGENKGPFWTGRDPTF*G KTKKKTNPCKKGGKGGPPKPGQFFFFF LRRSLAWSRLECSAAISAHCKLRL
1780	15681	A	1791	314	1	KTKPFFLKKT*PKKKKKKGGSC*DKARY QTRKG/IVNLGH/HPSFLFYFILFFETE SHSVGKAGVRWLRANSLQTPSPGFQQFS RHSPSRKDYRHPPKRPQECVQ
1781	15682	A	1792	104	409	EKQSFADFWDHFDLYFDNVK*KEGESKA GEFNASTGWFGNFRKRL/RFKNVRTIGE PASVTQEADEFDPNFKKITEKGYLHG KFLMYHEAAKYLNFWCPTK
1782	15683	A	1793	392	2	GERERDRL*REERERERERERERERAR ERERARQGTSTVESRF/HSYCRDQDVA RPKAKGEVAAGRGSPDGLQVGRGQ*PGP SLRPGPWREWGPFATYLACGGPIPTGEVE

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						SGEEWAQQQGEWGQALGPP
1783	15684	A	1794	405	119	IIKMAIVPKAIYRINTISIKVPMAFFTK \LKTIIKFI*N*KRARIKAILSKKNKA GSIPLPDFKLYYKAI VSKPTWCWYKNRP IVLVHSRTARKK
1784	15685	A	1795	455	3	CSVTQAGEQWCNHSLSLQPPGLKWS/C PSQLPK\WNYRHVPPRPALTAHPALTAD F*RRKEYKLMRHRGKKWHDFTLRSKMK AMRHEYHSFLTYPNGHLYLHWQFFFDFT ESHVSQAGVQWHDLSLQPPPPGFKRF ERVGGGNSGAD
1785	15686	A	1796	2	134	PRIQHCTPAWATPQDSVSKRKRDMTDD AI*KG**ATTNIYIHKFYNLDEIDQFL KKHKLPLQLTWYEI/DNLNSPITR\IEFV ILNSKKKYPGSDGFTGEF*D*FCLETKK RYDYRPCNLKRIISDYNKHLHT
1786	15687	A	1797	1	404	PTRPLTGSSASGMMVEIFPKTYLISSAC WVKISKIDCLKLFSPFFFGFLEGGFYFC PPNSRGGSPGKFGLEPLPPGLKGIPP PPPKRGGEFGPPPTPAYFFFLWGGGV /PP/AVGGGGKPPPI*GNPPPPPPQ
1787	15688	A	1798	2	383	SGWLWACRSPDSEPLACAPGPRQ*GAYH PGQQLWMVR*VSQCCWPTPPALHSIS\P RP*LPPRRAGLGTCSPP/VPESPLPPW APAWPKPPRRALPPA/PPVPGPIDRPA EECRMVRDWAAPPAAP
1788	15689	A	1799	35	410	ATGPSLGKVC*AFSFL*PKLDFWHLYF QASGFL/CHNSPSQTNSSSFGKHYGM VLRVNSL*PDHPWNEFYFLNFFIFYRDS /SLTILPRLVSNS*AQTILLPL/PKVL GLE
1789	15690	A	1800	65	415	KKGVKGGPPPPQPLGV*GPPPEKGGPGP F\GAPKEKPPLALGEPKGP*RGPKGF FFKKGLEPGAPPPKPRGEKPPVFKGPH PFCKKGGGDKREKNGGL*RKKPTLGN PPPG
1790	15691	A	1801	417	3	NLGPNIFFPRAPQNWGPAPPLFFFLKKN FTWGGGSTPLFP/LNLGGLGGPFPGLEV YAPPSPHG*PRFFFKNQKLPPPVWALY SPFFGOWEN\RKAPPGQTLFFFFFLK* GQDLPMQLLVPNYWAQVILPPWPKV
1791	15692	A	1802	1	431	QPCTPGLK*SSCLSLPSIGDYRC/RTTV PS*FFFFFLEKGVGFIPRGGIKGLDNC* LGPHPELK\NPPQNSQEVGTGPPPR PG*LFFFETFFFF*KGFFILAQP*MK WGALKKTPPAFSKRGGRGTPMEPTH FLKEN
1792	15693	A	1803	256	399	AIKNIHDS*EEVKISTLAGIWKKLITTL IDDFDGFKTSVEEVTVDMVE
1793	15694	A	1804	407	2	FEKANLFPFLFKNSGPPNVPGRGMAGVP KFCCPSKRKVPGPFIFFLRRLFLFYKCR RPPLFWPAFGP*KFFLEQVFAPAF*KPS PKKRAPVFFFFFFF/RDKVWLCHPPWS AMA*SQLTVTSVSWAQAILLPQR
1794	15695	A	1805	429	116	LLTKKKRKKKPLACGESGLGGP*GTVTG V*QAEDTHVIW\VLSSAPSLSSSEMTDS MPGHLPSKDSRYGMEMLTDKKWTWDGGA WDSSPQGANRGRARQASGFS

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1795	15696	A	1806	2	408	FVIFVFLVETGF\SLARALACAISNS* PRDLPTLASQGAGITGVSHRTWPRRSCV F*EAF\TLMVLHI\PPSLLWHSVFTHLL ALSS*CFLFFLRGPWAVTQAEGQGHDLG SLQPPLPGLKWFSCLSLPS*NYR
1796	15697	A	1807	1	196	FRLGASLDLGGCSGVSWTPAPPLPPPP PPSAASGIS/SGSTSAAGL*SCRTAFF SFLSSFFFFFLKKINPFPLGGI*PFKG GPRLV*GNI*PPQG\DFLGTRGGKKP WGGGKFGQGGNFPPLPKPPGPQKNPP \PPPPPPSAASGISMAHLQLPACDRAA QLSFLSSHLFFFFFF
1797	15698	A	1808	395	3	LGKKMNNPKFWQGCETATGTL/M/HCWV CKFVQSFWNTDSIY*G*AAATHDSAMLL LGMHSMPTCTFVHQKT*TKMFIAALFIL PLNWKQV/RCP\SVI\DG\YIPTMDQSTAM KMKNLHAKTWMNLRNMLNEKPR
1798	15699	A	1809	7	454	IPGSTISLQPPPPGFG*FFCLSLSSWD RQFAPPR/LANLRR*T*LQSA*LWR\RG PILDEMKSFMNCNSLTEGVKGRVEMMS QNGRLLTKFCHVGQACLKTPDLK*SARL GLLKCDWYSCPEPCLTQMPFSFFLFF*D RVS/PLSPGWS
1799	15700	A	1810	20	355	PQCAHGCRAVAPVCVCFVCVCVSHCV SMCMCGEVSAGWTLCLCLST\CSGAYA CDWCGG/CYSACVCARVCACVCAQLLTC IGMWE*GQAGQGEVLLDPLCLCSWAP Q
1800	15701	A	1811	3	414	SSKNDNNSLQEFMDKIAGMKKNLNLTE LNNTV*EFHRAITSINNRIHAEERISD LENWLSEI\NRQT*KIVTRNEQKLREVV DYVKRLNL*IIG\VFEREKKAYYLQNI FEDIVHENFPRFARDANSOIQEMQRT
1801	15702	A	1812	1	443	AGKSPSPKKFKKGGGGGRWS*FLGGAGG GVPPFRPGIQGSNYRFF/SPPPPLGEKK KPPFKKKKTPQKLQNGNPHPHYFNPRVH GCREQQPWEKAPDATRQPHYADKHVEAG EPREPPKPHSEPLFSSPRKRPLFTRST /SGASPP
1802	15703	A	1813	411	66	WKNNVFNKECLER*IF/IIQKKLDP\F LTRYIKIKSK*IKDLNIRLEIKKTPGKE SVTLAKWLIRSPYLSFP*QIQSQ*INS YVLIKITKEERWSTSKEYQKPWRERKAM YKIK
1803	15704	A	1814	369	20	QEVRPSTYLSSSNRKYVKDSNARFTKEA IQIANIHMKNCPTSLIVGETHIKTSKGY HYVPFIRMAKILKD\CNRRCGETGLIHF *WEWKMVQPFQKPF*WFPKKRKIH*QFD LATRS
1804	15705	A	1815	2	675	GLAILGRRLRGEACTRSPFSSILIFMVS MGEWPGVP/GIKGTRTGAEAVPTRRRKS SIWPQTGGAGESSG/PLRGLPRQKPGS PRGPSGPPQNCARWWHPQAAPLGACCF GPEPSRLPPWRQGNWCLPSTPSSA*EG WR/FVLQPGFL*SPSSLASICPGAERGP PGSSRP/GLRGAPGG
1805	15706	A	1816	273	2	MESHIMWFPTIGFFHLVQCLHGSPMLQC IAVLHSSYLFIYLFYI*DRVLLCHPGWS

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						AVVQS*LTGASGSW\LRRSFHLSLF*C*DFRHEPR
1806	15707	A	1817	40	404	GLHE\PGVQGCSEL*SHDCTPAWVTSET LTLKLLKIKKSKKKRANPRGFERPTFG EAGPGGLLKAIISKPRVIQGTQKSGALL GFNSNGGENHPPQKQPYLGGLYAKAHSP RGCGPPSPCG
1807	15708	A	1818	392	3	EKYNMSYDIKSTNHRKNCKLDFIKI/RN CCSLKDTINKMKMQASNLEKIFAIHMPD RGLIFKRKNSCNLVR*QPPFFKEAKDL NTQKSQ*TNG/HGSKETSLIIREMQIKT T/MNYTTSIPT*MLKIKKMN
1808	15709	A	1819	311	431	EVVGRWVLTPTVTPSLWEAEAGESRDQE *KLCTTVEK*KTISN/HDVPIRSSWTGM VAHACNPFTLGGRGG*TRSGVGDQPD* HGEGL
1809	15710	A	1820	68	410	AKKNQGPMPVFGFGGIKPPPKQKVRG GFFAICPKEQVFFFWRAVVQSLNHC SLQPQPPGLKQFKQSSHLSSLSS*GYKH VLPCPANFILFSLVETGS\SIYFPGWSQ TP
1810	15711	A	1821	408	1	TPFFFLRVLRLTPLLGNFFGPGFPWPW GFSPGPLLKGRP/CFPIFKPIFQPGKW GLVFFFPFFFPYPRGSR*NLKKIFPNF PFFFPVFF*ILNPPFFFPFFFPFL*D RVSLCRPGWSAVARYRLTASSTSQ
1811	15712	A	1822	362	76	SEIAPLHFNVDRLVSLHLETNKQSNKQT KKTLLIFRDRVLLCRPGKNA/VEVQ*LP AASN/FLRLKQSSCISLSSNWIYRHAPP HLATVFNFLLIFE
1812	15713	A	1823	314	2	VISKPCPRELTCITYGVSLTQCSMFGRM KGLLLIWPVCEVRRASGRPPLMGSEEP LCPAATPSGRCTQQ/LH*ERAMMTMAVL SNRKGNGVGR*RNQIVAVS
1813	15714	A	1824	57	389	NLHLQLPTYTDADSTGPTLSGMNVKNL HWSYEYKYSITGVQWLLTGLSLPLPBR FKCSCLSFLRRWDYRCAPRRATF*FL VETAFLERLTSCDLPTSASQSADITGV
1814	15715	A	1825	410	70	VPIMSATQDYRHEPPRPAGRFLKLLKME PPHPALLLVGI*PKNMKSLLKDVCTPM FSGTLFAIAKIQKKPNCPSMDEWINCR NY\MHIYDGICYSALKKNEILARRSGTR L
1815	15716	A	1826	2	411	FLVEMGF\SMVLVIAGLKLPTSGGAPASA SESAGITDVSHRAWPVFFFLKRCVLVLG RS**A\WPHTNLIPPLPSGIKGDLC PNS AGGWEKGAPPPSPGKF/CEF*GRTGTTN FARG/WTKTPD
1816	15717	A	1827	276	3	GRPGPADFRVRPQLLQRFLLIYLFTEME SCSVTQAGVQWCNLGSLQPLPPGLQ*FS CV\K*FSCGLLSSWDYRHMPPHLDNKS IFSRNGVS
1817	15718	A	1828	1	391	LEPRRRFLQCVQDCATALQPGQSKTSL QKKKKKKGGPP/S*YQKGQCGPSGKKGR GVAGKGAFGPGFGGENKTPPGGGPTGEG PFPQKGVVGPSQGPTKGNLWGPGGPKL GGKGGPPGPTKGGGGPSSF
1818	15719	A	1829	2	134	DHLSFVVWNQPGQHSEAPSL/LINIWKL

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						AGCGGAHLSSHL/LREDHLNLEVQGCSE P*IHACTPAWATE*DPVSQTKLN*NIWK LAGCGGAHLSSHLGRIT
1819	15720	A	1830	427	107	VQHQPQQREBSPSIIITQKLARGGARCL *SQLPGKLRLENRFN/SGSERSHQCTPA WVTDRCCLKRTGITRASSQRLSVGIKQS CLNPRTAQLQVSAQSPSTVSTNL
1820	15721	A	1831	3	540	VQFPNFKIYYKATAIKTVL/OHKQR*ID E/MNKI*TPEINSYVYGYLNFNKDAKAI QWGNDSF\FKKWC*DNWISACKYSQTSV SASSASSSSS
1821	15722	A	1832	385	2	AGRQSETPYHNSTIMKVSLLQVCVDLSCL LGPGLSLVQDSENPAPQRKFLRLGSFWL PLSRFSRVGWPLPHWGQRSSGFSLPR\ P P*SQIPAPRSPPAGPVPARSWVCGPRP QTRPLPAERPSRPRRL
1822	15723	A	1833	7	399	RISRSYLSEYGGSGKEHPTLGASYARIM VFG/VFIIYF*RQCLA*AQWYSHSSLLP QTPGLKHPP\AQAS*GAGTIGTHHT*L TFAF/IFVLGCFFL*NKISVTQAGGQGC NEGSLQPPPPGLKRVSCSLTLP
1823	15724	A	1834	2	306	LARLVSDS*PQ/CDPPASASQSAGIICV SHRAQPAEELKVFGTLCLEPQRPTPDI FIIPYLFC\LFEMESCSVAQAGVQWRIL GSLQPLAPGVKRVSCLSPP
1824	15725	A	1835	12	400	KKGMVVKQLKVGKKPFSCWGPNNMKRD SPVFHHQDPIPIPIFFFGNGFLFFPP/ LAGGOGGNLN*PNPLPWGLKEFPPTPR GRGEKGGAPPPINFLVFLKKGFFLGGGR GGLEPPPLGDPPLPPKRG
1825	15726	A	1836	220	401	KGSFVFIPQPEGEPPFLG*LKPRFPGLK QFSCLTLLRSGNYGPLPPPVIF/CGFL R
1826	15727	A	1837	12	357	GLLGQMNGSLGTQTSYEDLMSSS\FKP NSPPPTPS/VRTGHLPK*PLESSNGPPP PQVSHSFQGWARGHPSPPPQWNTDPS PQQYTQCSKTD*PPPSPPYLGQEGSNA PSLA
1827	15728	A	1838	8	380	LMKTHAKLLNKRAN*IQQYK/HH/NQ MGFILGVQIYFNF*KINLIQLINSVKKK KN/HSSSSSSSSSSSSSPVLIKSLC NLGKNKRNFCLTKGIYKNKTE\NSMKI ILNGEQLNAFPLRLGK
1828	15729	A	1839	2	444	VPGDAKWFSLHLKDAFFFIPLVPESQY PFAFEWENPNTREK\TAVLP*GFWDSP HFFAQPLERDLRGLQLEDGSILQYVDHL LVYSPTQEASDQNTIKTLHFADRSYKV SKKKAQITLQQVHCLGYILTPTGCK/LS PERVQAI
1829	15730	A	1840	1	642	EIKGIQIGKEEV/SLFADDIDYLRIDS TKKLEVICELNKVG*KINM*T*IVFLY IGNEHLELEI/R/ELMPCIKTSSTMKYL EINLKKDV*DLYTENYKVFPREIKIT*A NQ*EILCLCSRRRLNTRM/STFPQVFCVY YAI PVK/IPSRLFLVLVDKLILKFI*KY RGPRTAKTTLKKKKKVRLTLLIFKSY KTIVITIGWYGFQDRQVD*WNRIE
1830	15731	A	1841	3	423	HRITSE*DLHLARELIW\SMYGSLDHKN

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						YDAELDRMAMPCLCATAGALPPGYVDAS SSSKAEKKATVDAEGNFDPRPVETLSVI IPEKLDSEFINKFAEYTHEKWAFVKIQNN WSYGENIDEELKTRPMKR\PY\KTYSEK D
1831	15732	A	1842	33	179	YMLGGRGCSDLRSHHCTPAWVT/TA*LS KKQYQRQQNRLQYHLQEYERKK
1832	15733	A	1843	349	10	LAGGLNSMEGER\LR*EREECTQQQMVH DKYCKDLMGFGTKPRHITPFSSSQAVQP QQSNALVGLLGYSSHQGLMGFGASPSA KSTLVESRCCRDLMEEKFDQRK\QWVLK CR
1833	15734	A	1844	15	856	AAEQLSFIYKLPQNPSFSTPGSSLSGTH GMQTMLGSTHLPNLTDMLGPELVQGIP SPGCACQGRG\GGGRECCSPPGVSEPG \SAVGRGAEGPGGLTRSGGAASALVRP GEKGCWCRTASGAGPQRRQRTTRPGSWG LSFSQTSEEKCPSPAGSAGAPVCQRRQ SSFAGGCGTGAGAPGST\GDAHQAQGS GGFLRLSLPAVGGPRPGPSFLKTSGSGSV PQGVPIIWSLT*RALAAPGSQGPAGLAV SCTGGRGYRDPQAPGTGAG*HGNSTRLR GP
1834	15735	A	1845	402	2	SKARRQGRPLRQG*APG/AARIPEQKRI GGP/EERRRPSARGPRATRVAGEGPKPK GQTAMAGGGHDLPLPLPPARSRSQESIG RSRGSGHSQEPPAPQPSGGDPSPPQERN LPEGTERPPKLCSTLPGQGPPPNV
1835	15736	A	1846	446	32	TSRKIS*KTGNQFLMKECSCNSHHKAAF TKKDVLNI\LAVVKHVNTKASETFHFFQ SGQAKVQQGFVKEGCELINEALNLFNNV YGAMHVKTCTCMRLDLRLQYIMGDYABA LSNQKAVLM\TERVMGTEHPCIRPL
1836	15737	A	1847	440	4	VDGRHVEVSKKGGQVNYQAG\KTVEIWA DKLGCNMLGTADMVECLKSTRYKELIQQ AITAGGAPIAFGPVIDGNVPGDRQILM EQGEFLNYDIMLGVNQGEGLKFVDGIVH NEDGVTPND*KFSVSNFVDCMRPRRGPN YSRFQ
1837	15738	A	1848	526	0	PRRDPPPKRQTPIPTHVSPVWEKGPWGP APLRPDHPSLSPCPAMG*K\PGLPRGCP QTOISPLFNRSASPPLICHHHPSEF\K PGPEPPPTPSSSIPSLARFTRPGESSPL PPPQTPSGPP
1838	15739	A	1849	417	31	QATGQECGCHRGPPPGPAGETEPQAPL RLPGGTGIPWGAGILCPS*LPGPSLSLSP AAGRG/SGPSAGPGAANFSSP*/PACPS SSRSAPVGGAGSFRRAGPGLFYTLPAFP WCGRGASNKIIQMPGLVC
1839	15740	A	1851	3	285	YTVCECVCLCVCLPVSL\SLCLSVSV CFFPSLCGFVCVCPACVSLAECALCAT KRFV/CMAACLW*ASFVSTWVMRPAVN RFRRGGSALGA
1840	15741	A	1852	128	524	KIPGLGQRSEGVGQKDDLHVTAPVPTH GWGEGAASKPTVLP PPPP\PDAPT VFFF FFFFWEKKYFFGPPPGAGPQIYLLGPN PPGFKPFFPPHPQAAGI*YIKPPWPYKC PLKKRGVSTLAP\GFPKPPP



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1841	15742	A	1853	1	1648	MTVPLHSGLGKGVKPERKTTVRRPFVSA GKKYACPFKKAETPQWRRLMRPKAPAA SLLATFPISQRLIPLTPARKHCPSESET STWVVS KAPATPRTRGAGPTSPPRPTRR R\*ACSLQKLFAVEEFEDDFLSAVED AENRFTGSLFPVNAGRLRFVSSRPQETVQ AQSSR/PAAVTPHC SLRGFGPARLGP/P ASLPPARPVLTA/GPSCIGAAPLRPVST SSSWIGNQRRVTVTEVLRPARPQSSAL HPLLTFESQQQVGGFEGPEQDEFDKVL ASMELEEPGMELECGVSSEAIPIPLPAQQ REGSVLAKKARVVDLSGSCQKGPVPAIH KAGIMSAQDES LDPVIQCRTP\DPD*DL VLWVTF LFQ/PALTVP TQQLHWEVCQR SPVQALQPLQAARGTIQSSPQNRFPQCP FQSPSSWLSGKAHLPRPTPNSSCSTPS RTSSGLFPRIPLQPAQPVSSIGSPVGTP KGPQALQTPIVTNHLVQLVTAASRTPQ QPTHPS TRAKTRRFP GPAGILPHQQSGR SLEDIMVSAPQTP THGALAKFQTE
1842	15743	A	1854	235	223	IHKFIHQIWLAKITCQRTKV*KERSVLL PTSFSFPVPSQGHYTCKQLCSLADLSQ PDLVYKFMNLAVLHAMWNSRKVSCYPWT MIYFLHANRT
1843	15744	A	1855	373	3	IKDGIYRYFYKALDSFCLCCEFMNQFFS CMDRELSQR CFLNSAY*FPSNL*CYLCY LFFFF*LKKYFLTF FLDRVLLCCPE *SAMVHS*LTVP LDFW\VKGSSCHSLLS SWDYRHALPHLY
1844	15745	A	1856	378	1	RQRHSPAGNTGRPQVTPCG*ISWPSITK DRTSMSSVTSGALGHTAASPHARLLPLA LPSVRTQHGSPPPGQEQTIIICPSNLPT HPSLPLGMHPSVRASPLCK/P/SPPSI PASVHASKHPSPPVY
1845	15746	A	1857	3	379	YMRKVIEVWFLLLLLLFFFRGGFLGQ GWGPPAPGFSGKKNPQGLGSSNLRGPW *TNP*PVP GGALFLVGPPTPAEFPPKNF SRGFLLV/ALADF*TRRLVSPHGG/RG AKGTPAFLESMPPWMP
1846	15747	A	1858	452	1	GTHGLLLGSGPF\RQVFKPDNFVFGQSG AGNNWAKGHYIEGAKLVDSVVDVVQEE* ESCDCLQGLQLTHSMGSGMGTLFISKIR EECPDCIMNTLSVPPPKVSDTVVEPYN ITLSIHQSVENTDETYCIDNEALYDICS RTLKLTRCI
1847	15748	A	1859	1	385	NTSSDYIFPFFFLFRNSIHSVTQAGGQW HNQGS LQWPWSRLK\CPTASASICLHMP PFLANFLIFFVEIGSPYVAQAGSRDPPA LASQ/SAGITGMGHCTQP*VFLFFFFF SFRKKCSWP PPGGPPIF
1848	15749	A	1860	470	17	TEMDSRVRPRDKLACTTKCSKHIFDAIK IT*NELASAD/DFPFTLIYIVLKG/NPP CLQYNIQYITRFCNPSRLMTGEDGYFFT NLRLGTHCSWLMMTMWTCFRAFRISSQ WMSYVLRFRNGITGVSHRAHP
1849	15750	A	1861	3	790	CSRPEFPGRRFVEAVRSKPYLSLPF*SR *SFFNVPAE*TSAKDILASSEFIKQND VSS\LQKFMPQEVK*LDHIHTA*ADGSW

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						KAELERGPDSAPSFPQKPAASRQPEL GELATFLGRVDPWYQSNVNTLCPAIHKL AEMPPSLDTSRTVDPFILDVITYYIRMG TQPIYFQIYTVKIFFSGLSQDPTEDIFL IELKVKIQDSKFPKDGSPRRRGVAEGP GAELSLCYQKALLSHRPREVTVSLRATG LILKAIPASMY
1850	15751	A	1862	192	3	SSGSHSVTQA\GVQWHEHSSLLP/LLT* PPGRK*ASHLTLASS*DYRRAPHPANF *IFCREGV
1851	15752	A	1863	82	370	SLCQKRAFVGEKLVHGLLVSPSGGRVPS CPDPWGCRRPRFAIAVVSFLKLRVVIPE VSILPEDLEELYDLFKVRSSGKMRGSRP *AGLSRG/DPACP
1852	15753	A	1864	2	325	IQVYSISHLSIYLF\IYHLSRGS MHVSM SLSI*SIYPCMDV*MYLSNLCMHVYIYL FYGSIYRFYLSICLSVYLSIYLSIYLSI YLICHPSIFKTVIDEHAIFATWRH
1853	15754	A	1865	3	377	YSPWCKLFRELCKINVPD/LDSPLLSGK EFNDTTHNTFDHMRWRTKEHNEAGWLLLS SVDKVMKENDLRDSNSWLQKQV\*PLK SAKTALSGSLNSCREKAEIVEKQTSLS M*VADLQRKMHVQP
1854	15755	A	1866	10	378	GWKNGEFIDAL*KVYGHKAPNKS AVYKW IT/*FKKGQDDIEDHDSGRAS TLRKKI HLVYALIDKD/*RLTAAIAANTIDISIS LAYRILTEKLKLSKLSTQWVPKQLCPDQ LQRRAE LPMELK
1855	15756	A	1867	346	1	DILVVKLQKPQPNKGKMLKA AKERKKFAF KGV PVRMNADFSIAAMKA/RRRWNS IFS F*KENNCHLRLLYS AKNIFP/EIKTFSD REFVTIRSAVKEILKDWLWAEERLSHVK SRNV
1856	15757	A	1868	1	377	GTEFFORTQCKGIQ\YVVG LI IKASSDP TCVEKEKVYIGKLN MILAQMLKQEWTEH WPAFISDIVGASRTSKSLCQNNMVLK VSEEVDFSSGQITQVKS KHV KDSMCNE FSQI*Q/LCQF
1857	15758	A	1869	90	384	QWLLFTEYSSLYHPVL PFFFFPGGRTG PNPPAGGEGNETG/PNGSP TPGGGNPP PLPPGGLGLLSMPPPPRQILLMETKKRP PP*TNKCCSPGYSP
1858	15759	A	1870	2	578	FVVKHALLLGLDFLPGKMAPWSGQCSL GHTEGGTSWDFAVGGASWRLKVVCVKGD SHKGPATPIASCKGPLGRPCPLLAQSKA *GS*KRG/VAPGSP*LALGMGGG\DRIT LISQVHGNQVTQIIPFSTEGETKAQRSP SLPPRD LIRGRHSWNLDSTQLLG YCPLL PPPLHPAGPLVPVFTNGEIQKENSRE
1859	15760	A	1871	1	382	SGQDAGSCLLYGAGSGAMVSGAYNPYIE IIEQPRQRGMRFIYKCEGRSAGSI PWEH STDNNRTYPSIQIMNYYGKGV\RTILV TKNDPYKPYPHDLVGKDCRDGYEYEA*FG QERRPLFFPNLGIRCA
1860	15761	A	1872	490	1	ADSLSKDPGRPLHPPNIWGRGRQ*PGE TPQ*HRRSCASQDPGRSQ*PGKILPSPK PGRPPMTGEDAGPPK\HGPNPSPNDQKK NPPPK*/PQGNRIHRDPRFPQP*PRKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SFPNNLGDSNDQRSRFPVA*KNLPQSSS GTRAI GRELYLPPQPGSSAFPNSTT
1861	15762	A	1873	373	1	GGGVPGALFSHKKKSLFFPPPPFFFRK GL*NF\KIKGCGSPFLPLFFLEKESCF VP\RVECGGVLGPCKVCLPGSPFFSAS AS*VSGATGAC/RPRPGKFFSPFFFFYF LVEMRFHRVSQDV
1862	15763	A	1874	3	374	YMLGKEIVSKTKIGQELGLLNQ/TSQVV NAKEKFL*ETKSATPMNT*IKRKQNSPI TETEKALLVWIEDQTSNILLTQNV I*N MALTLENSIKAERGEEDTEEKLEGSRYW FMRFKKKKAISIT
1863	15764	A	1875	2	364	IHSGKGESLWDLGLDTEFLDLPSKA*HI KAKNDKLDLIK*NFCSAK/ET*/IRMK TQAIHWERIFVNNI*NRKLVIYKELLKLR N\KKNTIRR*AIDMDRHF TK/EKMPMTN *YTKGCSISLVIL
1864	15765	A	1876	41	461	GFLYLCSSSEIDPYPSPSKKIKSEWIRTY WMKLLSENATIMLKDSLSQV/FCVNI P FVQAAKAKIEE*DYIKLKWFCSAKGAI* KAKROPTE/W/DRIFANYPCVYGLITTT CMEFTQLTSLITTPITITLWPNRQSYHH NPT
1865	15766	A	1877	2	185	VRPTKLDPLERTQYTLPLLYKWNNAWM TAHL/FTA*FTEYFKS\SVKPDE*VREI DYRMLYL
1866	15767	A	1878	1	491	IHRLLWPPLSAARPPSRESGLRCRAPRR PASAAAATAASPS\PTAPQGPPR/RRRL LIQPPPLYPRGLFTPGVPP/LAPGGSREP S*SLT*DARTLPLPVLGPRRARLLGACP AVQAEAGVDPVGHLSVLAAPCKQP*TP PPACHCLDGEGRPSGVQAPLHKALYP
1867	15768	A	1879	24	449	LQPPLTWALLLQPPQPKSRAAFFFFFFF FGKKSQFLFGPPGGGEGEKL*REPPPP GTKGMPPPPPRERGGKRGGPTGRENLGI *RKGGVPPGGRGGGQTPNPGGGAK\PP KGGK*GGRLPPPQIKGPKRGRPKRKG RP
1868	15769	A	1880	190	2	PLYCHKVGQVGLLELLTSGDPPPLSLPKC WDYRY\DHHAQPSF*LFLSVQISGIKEN HSVVQPCI
1869	15770	A	1881	1	458	FAIRAGRNLDPKEFRYLRTVIVTAAVYW GLNSKLRCCLTS\LLTFQHRAGVSPYTSP FGFA*TCVFAKQLLEPILC/RPCFHRAP LLEKLRGHFAE/FP*QCFFR/QALGFSP /RSTCVGLRHG
1870	15771	A	1882	3	392	YMMRYHYILIRMAKVKI\SSTNDDTQ*L KLIHC*QECRMVQPLWKMV*QFLIKLNI *LP*NLAILLWGIYLIEMSTYEF R/RKI CIQMFM TDLIVIAKYWTQ/PQCPSVAGW IKQ/IRSIHTVEYYSAVKRNQL
1871	15772	A	1883	2	473	IQGGIAAYRVDRQERSNGRQGNRRNL SG TNMRRNKQKGLRRCKPRW/RSRGM AWK DKPRDAR*KSDRDRQ/RGETDG*RVSGG LTA*EAYRH\HRGQ\EAASQSGRSRQAG RQTP*QEQAGNEAIEIRREEKSRGQERE RE\KDRDADRHKG
1872	15773	A	1884	138	444	CYLTLIKCRIIYINDKVIVLTIVWY*HK

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						DRHID*WNRLQSP*LNPSTIWVQLILNN AKNTQWVKDTLLDKWY/ENWIYQCMRM PLGSYTI PMNQFKMNYGLS
1873	15774	A	1885	27	470	TICCYIFLFFSFFSFLFFFFFGKGVSF*S PGGENTG/ANLG*WNPPPPGKGISPA*P PKEPGMEGAGHPPGTKS*PGKFGPGPGG GPSFPYRGPNTWKGPKWFGGIGYP ATIPQKKQPEGKRGR\PGGPMSPYNGPP KTPTHGKGPG
1874	15775	A	1886	478	1	KNVQENSALQAAMCRKMLIVCQTQCIVIT SGESGAGKSVAAKYIMGYISKVSGGGEK VQVRRGKQDKLGRPHLHGSAAPICTP ASV*LLPTPPASAP\HVKDIILQSNPLL EAFGNAKTVRNNSRFSVSLCRPAWSSC SLRADLSTHTPTHTTRV
1875	15776	A	1887	1	402	HSLERPHYIG*LFKNIFSRD/RVFAMLA HWSRTPGLKQSTPLSLPKCWDYRCEPQH PAGSFFFFFLKNGFWGCSLGGRAGGQQ *LKS*WRPNELG*GNPPC*PSKEVGTG AHKKIANREIRTRACGGTNFSL
1876	15777	A	1888	511	124	GTRRQHFAGAHVPPEGP*S\MLDPKLG DDRPARDMWIREPGLLLPRAPAQDAGKY YCHRGNTMSFHLKITARPVLWHCLLRT GGWKVSAVTLAYLIFCLCSLVGILHLQR GESCPQWVCNPTPSSPG
1877	15778	A	1889	667	310	QLKP*ATKSV*KDTAFGIDVGNDFLAMT PKAQAMKGKIDKWGFIYR*SICTAKETI NRVKR*PRK*EKIFAKPTWQKGQIS/RI HKEFQQLN/KQKSNNLIERQTKDLNRFL SKECSKDL
1878	15779	A	1890	462	3	KWFFPLGPPFLPPP/PPPI*NPSFQKNK KLTRGGCARYFPPLKSRPRIPFPFEK GEGSPNSKHSPAPPFWGPKETFFFRTP PPPPPPPLCSFLKNNLFSYIPKGLGGK GQNFHSLFSPSFFFSIKKKLLGLGVHVR YCRVNSCTGFFVQMY
1879	15780	A	1891	1	455	NTCLGFGNGFLDATPKA*SMKKIINKLD FNETENFCSVKD TVKGMKRQATHWEK/V RKTHILYKDLILKIYNQLKHHNKTST IKQ*AKDLNREDIQMTNKHMKRCSGWGR WFTPIIRALWACKVEGSLESSLGNIV RPHRKREREIHCY
1880	15781	A	1892	1	537	RGGIQAPKEVSPEGRQEPARKSLI*TA* ETPP*SQ*/PIPEEP/TGVFMKKPVSVS LETGKHAVVVPKVNKGELPDNPTIKWFK GKWLGLGSKSGARFSFKESHNSASNVYP VELHIGKVLGDRGYRLEVKA KDTCD CGFNIDVEAPRQDAYGQSLESFORTSKR SLYALALEDPGM
1881	15782	A	1893	2	514	VRCQRRCHE*RACGSSLVNAKKLYEDAL MARKVKQSLFSLDVEDDEKFMMSLQ\ CSLAYGTLTKILSEKRSKSYGMSSVRM RSAGQTSKAHLHQPRVSQVLQVPAVNL LPFRKKGQTKDPALNTSLPQKVLGTTEE ISGKKHTEDTISVASSLHYSPPASPQGS
1882	15783	A	1894	473	2	VMGESRGFSPPPTFTGNGFVFFWKGQVS LFCPEGFKTLCSSSPPPPPQKAGVLGG SFHARPPPPFFFI*IPFFFGIKP/LC

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						SPPP*PL*KKRGIFPVPKGFCEMESCS VAQAGVQ*YDHGSLQWPPGF**SSYL LV*LSS*DYKCVPPHPMY
1883	15784	A	1895	613	11	FRPRSPACGLHAVSSPKLPGAQALSSPG LNLVFTAGSWDAG/LLRLSPRANNPRVA LPRVHTGPSST/DLSPSCPLGLACGFGT SQPACL*SPFLLLAPARPSGCAWPGLP VCSLHLRGWGADPTGCLDAWAMALAS LRPCLCALPLSREPPSPLNLDLVLPRM PRRAPVPLGRTPHSLLLCHVQSPSEQ PSKGPERL
1884	15785	A	1896	20	449	KFGYSSAAARRQQLGWAWL*YSFPLQL EPSAQTWGPGLRLPNRALLVNVKFEFS EVSPCVACGIQAALSMGSTSSSVKLSHP QAPLPQWHQMVFARCLCMGAQLNVPP\ ESFTFQVSTKDVPLALMACALRK/KATV FRQPL
1885	15786	A	1897	393	3	RPTAQSKGNI*VRVAS\EALSPKLLDFL PGKVLNGEKVDVRPATRQNLSSQFEAQA RKECVRVPRGGIPRAHSRSDSSDSADGR ATPSENLVPSARVDKPPSVLPYFNRPP SALPVMGLPPPIPPPCI
1886	15787	A	1898	395	217	RER/CKSFR/PPA/HLQAKIKGAQ*QVN QAAAAQAAAPAAAMVSRDISSLLVSSQK SKVSNYM
1887	15788	A	1899	1	375	NTVLVQ*NNKAWMTVHPF/TAWFSEYFK ATVEIYCS/EKIPFKILLVFARVHSHPR TLIEI*KEIYAVFIPANTPSILQPMDHG IILSSKPYLRLKASRAQRLTPVIPALWE AEAAGSPEVGSSGLA
1888	15789	A	1900	47	326	VKSIIQFNSKNEPGKHDKTPSPEKTQIV WWLGSELRSPPSYSGAAGAEEMGRSL RSRPQRAETAPLHSSPGSGSEMLSL*RO HLTPTAWAGVQWRGLCSLRPRPPGFK*/ FCPSQHHPQPPSSWDYATRCQATKQFVF FLEMGF\VMFARLILTVELNN
1889	15790	A	1901	181	837	AGRVDRREPMTGTGCKELETGSRETRS ASRWGRGRWRLGQACRPQGLPLSTFHL GAQAKARGGTPLACSSHLPNSHVGSLSKA QRDEAMVQSGLAPAVSSTCTRWT*GSEW **GLHIVAARRQQGREEEPRTTAAPET LCFQQTSWASSCSLEHSAQPSEVQVRAL SVPSHSPMWV\PQLSLPRDHRKPPGE
1890	15791	A	1902	1	385	YTWGFRGKKPLIHCL*EYKLVQPLWRAA WRFSK*LRVEL*FNAISPLGVPEENK LFYQNSTCTCFITALFITGKT/WNQP
1891	15792	A	1903	207	3	FREMEFLHLGQAGLELSTSGDPTLASQ NVG/HYRREPLRPANTLQS*PLGLKQPS CLSLPSSWEYRHMV
1892	15793	A	1904	2	391	IQPLISQRKYKTLGQNSLS/CCAHP/PP HFFFVLDSYFHSLLSQKNAPFT*G*CP YWYSKSYSLIHSWSSSILPCPLTSSGF PSLPPSYQPLPCPSLFL*NSLSTLCLL FFSLLSQPSFSNRWPSQVYL
1893	15794	A	1905	3	424	YRAGCLQSLPPPLLLFLPCDVPFPSP S\LP*VKASCGLIRSQQNVGTIPCLQNR KSNKPLHKLPSLRHSLRAMQNRILPILR IGKFF/IFFS*DGVSILCHPGWSAGVQLQ

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						FTALHLL/VLKRFSCLSL
1894	15795	A	1906	2	389	IQRGLDKSCLITDNIPSSQSLIQKKGVN PSFKSMKADRGKEAAEEKSEASRSWFM EKERSHLHN/IK*VQGAACYPEDLASI IDEGGYTKQ*IFNEDY/MWKKM*FRSFL TREKLTPGFKASKDRRLTFLV
1895	15796	A	1907	458	13	AKEETQSVVVDFFPM/VPQGVVYNFFVSR NANLSTIKQLLWHRAQYEPFLHMLSGPE AYVFTCINQTAEQQELEDQRRLCDVQF FLPVVRMVDCEGARVNKLLSSQISLFIG KGVRELDLSLSDPEVSDFTKMCQFCEKS AAL*DQATS
1896	15797	A	1908	409	3	EKTDGLYRASQRGKDLRRLCAQSFHASW KGMALCALIHRRRQ/DLIGYAKLRKDD PIGNLNTAFEVAEKYLDIPKMLDAEDIV TTPKRDEKAIMTYVSWL*IVIAGAEQAE TAASRICVLAVNREKKKLMEERV
1897	15798	A	1909	116	379	HSGPRREGALLLPKCLPHAKRCLLFPKM CSDGATALCCPGWSSAAPS*LTQSP/AS TSQAK*PSHLGLPSCWDYRCIPHPANC LDYYY
1898	15799	A	1910	418	3	QD*YATANRWFICMLSQACFLPSL*PAH LL*L*QLMLFSFPGTPVFSYGDEIGLDA SALPGQHMEAPVMLWDESSFPDIPGAVS ALMIVKGQSEAPGSLSLFRR\LSVQRS KERSLLHGDFLAFSAGPKLFSYIRPMY
1899	15800	A	1911	394	3	ILEAYPEVKDPAVKGASSKKEMYGH*/A AEQALPVASEQEQQRHERSEKKQPQVKE GNNTNKSEKIQLSENI CDSTSSAAAGRL TQQRKIGKTYPPQFPKKLKEEHDRCILK QENEEKTNVNIMSKKNREDV
1900	15801	A	1912	499	141	PGLGERDWTISKYGGQAGGSESTREWASRC G/IRPGGDAGQQQPRPE*SVCPRGAHSP GPGSWKASPAWHAEPGGRCSGLGVQKE GFPGLHLLQPGCRTPGPGIRKERFSGYLQ
1901	15802	A	1913	127	387	ISFVFPPPTLEKMPQLKPEITISMTGLNLF QHLCLNARLATSAYDGCNSSEV/CDLDDL LY*AALFLKLDYQIRFPNYFSTKYRIYY LCLY
1902	15803	A	1914	504	0	PGPGQRKHSTAPMCLLNIAQILRFVLA NQIYKCIKRIIHDQVGFIPIMQSWFNI QNQ*\INLIHHINRLN*KNHMIISFDKT HHLFIIKTFTKLGLIEGNLLNLIKNIIF/S KNPAANIILNSEKV
1903	15804	A	1915	46	415	YTSNKQLQIQILKITYNSTKKYKILINW IKDVKDQYTENQKILLREIKDLNK/YRD TSCSW/NIVQMSMFS/KLIYRFSEPPNK NLSTL*ILTTSF*FAWKYTGTYIKVMTM KNRVGRLSLPNFQNY
1904	15805	A	1916	420	1	ENADCVERARKSPDSIP*\RGGQISVTM VSPNEQEKAGQLAIGVRAVRYNGV\LLA KMWRKKLHLTSLANLEKIIAIGLFPSNF ERKPPENTFLKLTAMATHSESNSLSCFAQ EDIAICRPHPAIKMPEKAEQYKPLTASV
1905	15806	A	1917	384	3	TRTITSGQYSTHVIRASRVPTRS*VPVF RSCTSNRRFSQAIEPRVMH*KVHIRAST VRYDSGGHVAVYPANDSALVYQLGKILG ANLYVVMSSLNNLDEESNKKHPFPCHTS/

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						RRALT*YLDITNPPMY
1906	15807	A	1918	405	105	KAEAQRREITCSGPHSQADSAWHPLVTW WH*PPFVARSSQEPGVHSPVP/HVCRKI LLIRPKMALANEGNYRELRFWFTPWSRSR *VGCLTTPGMCVKHLRCV
1907	15808	A	1919	409	3	GGQEEGVFRVLNSKEFFTERGKP*IPPV KDQEI IH\PTKFNHVAHMGPGDGKQVLM DLPLSAVPPSQEESPGPAPTNLARQPPC RNKPYISWPSSGGSEPSVTVPLRSMSPD AQDFDKEPDSSTKHSTPSNSSNP
1908	15809	A	1920	9	470	APARNPLPRPCTWPTGP*CLRPARPPVA SACLCGGTWNLALWLCSPGT/PVPFLTP PCS/SCEVQQPASHSVASNQSKPAKSA AVAHECPGGTGSADPGWPPGATCPESP GPATPHTLGVVEPGKSSPPTMEEEPWAP QGSPCWTVRQRTMM
1909	15810	A	1921	556	1	IQLWALGGILRRVGRDPPSHRIGKEPS AMAGQAGNGDGEESG\GLAAVPHLP *SQHAAHPLLIGPPGQQLGDSKV*GFP SPRLEENTLENGGWGSKQLHGSPGSQHA GGSWKNGETSLKG/PH*ADGAGRHTMPQ SPPSPFFKPHSV*HNPPAS/PPPHGSPA PSGTSPLPMSAVSLLPSSL
1910	15811	A	1922	567	41	GGWGETFSRLGNDLQAH*SRFNAQAQE ETSR\VLAVSLINEALDKGSLEKTLAL LLPAAGLDDVSLPVAPRYHLLLVAAKRO KAQVTGDPGAVLWLEEIQQGVVRATQDA NTAQRMALGVAAINQAIKEGKAAQTERV LRNAAVALRGVVPDCANGYQDLESAMA KIQRPAAV
1911	15812	A	1923	2	405	IQCGGITSSSVLHGMVFKKETEGD/VTS VKDAKIAEYSCFPDGMITETKGTVLTKT DEELMNLSKGEENLMDA*VKAIADTGAN VVVTGGKVADMALHYANKYNMMLVKLNS QWDVRRCLKTVGATALPKLTPPCL
1912	15813	A	1924	510	37	LLGHAFHVQSSSGRPQLAEASGHSHLKK GECVQORTGNVGLSPNTARWGTPLGPSI SSSAPPWSFSAFPGPPSGK*AAKDGP CSLKSLKR\RSQGLR*TRSGSPSPMP PSPSPS/ERPPGDEGLLPCTPRGGLPG PKINTACVCAADISPGLEPV
1913	15814	A	1925	74	429	ATIPGHELLLFFFLFFFLGKGAWPL G*GKG\GGPIRG*GNRAPRG*REFPPPT PGKRGNTGGGQPGQPIFGFLKKKGAPP GPGVPKTRGQIEPPPPWPSKRAGVTGWT LGPQKV
1914	15815	A	1926	515	304	ALAASLALALNGVFTNTIK\*IVGRPRP DFFYRCFP/GMG*PHSDLMCTGDKD\VV NEGPKETSPSGHSSPV
1915	15816	A	1927	1	433	NTVGSNKKSKKLYFAEIEKSYLNFIVNL KGPQ*VKIILKKSSVTKCTLIHNSKA*Y KV/LKIVWYWRDTHM/DHWNISIKQHMW KQFFDGDTKTVQWAKDCLYNNWCWEK\W ISTSNRMKFNIPYTP*ANINCHQDPNSK ELYRYKN
1916	15817	A	1928	316	356	GGT*PPQAATPIS*LPLPITSSL/TLPP APSLPLQIAPISDPSPPRYS/TPTPPI SLGLAPPTLLIPVPSLVPSPRLNSTA

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						PP/TFLTGSGAAVTVVSLAVSLSPAPAS AMDKAQNM
1917	15818	A	1929	490	11	PTRLTCPGSHVPGPVTFPPYETHSMF\ P PCHVHPLVQPPGSSSHVPGPVTSSPSPPS ATHIHPLVQPPGSSQLPNTWVHPSQRM TWLQQHPLPLAPPQP/PSPGSICSMTH LTEYLASFAPQ/PREQAPQGGVPTSLP QW*APQPTAPCRATOSQQLLDG
1918	15819	A	1930	1	552	RNPKRAFPSPPIAPPS*NQENERSRH PQSL\PFVKSRKRAFSP/LSPCSSFV KSRKRAFSPVPAPPS*NQGNERSRH QSLLLLREIKEMSVPTPSPCSSFVKSR K*AFSPSPVPLLRDHTFLPLPEPRQPS TVPVGCGFSGSRIPRRWNHTGCAFLICH SARLLCDPRVSSCVVRHS
1919	15820	A	1931	414	3	RVPGESRK*ERVLDNRHKD*EGRRRCNI \MGKRVDYTT*TVITDVNTLSIDQGVH RSIAANMTFAEIVTFNIDRLQELVRRG NSQYPGAKYIIRDNGDRIDLRFHPKHS LHLQTGYKVKRHMCDGDIVIFNRQCI
1920	15821	A	1932	521	103	ATEPAGVRLKEGGNITESFVTGVNISA LADFSQDA/SRYS*KKQVLVPYRDSVM TWLLKDSLGGNSKAIMMATISPADVNYG ETLSTLRYANRAKNIINKPTINEDANVK LIRELRAETARLKTLLAQCNQIALLDSP
1921	15822	A	1933	1	490	NTGWVVRKGEENGTLVVRRLPCVPLCSS AGGLTEDEGELCAAGFLLAEDFGQAL QQLQTAHSQAVGAP/KGGDQVLGGGTGA PPTAYPNHALSIS*IPSVSWHDEGALPA VKIEILGIHLLPERHALLSLVQARSGL LLHGPPATGKILLNKAGTTECCLT
1922	15823	A	1934	383	151	EVAFLENLIKDDIERGRPLLLVANAGT AAVGHS\S*LGRMKELCVQCVNRPKMEG YMHVSQHPVPESHKMRKAIF
1923	15824	A	1935	379	1	YVPVVS KDKEYFFNSQ*GLTTHQILPYI DGRFHVQKISAEADVKNLVRIAIQILL *VGLQSYLGQGHQPGKS/CRGPGCEGWE GMVLRS*AQLSLSGTTAL*HWCPSRKL IQFGIIKNLIRRLCI
1924	15825	A	1936	376	2	GCLFIYMKPTAMSSSQVARSGEVSPFTA VPA*S*K/QGHGAVLGCHITSEACFOAC FPFLRPGRSTCFA*SGC*DVERSSSHSH GTAHSP\HGTAHTPMEQHTHSHEQHTHS HEQHTSHGTAHMY
1925	15826	A	1937	426	1	KHGEIIDDLLKVYRDNASKKSAI/YSKW ITHWKKRRDDVGEEVHSSRPATSVCEET IHLVCALI*ED*LIAETIANAVGIPRC SAYTILT/E/KLKLKSLSTRWVPK/P/L LPAQLQIREKRSMAILNKWNQDHEAFLH IIAGLY
1926	15827	A	1938	2	469	KRRKLVSSIAAAIHPALSS*TRQRFLL LFLFHI VREDLVQLRIKKKHTIQGNVE VKLL*PTDNILCGKLYRFHRSTQKVLQ LI/NFSIVAAYKINMHISLVFLYSNDE* LENKTKQTSSFTIALKRIKYVGSNKKSK KFYFAETEKSYLDFIWN
1927	15828	A	1939	468	920	IPLSTHSPGMGTSTHLSRHHLSFWTYH ERLLNPGRETDWA/IMLFRWGGLMLPRL



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						VSNS*AQVIPPTSASQSAGITGMS\HAS GHLIFNY\CSM*WLHLRNSQ*KRCTGQE TGPCPVTQDGVQWSNYGSL*PQTPRLKQ SYHVS LPSWDYS
1928	15829	A	1940	448	474	GIPGG*GSTTRNALYHVMNGEDVVILT CKHGKDWQKHKDSRCDRNTYEYK\YDF GEMLNATFCLVHRGRRHGSFRFLEAMQ AACVPVMLSNGWELPFSEVINWSQA GDERLLLQIPSTIRS IHRDKI IALRQRS QFLWESCIATAIEDPNLIGVVR
1929	15830	A	1941	1	423	NTTLIFAGGM*NVC PGPLCARLLHRS LT HATPD PPLLTLP*IPTPTSSRCAPK AP PHLICPTSCPLCSKPHWPP/CSSCQ
1930	15831	A	1942	48	417	RLTMYQVLYRLHCTALQPLPRVK*FSC LSLPSTWNYMHMPQCPTNF\CIFTRDEV PPMLP\SWWRTP
1931	15832	A	1943	450	2	VHRRSNRQNMDSR*RGAMQSVESV\GV PY\EQ*TIVDGI\NSGVWEGIAA*IEE RYPEEFALRDQEKYLYRYPGGE\AYKVE TIKLNVEAVNTRDKPTNIFAKNQAPVR MRRNSFTPLSSNTIRPRNYSVGSRP IKPLSPLRAQECI
1932	15833	A	1944	451	3	GRITRHLPRRAEDDREREREPSPLPSRH PMFPPSVTPKASSDWP/PASSIPCQACH G/PPFVSLPRKPAHRSC\VFVFP\ASGG DTSIHSGKT VYVKRSQPAWPVLP PGGL*APSHGAPSPSPDQHRHCPEI\R*DLL PAPAPSPFSIPPLY
1933	15834	A	1945	402	3	VRLLSWKVMYP*SRSKASL/HPQITAS LTGSCVNCIVILILNFFYEKISAWIAKM EIPRTYQYESSLTLMKFLFQFVNLYSS WFYVAFKGFVGYPGKYTYLFNEWRSE ECDPGGCLIELTNQMTIIMAGDV
1934	15835	A	1947	1	405	NTGWRVFALCSLKGRPRGIERV/GGKK KKKKKPGGPLGPAQKTPKTQKGGGAQG NRGKPLPFSGGNFGNGRIFGNPLPAPGP GGGGGPR*KTR\KRKNGNWDLLKGGGKL VFCPMVGKLSGVPGV*QKNFKGGW
1935	15836	A	1948	443	1	LTPGAANASLLG\CCMEDLSVNG*RGQL WEALLTHNMVAGCRLEEVDNAYGHYEF STLAPKAWLSVELAEPVPEGLPPVFA NFIQLLSA/PVVVTEGGTAWLEWHVQP MLALMEALRKSQVLNRVT*GAHYSDCI AAALRIKIT
1936	15837	A	1949	396	2	GNGRGGSVPPNSLNEDGISCAI*/RHIN WLNG*TPTIYCL*ETHLICK/DH/HRLR VKGKKKILHPNGNQKPAVALLT*GQTD IK*KAIKSNKEGHYEIKGSVKQENITVG NIYAPSTRAPRYKKQLDLKGVN
1937	15838	A	1950	419	1	RWQ/PSARPPTPSGK*GASLPARPSGT *GALLPGCPVWKVRSASSWPPSRLGSEE PLCPA\PSHLGSEER\PSRPPSHIGSKE R\PARPPIA*DVGSASAPP/LPSGM*ER PAAPPSGR*GASLPGRPSPEMWGVPLPR RPVWDVRAPSRAPVWEVRSVSAWPPHLR REKTLRLATAPV
1938	15839	A	1951	422	3	QNHVIMSE/DAKIAFGKIQYPFKMESLN TL*MKVNFLNLIKITQKNPIANTMFTGE

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						MLE/AFLLRQGRSC/CSLSPTLFITLL EVLPS*VWQEK*/IQG*EREE*NCDFVD DMIVYVEN*KKPLYNLL*IIS*VARFKV ILDTCI
1939	15840	A	1952	2	409	CAHYSKNPPQRPLRTDARLPAV/DFWSL GAILFMVGCQPPFQEANDSETLTMMD CKYTEPSHVSKEGKDLITRTLQIDPRRR ASLQ*IENHPWLKGVDPSPATKNNIPLV *YK\NLSEEHNSIIHRMALGDITDR
1940	15841	A	1953	2	367	IQCVRL*VHVCLCASSCVCI CLYVHATL CVSTCL*CVAVCM/CLLCACATVSACLC /V/CGCVSTCVCPVCTCDCVCMASAC VCT/CLCVCTVSTCVCBRLCVPTCVCR CPCICSSLNGNEWMG
1941	15842	A	1954	374	2	EAPWLLRAGRGA LPPCWSKTPPSPLLF\ PPLLPGTLVYQPWVPLPPWNRLACAVTL ST*ARAGTSNPSWHLPPVSTAPQHPSTW QSPGAGTMGDPSPSPWTSLLPGCCHNP CHCPFPHHKPTRV
1942	15843	A	1955	1	411	NTPSPELHPC*PGL\PPLSPPPQQPPTW APERTSTQQLPILCLLPSAHTDAPCT QPGSTLPLHTPHTQQAQGTAYQIHTT*A APPPGAKPG*RCPPPPPSRQPQRMQTPA PGNPQPCPRLTTLTRVLVPAVPPPLPI
1943	15844	A	1956	33	451	RGRNTFGPLQSPPPRFK*FSCLSLRSW EE\RDYRCMPVHPANTMLASLVNLS\CD LPALASQSPGITGVSHPTPHLS*FLMP LE*GHHHLLLVLSQPPNMPP*FQRFST GQLECSSFRNLIVSPSLNFHSDFLIT S
1944	15845	A	1957	3	399	YMQVRTTMSDSSHSISKINTDNTKSCK G*GSTESLFHDRWEYKFVQLLWETVWHY VR*TFTILYNPEIILKR/IFRHTYKNVC
1945	15846	A	1958	47	399	AANPTLPAVFFFFFLETEPPFGPPGGR GPQSRLTEPPPSGVKPIPR/PPPPGEPE KWPD\QGGGGGDKPPGGPPP*ATQON SAGKKKKKKIPRPGAAGADPLLPKGAGG EEWLDPA
1946	15847	A	1959	407	238	TQAFALI/KDGGVIGGICFRMFRTQGIR EIVF*AVPSNEQVKVSGSPRRQPCTAH S
1947	15848	A	1960	106	1854	NEAVKSKPNQTRNHKEKNYVHLPDAGP SQPASAGGSSSACRRSTKATLHKRWVSS PAGPGVQPLSWQHPPMA*GLQGNPSQ AAAPPARPGLVSGNCLT*EMAQAGA\GT GGSLSASLGKRCPHIPVPC\PVL*GLC VPGRSSLGELGGNPVTVQSFPGPGAESD PW*GDAECCSLLQASFGDRAGWSIR/RG SVGRPAGVPRGKGRKPTLSGA/SGPGSV LGGFCCPEPLSREAESGMVQE**GRFWT QERTPTGR*GCKVAGYLHSSATVGHSG AGAGGSPGKTSATLDVGQGLGPT/PSGP AWDRTINGYMEKAALPLCNGKVTGNTQCG AQPPASGPSFWVQPLLLRQRLRQSTGL *LLFPGVGGGLQPGEG\GQPFPLSPWGS LTGRKNSNKARPGGNEGTEG*GARNGAS LTWVWTVPNGGYCPQAGRDFWLVDSEFK PSLGLRAMV*NSRKAPLSFEDGRMGTV*

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						PQQEGRASHRKGDGSLSPHSGKG*DP*G/PGGKERSISPPLPRGL*GP/VGERGRNGDWPW
1948	15849	A	1961	76	427	QRQEPPTPGHTTSGTRHPPGPGGRGPIQT HSHSHLFPWLETSAGSSPPNFLCSLPFY TPLLRLLPSEFLCPSQTTQRMPIPAHP SPASPCKVP*DARGAPAGGAPSTL/RGH HPPHP
1949	15850	A	1962	375	131	FLVGRIRLLYCLRELFFVYLLREQKAKRN SQWVHTLPISRRHVDVPCSPSINRNR GRDKKRPFPL\CVDA*LHSPSVVIQ
1950	15851	A	1963	89	538	GLILLQKWHPGAVSSMVERG*LLHSGLF FSFPDKVSSVVQAGVQWDLSSLOAPAS GSKRFSSLDHRHAPPHLAHFCIF/M*T QDFAMLARLGTSFIYLFGCCC\FETGSH SVAQAEVQWHNHSSSQPHSPRLRRSFHL SIPGSDHNRNAP
1951	15852	A	1964	402	42	CCHYPGTPGLQGRLSASHQAS/SGPQLP APLPLOVLPLFALGIGVDDVFLLAHAFT EALPGTPLQVGPCP\QGSSEAAQLTG*E PLGSSDLGLLMNLGASCPHL*TGEIIVL CPKGYCLDQ
1952	15853	A	1965	8	14	SSRAAACPPRPALSLPRPPVFTRRMGPQ GSGLPKLPVSAPSSRMGSFPAPSPLLLA SGDRHLCPDAAALPLLAETGCDL\PPG H*PPSPGGLHPCSPPS*PLIL
1953	15854	A	1966	521	2	YELYGITIKRHRREVSNQVRYKEHSIP PDYVSSVPTDPTWGPERRREESSGHFMV DHTGTAAGGGGGMILASPKLGATPLPPE *APA/PPPPPPPPPPGVGSGHLNIPLI LEELRVLQQRQIHQMOMTEQICRQVLLL GSLGQTVGAPASPSEIHGTGTASSTKPL LPLTV
1954	15855	A	1968	111	395	YLMRGFLLHHNMVKGKEDERKTKGARLI LFFFFFFFKKESPPPRVEGRDP\NLGT* NPLPPKVKLSRPTPEKWEPGAHPHCP NNFLFFRKNNGS
1955	15856	A	1969	413	101	DVNRHFSKKNKHCQ*LVIKEMQIKTKRR YHFSPTRMGKIKN\KKENKFWQGYGETG IFTHCWWECKMVQPIKKTWVQFFLKVK* LLVFGPACKELGSYYSLVTKS
1956	15857	A	1970	411	1	NLTPALCTKVHFKWVMDIKMGKTIRLL ENNTRKYLHNKIWKGLNRTE\KP*TIK KKTDKFDYDTIKNLSSSKNKTRQIDWE NIL\YLQYITDK*IIISGIHKAFLK/YK /KKTNNPVGKWARDLNGHLIKNDIHM ACI
1957	15858	A	1971	3	828	GQACHFIFRSAQAGGSRLRIWRKQLGL WRVICALIMPALEHSFPTRLQGNVPGP SISLDTSC/CNRCVWEGGR*TGPGLP SLGKVLVEGIPSESPGPTASHPCSPRP DPDQ/LSCISAPSATPTVH*SHLTLP MPGPG*GLHLSAQPGPRKP*PGCSGLGG GDAAPRGMEKP\PPPQLP
1958	15859	A	1972	398	3	GPGCYFSVRLQCP/RKIPAWKRAVCSAT LI\SLQGPSLSAPHVLGLAALAVHLGES RSALPEVDVGPPAPGAGLPVPALFDSL LTCRTRDSLFFCLK*ALLPQSRLSSLSK

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						SDTCSFDKIRRRDRHADIPPLY
1959	15860	A	1973	2	433	QDPTKMTKEELNALKSTGDTLG/RASE VEVKNEIVANVGKREILHNTKEQHTED TVKDCVDIEVFTAGENTEDQKSSDTPA FLGTLGATYEEQVQSQILESASLPENT AQVESNEVMGAPDDRTRTPLEPSNCWSD LNNGS
1960	15861	A	1974	373	580	TIFSRQVLRIQNALSDKPNVSTVYSNNG SELHGTSEASV/YHWKILISTEYHKTL
1961	15862	A	1975	47	413	KWKHLRGSEHWRPQENQVHQRIAE LRKA GLWSQRR/PAEAAGGPRPKSHWDYLLLE MQWMATDFAQERWKVASVKMVRARARQ LQDRTRREAGARREEPSRLRQTSPLVPE KSSVPGVLVLR
1962	15863	A	1976	444	3	GYERSRGTSGTHSSRDYDGFQATVK WAMLDQFRMLSPCSKEVMHQPFFYLKRV EIMAQCEEWIADIQQYSSDKRVGRIMSRH SAAIKRRTGQLREELLKLPCPEGLDPDS GDAPEVCRAATGAETIMHDQV/QPSSS KVLPSDFQ
1963	15864	A	1977	281	567	PRSSLQGGELSRPWGRKGNFPGPVPPP QRMFYDSELFSGISDPSCCF/RSAPTAD QVYGDQDMHEVVRKHCMYDLVRKWRPLG KGQGGKISSPHRP
1964	15865	A	1978	357	2	KQILGPPHPQAQPGRVPPPHGPKDAPL WSSRAAPPGRGLGRAGPAAGVEAGATLR DSSPSTWTREGLHVQAQRKRPSHVHKG/ SGPGCLEDEGFPSTSLRLQAQLAEIGRGN GLSVRRQ
1965	15866	A	1979	29	434	VQAEAEGLPGDTEHPQPQLMSRSLLEGQS DVTIKHVACGDDFTACLTDRGIIMTFGS GSGNCLGHGSLTDISQPTIVEALLGYEK AQVACGASNVLALATERELFALGRGDSG RTGARTKESH/YLPQQVPM
1966	15867	A	1980	3	2082	SSEGYLRGNMSENEEEISQEGSGDYE VEEIPFGLPEQSPGFEQSPPEFEPQSPR FEPESPGFESRSPGLVPPSPPEFAPRSPE SDSQSPFEFSQSPRYEPQSPGYEPRSPG YEPRSPGYESESSESRYSQNTLKTQSP FEAQSSKFQEGAEMLLNPEEKSPNLISV GVHPLDSFTQGFGEQPTGDLPIGPPFEM PTGALLSTPQFEMLQNPGLTGLALRGPG RRGGRARGGQGP RPNICGICGKSFGRGS TLIQHQRIHTGEKPYKCEVCSKAFSQQS DLIKEQRTHTGERPYKCPRCGKAFADSS YLLRHQRTHSQKPYKCPHCCKAFGDSS YLLRHQRTHSHERPYSCTECGKCYSQNS SLRSHQRVHTGQRPFCGICGKSFQSRS ALIPHARSHAREKPKFCPECGKRFGQSS VLAIHARTHLPGRTYSCPDCKGTFNRSS TLIQHQRSHTGERPYRCAVCGKFCRGS TLLQHHRVH\SGERPYKDDCGKAFS\R ASDLIRHQRT
1967	15868	A	1981	2	188	LPETNFAELFLPYISQHNLRKYKK/WP GAVAYACNPSTLGGQGGWITRSGDQDHP GLHEEW
1968	15869	A	1982	3	424	EGQAIVERMNLCLKQQLQKQKGENRYR TPHKQLN\ALLTLNFLSLPKGRILSAAE

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						QHLQKPAAKTEAEQLVWWRDLITESWEI GKIITWGRGYAYVSPGL/NPSRHLKPYH ERMLRKRFRDEPDPPSCSHVKTDAEED PN
1969	15870	A	1983	3	399	YSKLSFKGTLTKFRRIYSSSFYKEFQGC ISDLCHP/R/TLTNCLRGELLKENLVWG AFGCHPHFPCYINKSQERNLLQALRHPT TVAFGETGFNYSYKCTMPVPEHHKVFKR QLELAASLEK/PLVILCQQADE
1970	15871	A	1984	1	405	RRHIGGGVRLYYIGGEVFAKSLSDSAIF AQTPNCNQRYPGWHPGTVCKIPPGCNLKI FNNQEYADLLDQSVNQGLEADY/QLTRM CTILMSLLKGWGAERYRQTATRTPCWIE LHLNGPLQRVDKVLTMQGYPSILM
1971	15872	A	1985	27	452	QGREHAQGGQSPGAGHLGPTPEPQPEPQ PRPSSQAVPAGRWEPAQE/PTRHPHRL SPASRPLGSPAPLVRSSPGRCRLHEHT IWSSTVGTSEVPAPSLGRPALEPGTV TSSVRLQQPHMHTPGKIMPDPSKRNGKF TFT
1972	15873	A	1986	414	220	GAEQEELLSP/GSGGCSELRSCHCTPAW ATRAKLRLTKQNKTKRESYRQGNQNWGR ILGELLGRL
1973	15874	A	1987	52	412	TRERKLFFACDNVWKHLKRYLRKNSFGE NLWSSRNIAKKKKKKKKKKKKTNFST PKNFFFKACQCMGKKNTHDFHEQNF EHALLQQLNINFSTNYIEGRVF/HPGAP IESLLLMCH
1974	15875	A	1988	2	143	EKRRLGLDKRTP/AQAFAEKMQEKQMER ILKKASKIPPPFVCMWSVDS
1975	15876	A	1989	3	163	TEFQPSK/WGEDLGDNWYEIFAIDLL CCHQKWI CHPLFLVGVVRAGAEVSGVF
1976	15877	A	1990	1	439	DKTAAEDAIRNLHHYKLHGVNINEEAST NKSKTSTKLHVGNISPTCNKELRAKFE EYGPFG\IECDILKDYAFVHMERAEAE AIKGLDNTEFQCKRMHEQLSTSRRLTAP GMGDQNGCYTGCKDGHWSKECSIDRSGR VADLTEQ
1977	15878	A	1991	1	145	VVAASKAMK/MGDWKTCHSFIINEKMNG KVWDLFPEADPVLLKRLRESR
1978	15879	A	1992	2	425	NISTLKKTLES DCT\KLFSQIGGEQAAQ AKVDRCLSDLAETNKFRDLLQEGLTE NSTAIKPQVQPWINSFVSHNIVEEEF NDYEANDPWVQQLILNLEQQMAEFKASL SPVIYDSLTLGMLTSLDAVELEKVVVKST FN
1979	15880	A	1993	3	449	VAGPAPGAGARFGLDLQFLQRFQILKV LFPSWSSQNALMFLTLLCLTLL\LKSF QFTCNLLYVSWRKDLTEHLHRLYFRGRA YYTLNVLRDDIDNPDQRISQDLERFCRQ LSSMASKLIISPFTLVYTYQCFLSTGL LGPVSIIFY
1980	15881	A	1995	1	410	SSRRPFTALKTKSMRDLNPEDIDQLITI SGMVIRTYQLIPEMQEAFFQCCVCAHTT RVEMDRGRIAEPRVCGRCHTTSMVLH NRYLFSDKMIQLPESPEMPAQTPHT VILVAHNDLDDR/VQPVDRVNDSGFF
1981	15882	A	1996	1	154	LFFFRLLVRYTKKVAQVSTPTLKGVS RN

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1982	15883	A	1997	2	475	LGKVGKKSWKHPEAK\KRPCGKN KKLRQTRREAOKE\LPDKV\RWGLVTP SETPVGISNLSPPFLGPRCL/QNPaelkp PWRFPWAQRPKAH\ERANAGPKTPAEQR KVKKIKKLKEDISQGVHISVYRVRNLSN PAKKFKIEANAGQLYLTGVVVLHKDVNV VVVEGGPNAPKTITRLMPLRI
1983	15884	A	1998	3	431	QLRTRDRGWPSRRPEREKRTSQSARRPT CTESRWKSEEEVESDDDEYLALPARLTQV SSLVSYLGSISTLVTLPTGDIKQ/SPL EVSDDGPFASFPSSSSQQLPPGALQG SGDPEGQNPCFLRSFVRAHDSAGESSLG SSQA
1984	15885	A	1999	1	400	ALDLRGLQILVGFPKRRVTTCSYPTALQ SEIEYQKKESTAVMRTPEPDSAYQASPR PYSAGPADSKKPTKGYCYNPTLP\RLIEI MTLEGGTTG
1985	15886	A	2000	1	372	QNIDLVISFFSSRLLQGAELSVERVLE IIKQGVVALPKDRL/RGSCAPTLAAGR SSGGQSPCMPGLCVCSFWVLTVSWLVQC KFPFLKFKYVEEEQPEEFFIPYVWSLVY NSAVGLYWNPDII
1986	15887	A	2001	393	1	GGTGRGGGACGGVGAAGSASGGVGRGA GGVIADSGAPGGGVEGGVGASGGWRE/G RGTSGGVGGSGGACGSV/GSGGAGGGV GACGSTSDGVGRSRGTIGGLGGSGSAGG GVGACGGASGYVGIRGAGGG
1987	15888	A	2002	2	362	WVTFISLLFLSSAYSFGVFRDDAHNSE VAHRLKDLGEENDKALLIAFAQYLQOC PFEDHVKLLNEVTEFAKTCVADESAEDC DK\SL\HTLFGDKLCTVATLRETYGEMA DCCAQQEPE
1988	15889	A	2003	2	358	EANRGWFIRLKEGSQLYNIKVGEEAASA DVEAAASYPEDLAKITDEGGCAKQQIFN VDK\QTAFSWMKRPCRTLIAREEKSVPG FKL/SKNRLALLLGANAAGGFKLKSVL CHSENSRTF
1989	15890	A	2004	190	1	DQTCFLSFTVKAVTFNGVWVWLTVPVIPA LWDYRH\RPANFFVFLVETGFHHVQAQAG LKLGS
1990	15891	A	2005	1	132	GMCHHAQLIFVF/CSRDRVLHGCSQTPC LKQFSCGLPKCWDYR
1991	15892	A	2006	2	134	PMTFFTELEKTTLKFIWNQRRIQIAKAI LTNQK\NKARGITNIC
1992	15893	A	2007	315	127	SEIAFFFCFLKIILDR/FSFFARAGL KLLASNDLPSSSSQGAGITGVSYGTQPV CFEYNVG
1993	15894	A	2008	3	325	RCSMLAVREM/QKATKRCHFLPTRLALI K/ND/GSNKCWK\HCWWECKMVQLLWKI VWQFLKLLNIELPFDPEIPLRDIYPKQL KTYVHTKTCGQMFIAVLFIILNPHLMNV
1994	15895	A	2009	369	3	VGQAGLEFLTSGDPPASASQSAVITGMS HHTQPIFCIFGFA/GCPDWSQTPELKQS AHLSLPSSWDYRCMPHLANFYFCRH/R VCCPGWSQTPGLK\YPPALVSQSVATTG TSPRAWQDTILPV
1995	15896	A	2010	114	287	APLCLCLRHLRLLIKRLTVLGTEAHTL\ NPITTRGRGGQITWGREFETSLANMVKP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CF
1996	15897	A	2011	218	346	IMKFNLLKFYFIYLFSSRQSL/SSVAQAGVHWRNLGSLQPLPPKF
1997	15898	A	2012	310	1	SSSSSNTHFGIPKYLINPDTCTFLA/KVNNSSLTGLEYTETLKPQIK
1998	15899	A	2013	3	301	SDCCASNQRDSGGVGPSEFARKHTLCV/CNSLDLIE
1999	15900	A	2014	332	3	LRDPLEEAVCPFSDQLHAGRTTALPKAVRQGHLSLQRLLSF/VCLCPAPRGAYRGRQAG\SLSCGGLHPVRASRLCLPKQAWAMAGAPPAWPRPCSLISDCCASNQR
2000	15901	A	2015	2	325	LLLHHAPPVNLFLRDRVSLCGPLCGPGCSQTPGLKQSSCLSLPKC/WDYR\RATAPGL
2001	15902	A	2016	373	3	WAHGLQPGKPKVDSLKKRKKKKGKKLNTPPLRSRTRQACLLSPLLSNIVLEVLPNBIRQ/QKKEIKGTHGTREELTSLFTDNMIIYVDIPKQSTKKNQGSYSVARPGAVAHACNPSTLGGG
2002	15903	A	2017	343	1	EFFFVSGSRATGKSSDIRATKYIWRVLEYLRAWPRGQRLKSS\HTSLLGSYHPGAFRGDKWSCCHQKDETGGGEDEVLLCCPGVLGCSALCRSGVVRTKFGIRGRPWKERE
2003	15904	A	2018	139	2	NSISTKNTKNWGMVAHAFNPSTLRGRGGOI\RGQDFKTS LANMVKP
2004	15905	A	2019	3	322	ARELVFFFGAYRKGFHHRDMKPKNLLCMGPKLGKIADFGLALELRSHPPYTDYGSTKWR/YRGNPALLRPTPMKAPPYEGWLHISGSSIWNITKSDSNFIFFKESKG
2005	15906	A	2020	205	377	NIVENIVFCWPGVCFLQTCTVCINPETSDE/WPGAVAHACNPSTLGGQDGOITRSGDRE
2006	15907	A	2021	3	324	KKWGKR\LNRA PNGRRYPETRWALEEDQCHICKELHLKTVRFHCTPIRMAKIHTDNPQSWPRCGTGTLIHCRRGCKTV/R/PLWKTVRQ/FL/RKLNIPLPDPAVLSLCIY
2007	15908	A	2022	2	382	RVSQDGLNLLTSRSTRGLGLPK/CWDYRC EPPSP
2008	15909	A	2023	1	421	RWNPGGRGCSELRLHYCTPTWVTERDSISKIAKNK/NNKRPRNNCR
2009	15910	A	2024	339	3	SWDHRRVLI FVFLVQTGFCHVGHAGLEL LTSGSQSAGIAGVSHRA\GQKHQFRPEH RFLKFGFVFRDRVSLCCPGWPQT PRLKQSSRLSLPKSWGPPATALDPDSSYLEEMVLS
2010	15911	A	2025	2	146	NTFGRSRQEDHLGPGGQACSELRS HHCTPAW\VIEQDPVSKKKKPPKP
2011	15912	A	2026	3	380	RLECSGGTSTHCNLR/LPGFKRFSCLSLPSRWDTYRLP/PFVFLVETGFHHLGQAGLELLTSGDPKCWDYGC/DHCTWP
2012	15913	A	2027	32	296	DYMNSLMYFHSVLVASTDEGFLPKTVSTQSAGITGISHCARPWIFF/CFFFFKNRKRTRFVAQAEGQGGNFGSLNPLPPGFRGFPCLSLT
2013	15914	A	2028	2	187	FTLLPRLECSG\MILVHCSLNLPLGLRWSCLSLSSWNYTCVAPFSIFYFIFLTW

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						GTTLNC
2014	15915	A	2029	197	3	AAGLSQAGMQWGDGFSREHLPSRFQRF CLKVPPNNWDYRHGPPRPVGIFFSF\LV ETGFHHHPGQ
2015	15916	A	2030	88	362	KFGINLKKKEKKGPQKNQNFPTFLFFF FFETESHITQAGVQWRDLSPQLPPLPG FKSLPSSWDYRCLPPCPANFCIF\IPDS VSLCWQGW
2016	15917	A	2031	7	131	GTIMAWAPGEGGCSEPRSCHCTPAWVT\ SETPSQKKKKGVLL
2017	15918	A	2032	1	343	LECSEPRLCHCTPAWV/TGDSVSKKKK KKKK
2018	15919	A	2033	243	14	QKLAPWPPQSAGNNRRVPPHPASMAFLT KIEKTALKFIQNHKRPQIA\TILSKNR VGSITLFSKIHMYMTTVIKTI
2019	15920	A	2034	238	3	FLALPKVLGIIGCVPPHPASMAFLTITIE DTALKFIQNHKRPQIA/KPILSKNRAES ITLFSKIHMYMTVIKPLRVST
2020	15921	A	2035	345	2	LVKIQKEMNVFMTANPISIPQFMDQGV SSCKSYFRNKFLYV\IAAMTD/SSNG SWQSEWKTFWKGFILDGKNTDDSWEB VKISTLTGIKKKLIPTSTDDFKEFKTLV EDVT
2021	15922	A	2036	1	140	GRCC\HELRSRHCTPAWATRAKLKKKK KKREKKTQKGNLGFWAF
2022	15923	A	2037	199	348	RSSNEGGRDCVFCFGRVSLCLPGWSAV AQLWLTATSTSQ\VKLSLHLGL
2023	15924	A	2038	3	193	NGLNAPT KRLRLANWIKSQDPSVCCIQE AHLTCRDTH/RCYLKG/WYKAF
2024	15925	A	2039	116	337	SKLLKILPRLCWGWQAPVIPATQVEEA EDHLNPG/RSRPAWATQRTPVSIKKKII LRPANGK/CHGPSW
2025	15926	A	2040	368	252	VFFFFALFYLFFFFFFFFFFFFFFFFFFFF QFLGFYFRFKF
2026	15927	A	2041	204	399	VSSHKINGLTV CSTSPFFLSLLPPSEES ACFPFAFCHDCKFPEAS/SVMLPVKPE L
2027	15928	A	2042	103	356	WHFSPQPPLPPP/PLPNPPPPPTPPPP\ PPPPPPPPPPSPPPPPPPSPPPPPPL PPPPPPPLSPPPPPSTPP/PPPPPPPPPP PLPP
2028	15929	A	2043	3	344	LYKWNKASLAHLFAAWFTVYFKPTVE TYC/SGKKKIPFKILLIDNTPCYPRAL LEMCEEISIVFAPATTSS/LKPMQGV IVTFKSNYLRNTFQAGGGEKKKHERKK NIIS
2029	15930	A	2044	2	349	PRVRKSPGPNFTANFYQTFKELISILL KLFQKKKIKKGENPPNSFYGAIIIPRI NPNMDLSKK/ETYPVSGRNMEAKIFTK FLAGHFQSFGREIHHQREFIPGIQGG FNIGN
2030	15931	A	2045	280	462	CXFFLVVVLVWCVVLLFXVVVLWLCFFG FVVCCVVFVFCXGVWFFVFFVVCVLCV LGCWC
2031	15932	A	2046	3	284	PSPFSLLLPPSFLLFPPSF/SPPPPS FLLLPPSASLLLPPCTSLLIHPPTSLQ LPPLPSFYLLLPSTISHHLPTHNLPTTS IQDPSTPCSIK



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2032	15933	A	2047	95	1	GRVDAILAHCKLR/LPGFTLFSCLSLPS TWDC
2033	15934	A	2048	211	1	EPTTMTGAKWGSSQTTTNYHMLQSLRIN VRVDFFFFFFFCTDR/SLSMPLRLVLNSWI PAIILPHPPQVLGLQ
2034	15935	A	2049	35	266	EVRRPSTWQPPRLRSEEPRLR/QPPRLG NIGFCHVGHAGLKLTLSSDLPTLASQA GIT\GHSYRRASEEDKKESSMSS
2035	15936	A	2050	281	3	QSNFKRALLSILLKATYRSNIPIK/VP MTFFTEI/EKVIPKFIRNLKRLRIAKVI LSKKNKTRRITLSDFKLYY\IAVFVA WYWKKNRLSDQWN
2036	15937	A	2051	251	12	ILRFFFLPKFLGFQKPPSLEKTHFFLP AF GNSLFWPPEKLGQKKVFFFFFFFLRQGL/NSVSQAGVQWHNLGLLQSPPLRLR
2037	15938	A	2052	2	325	ADHLRPGVQDQPPQGGQNGKTPSPLKIEK \LAGCGGGHPRLREENCLNPGGRGCSEP RSRRCTPAW/VNDSKTLARKKKKKKGVE KNECGRKVMRV/LQGPKAKVKPWGENL
2038	15939	A	2053	3	166	SLLLPRVECNGAISAHCNHL\HNLHLP GSSDSPASASQVAEVRGSLERSSSLA
2039	15940	A	2054	227	3	LNENIGRITGMSHARLILLFCE/YRVS ITQAGV/QHDPGSLQPLPRVFKQFSHFS LQSSWDHRCAPIRLAIFWVFC
2040	15941	A	2055	301	0	QRKSHMFLTINQKLEMIKLSEEGMSRVE TGOKLDLMC/QVSOAVNAKEKFLEKIKG DTSVHTQMIRKQSSINVDMEKVGIVWIE DQAP/HNHIPLSHLLMRAR
2041	15942	A	2056	1	109	RPLRRLRQENRLNRGRGYSEPKLC/HL CTPAWAT
2042	15943	A	2057	313	250	PQPPPPSPPPQSPPPPPSPPPSPSSP/ PPP
2043	15944	A	2058	134	2	EKESRSVA\RLKSGAISA\HCNL\CLP GSSNSPPSASRVAGSSGA
2044	15945	A	2059	120	326	NSLVADME/KVLVWVIEDQTSNIPLSQ S/LIQSKALTLFNSIKAKRSEEAEEKIF EASRDWFMRFKIKQK
2045	15946	A	2060	102	413	ERTGFRHVKGSGLEFMTSGDPPTLASQS VGIT/VHEPRTRPG
2046	15947	A	2061	311	1	FEKKQRFCKSGCKTPGKPRGPKKLGANQ FSGPTPLKNGVGFSPGPKGGFFPPPPGG FPAGRPKWLTRILGKGSLLRG/RYPKK GFLKPILGDNSPQRAPKRG
2047	15948	A	2062	229	380	WYDLGSLQPMPLRFKQASRVNLPRSWDY RHPPLSRLN\IVFIVDTGILHVG
2048	15949	A	2063	142	383	PQSCFSTHWQLLQKQETAGAVSVCVCT S\VCVCVCVCVCAGAMCVCAGA/CFC VCVCAGA/CLCVCVGA/CLCVC
2049	15950	A	2064	408	200	NLIQIKALTHFSSIKAEGRGDKSTE/EKF EGSRGWFVRFKERGHLCNIKVKHEAANA YAEAACSLSRRSS
2050	15951	A	2065	348	3	WVSPYSPCVVCVCVCVCVCVCRCWVSP CCPGVCMVCVCVCRCW/CFTM/CAQVC VCVCRCWVSPCCPGVCCKDWVSPCCTS WSILKLLSSGNPPTTVSQSAWITGRSHS AWPARA
2051	15952	A	2066	73	286	NLIRGLLESHILISMRYGYCKSYTLMSR DIPEALNKWKS/IPMFCSWSRRLIVSMA

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						VLSKLINRFNAKDVOH
2052	15953	A	2067	329	0	PSSTFLLPFPRPPSPPPPPPPPPSPP /PSSSPAPSSPH
2053	15954	A	2068	221	3	ELKVILHLCLDRDFLQSSIMKVLILKILI LSVCCVC/VCVCVCAVCSCVC/VCSVC /VCSVC/LC/LCVCVC/LC
2054	15955	A	2069	1	167	GTRENPLNPGGGGCSEPR\SCHCTPAWA TKSETLSQKKKKKKKISNYKTPFKSYRI
2055	15956	A	2070	2	354	ARACGLPSSWDF/SVENRFRHRVGQAGL ELATSGDPPTSASPECWDCHR\DHHTWP LL
2056	15957	A	2071	20	341	CIVTVNTRGENINICWSPDQGTTAVGNK DDVTFFIDAKTHRF/LKQNSSSS/SEVN EISWNNDNNMLYPDTGNGCINILSYPT ESRAIYQRPIFHVVNQDLPHGDVLS
2057	15958	A	2072	353	58	LQLLTTS DPPASASRGAGIADGVWFTQ/ SLNGAQAGVQWRDLGSLQHPHSRL/LL ASQSAAIAASARPPRLGSEERLC LAAH RLGCEPLCLAQSGK
2058	15959	A	2073	1	338	GSRLQRVCINYLRSFFPFSLSQGWINF TWLFCLCVCFLRDVSLCCPGWPSTSGFKR SSCPSSLRWYDRHMPQH LASHTLFKKL /TILPR
2059	15960	A	2074	1	322	GGGREAGEARGGGEGGQSGRRRRGRGG PRTGAEGGGRGAGETPGGGARP PEREQGR GRHSERQGPT/RQTKRPKTKTKLSQNK NT
2060	15961	A	2075	450	225	TFVGRGCSELRSNCNTPAWVTD\ETLSQ KEKRGVKIGWKRRTRIISLHLP GSHE KFNNLETVKNCNVNHFCRLNT
2061	15962	A	2076	2	470	TPQNKPHPTTKNTQPQTQK/PTQTQP /TTPPKPTKKNTTPNPAPPNTQKNHTTK PTTONPHKTQKQKNTKPNTQQONKPTN QNPKTQTQKTTTQTKPKPKKKKKKTADT TSPNPISTKKIKLAEP
2062	15963	A	2077	304	1	NSATPPCSPTA/KPHPTPTPPPTSFP TCQHSPTKICPQARPRTPPYAHPPRCP RKII PKGRRHPLAPPQAARDLNYYHPI IWRGRVCVCVCVCVCARA
2063	15964	A	2078	167	1	TILTQNSTWSNVLLWQGAVAQAC\NSST LGQGGRITRSGDRDHFGQHGETLSRA
2064	15965	A	2079	3	364	HETRSRHSCAWCSAALWRAVASRC PSS /IPVTPPQCPLYW/WKVPLQCPPDL
2065	15966	A	2080	303	2	SKRGRPSGHECPFLTSSSCRHVASCTI RTPRRLCKSQLDRCSPLKERHKFGLSR VLSAMTQSGIY/WQPPPEFKRCFSCLN LLSSWDYRHAPPRARA
2066	15967	A	2081	4	326	AGITGMSHRAWLFLYFLNKFAPT\YGLV LNFLPHKIQEPSLG\SGSGP/LSCNS
2067	15968	A	2082	1	343	PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPSPPPPPPPPPPP/PP PSSPSSPPPPHTPHP
2068	15969	A	2083	330	88	ACDRSIISRIRHEL\EOLCKQK\SNNP IKKWPKDMIRYFSKQDVQTVKTMNKCST SLIIEMQIRSTMRYLLTTVRTPHPS
2069	15970	A	2084	1	340	RVRSHGTTHLAQLIFVLLVQTGFHHDGQ DGPDLL/NLVIRPPOPPKVL

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2070	15971	A	2085	2	348	ARALSLGANAAGNFKLRPLLRYSQNPR ALKNYAKYTLPLVLRHWSSESLETAFT FTEYFKPTVETCYSEK/I/SYKALLLI EKALGHPRALMEMYKDISIVFMPVNTTS LLQPM
2071	15972	A	2086	369	2	KGLPPSPANLFFLSVY/MGPFMFTRLL ISCPYPPSPASPSAGIKGLNPPGWPPF SFFYQKFVRFVLARNRTFGFVDYFSIL YLIYGCSNLYRFLLSALYFFVSFVFL TQGIAMVPRA
2072	15973	A	2087	314	3	LLESVGPTRNSRPFKGLIGRILLDEPHY PSLVSDDLPASASPNAGRILPFFFFETG SHS\TQAGVQWRHHSGLQ\LKRSSYLSL TSSWVYRHTPPHPANICIFRA
2073	15974	A	2088	330	16	CPCFFLSALSVLVGWCFAFVVCVGC/VW CVCFFVVFVVCVFLGCVVLCFCF/VCL VGVCVVFVGGGLCCVCC
2074	15975	A	2089	1	337	GTRTFLPPSYKDPCEY/IWAHPDNPSS SNCNMLNFTSD/PPVHSSGNWKLSSP NRPYYSYTATPHTDPTPLPSPNPSSP SPSYPLSDSTICQTTPITPITSSHTL LTS
2075	15976	A	2090	350	84	QRKENKTRKRATERRDESREEKAGRKE GENQEKRNKEQQGRQRRSRDRT/EEKE EAKRREHKNPKKKTKPPQKKKTEKK KTDNLSN
2076	15977	A	2091	1	355	SDPPTSASQSAGITYVSHRTWPLLEFSG TSIRLAGKPAGVLVEVTGK/SVCGGV KTHWNECHTGYPKCCWSSQAGESSLQPP PPGFKRFSCSLPSSWDYRLLP\QNFC IFSRDGL
2077	15978	A	2092	27	345	ASIPCLKKRKKKKKTGKPPF/GGPKP KRGGGGPPPTKRTLFPPQGNQTPGGV S/GPPKGDPPFSPIPPQORKSPFEKGG KKGPPWRGVKREKGFHFKNFQK
2078	15979	A	2093	3	301	HEHVAQAGLKLGLSSDPTLASPKWDC KR\DYCAWPHIFPISGLYVFFPLPRMS PHTHHKYTRTFHYAHKHCACLTNLLL RAQFQCHFGKGVVDP
2079	15980	A	2094	76	342	WFXFFFLFVFFVFWFVFCVFCGFFF FCFFCCVWFVFGCLFLCFLFWFCFFV FGFFGFVFFVFLVFLVFCVFCGFFF LFCFF
2080	15981	A	2095	115	325	MDERKKIRGGGRQGECKIHCKKLSFG IRSYPVEN/F/VDTMYDLQPAYKLN LTNADPCAVRYLLFDQN
2081	15982	A	2096	80	227	SCLGN/CIHLYSHSPTLSFTHTHTHHT HREREREREREICIMSVYA
2082	15983	A	2097	308	1	NSTVTMENSNIHYRTRVFTEAQFTIAK SWNQPKCPSILEWIKK\WIYIYCVYI CVCVCICVVCVVCVVCVCIYIMMEYY SAIKRNELAAFAVTWTRA
2083	15984	A	2098	2	361	ARACGLPSSWDF/SVETRFHVRGQAGL ELATSRDPPTSASPECRDCRH\DHHTW LL
2084	15985	A	2099	1	221	LLWRLRHENHNLGGRGCSEPRLHCTP SWMTR/GKTPSQKKTKQPMWQNLCLK KVFGNTGVREIFNGIKLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2085	15986	A	2100	186	2	ERVYVCVCVCVCVCVCYQCYLPQIRSL/V ASSLKANARVCVCVCVCVCVCVCVCV SLWHPLTA
2086	15987	A	2101	305	2	HNILLSQSLIQSKALTFNSMKA/E/RG EEAAEEKLEASRGWLMRFKE\RSHLCN\ TKVQGEVASADTEAAPSYTEDHSKITDE GGYTKQQIFNVDDKASYWNMS
2087	15988	A	2102	6	166	EQTALETILARAIROKETKGIQIRKEEV KLCFFVND\MVLYLENSKDFLKVDA
2088	15989	A	2103	53	176	EIKNNRPGMVAHAY/NPSTLGGRRQIS WGQEFETSLVNMVK
2089	15990	A	2104	3	267	FRHVGQGLKVLTSQDPPALVSQSAGIT GVSHCAQPIVGDFNTPLSIL/D/RSTRQ KINKDIQDLNSALDEADLLDIYRTLHPK /STEYTF
2090	15991	A	2105	268	3	PPKEHGSSPATEQSWMENDFDELREEGF RRSNYSE/LREDIQTGKEVENFEKNLE ECITRITNTEKCLKELMELKIKARELRP ECRSLR
2091	15992	A	2106	3	170	GFHHVDQAGLELLTPQVIHP\LGLPKCW DYRREPPCLASPHFHQIAISQKRHREAK
2092	15993	A	2107	1	398	SARGPDGFTAIFYQTKEELVQILLKQF QRIKGEILL/KNHYVKPSITLIPK\PG\ RDITKKLLTRSFVSLCPVLSPLQSLQS RPSSLSMISLHVSFVLSASAPHVHL CPTCPTLVLSGSHCCVSLFFF
2093	15994	A	2108	3	370	HENWNNGWGDSTIYSMKYLYFKPMLRP Y/C/SQKKIPFKILLFDNAPGHPRVLM EIMYKDEMF\MPVNTTF/ILQPMQORV ILTFKSYLRLNTFHKTIAAINSYSDGS GQSOLKTFWKGFIVL
2094	15995	A	2109	1	213	HFPVENESAPG/FKAAGDLITLLGGNA AGDFKLKALLVYPSENPCFLKGSFKPNL PLVWCCHKAWVQLG
2095	15996	A	2110	391	3	KKKKKNPHRKKIKRKKIFNAERNKKR AGVJIHILDRDLDFKQQTIRRDKR\GYT MINGTIQEVITILNIHAANTKAVRYIK QVLLKLTTELGPNTIITGDTNTLLSTL NRSSRQKNQQTLDLICI
2096	15997	A	2111	188	365	FQNTIHCVCVCVCVCVCVCL/CVCFCV FFFCLCGGFMCGCWCDFCILFCFYGVG FFFL
2097	15998	A	2112	3	340	RMESALDRKQFTTVVGDGDFHAVDEY KPHDATTNPSLILAVAQMPAYQELEEEA IAYGRKLGGSEDQIINAIDKLSVLLGA EILKMITGRVSTEVDARLSFD/SDAMVA TA
2098	15999	A	2113	11	305	FLFTDFCLFMTHILGHKINYITN/CKRN VIIT/SYFSPHNRKIKSIRKISRKSS NTWKLNNRLLHYPQIKDEVSRIRKYLE LNINENTNF/QNLWDIHK
2099	16000	A	2114	3	387	QTNH/NIPLSQNLIQSKAITA/NCMKAE RSEEAAGKFEASRGWFMRFKSSY\IKV QGEAASAGVEAVIYPDLAELIDE/GCY TT/QIFSVFQTAFWKKKPSRTFM/REE KLIPGLKASKDSSSLLRVHAAGD
2100	16001	A	2115	152	393	VYCPICWLVEFFFCFCSVLILFVMFV/CL CFSFFCFLGFVVVFSSFYLFICVFFFI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LGCLFLCVVFDLFLFVLVLCLEFFVS
2101	16002	A	2116	2	373	ARACLGLPSSWDF/SVENRFHRVQGAGG ELATSGDPPTSASPECWDCRH\DHHTWPLL
2102	16003	A	2117	3	449	HEFDHAMLQAHRAHHLAIDAYHEFEETY IPKDQKYSFLHDSQTSFCFSDSIPTFNN MEETQQKSNLELLRISLLIESWLEPVR VLRSMFANNLVYDTSDDYHFLKDLEE GIQTLMGRAEKRHCRVTQNLKQTYRR/F DTNS/HNHDALL
2103	16004	A	2118	146	15	FFFFYFFFLFFFFFIPFLFFFFFLFFFF FFYFIFILFIYSLLVF
2104	16005	A	2119	406	3	LFSVNETGFYSKMLSRFTTATEETSIPG FKVSKDKLTL\LGANAAGDFKLKPMLIY HS/ENPRALKNYAKFTPPVLYKWKNKAL MTTHLFTARYTEYFKPTVETIY/ILLID NAPTHQRALMEMYKENVFMPTNTSI
2105	16006	A	2120	109	396	YYFYFYLVLFYFFIFLFFYFFFFFILLL FYFFFSFIFFFFLFVYFIFLCYFFLFFF FFFFYLFYSFFFFFIFLFFFFFFFFFFFF SYYLIFFLSYII
2106	16007	A	2121	15	413	IVLARNTNFWLSFLFPVALGILIVLKGV KYIFWPLEYQCQLKMFVSYSFHY\FELG SLLFLKYGFHMYLILL/CIFIIIMCFF IKYSFFFCCLYHFFFSFYLFFLYFLIF\ CYLVILFFSFLFLFLSSYCFFF
2107	16008	A	2122	1306	429	SSSSSSSHVLRITIKDEDFKILEQRQVV LSEKEAQALCKEYENEDYFNKLIENMTS GPSLALVLLRDNGLQYWKQLLGPRTVEE AIEYFPESLCAQFAMDSLVPVNLVGS LETAEREIQHFFPLQSTLGLIKPHATSE /HKRGPSMMILTKWNAVAEWRLMGPT DPEEAKLLSPDSIRAQFGISKLNIVHG ASNAYEAEVVRNRLFEDPEEN
2108	16009	A	2123	3	206	LRRLRQENHLNWRGGGCSEPRSQHCAAA W/VSNSETPQKKKKKKKKKKKNLPS ALKKTYSQRGKLF
2109	16010	A	2124	23	401	IASGRPFFFFFFFFFWPPPPGGYPHFS FLKKKKKRGGGGKSLPPGKGNPPK\ WGFPLFPPLFPQKTPPPFFFYKTPPI PPQGRGGPLKFTPPGGGGGNPTILLD KKRGVLGPPFFFTN
2110	16011	A	2125	3	439	MFDVSLTLTFTHSLFHFSPQFHRKCELST LCDGGELRDHILLPTSICPITR/DKCS PGECC
2111	16012	A	2126	1	213	HFPVENESAPG/FKAAGDLLTLLLGNA AGDFKLKALLVYPSENPCFLKGSFKPNL PLVWCSSHKAWVQLG
2112	16013	A	2127	104	419	NSFFFEELYNPFGLGKKTFFGGGEEF GHTPPENEALGGKNKFFTGGGGQTFNN GEEKSVSFVISIEKILHRALL/AHALCK NCVVELNFGQKEEPFFPPPEEF
2113	16014	A	2128	399	140	PPPPKNFFPPKGFPG/RG/VGPKFPP PKKRVFSQKPPRGFFYPPLKKNNPFP PGNFGPPRGFFKRPPPPFFFFFFFFFFFF FFFFF
2114	16015	A	2129	10	457	KTSWTWCPVPVVPATQKAE/AGGSPEPG RSRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2115	16016	A	2130	409	0	PPPPSPSPPPPPSP/PSPPSPPPPPSP PSSPPSPPPPPSPPP/PPPPPPSPPPS PPPSPPPPPPSPPPSPPPSPPPSSSS SSPPPL
2116	16017	A	2131	317	177	FFFFFFFLLLLLLLLLLLLLRLQIFFF FLPLLFLFLFLFFFLFF
2117	16018	A	2132	3	542	EPWSVAQAGVQWRDLSPLQLPPRRFERF SRLSLPSSWDYRRLPAHPANF/QFLVET VFRHVGQAGLELLTSGHLPALTSQSAGI TGMSTRS\RPGFLEKV
2118	16019	A	2133	146	439	LKSVTSIAKTWIQPK/CPTNSEVDKCPS TVKWLKKMWYI/YFTMEYYAAIK
2119	16020	A	2134	95	1	GRVDAILAHCKLR/LPGFTLFSCLSLPS SWDC
2120	16021	A	2135	2	380	THTHHTH/THTHTHTHTHSLS
2121	16022	A	2136	4	337	KRNNKAWMTVHLFTAWFPPEYFRPTVETY CSEKKIPFKIL/LLVDNAPGQPRVLVEM HKEMNVVFRPANTASILQPMNQGGISTF NSYYLRNTFHKAIVAIDSNSSDGGFQNK
2122	16023	A	2137	2	356	PVSSSQVRASVYLKKKKKKGPPPEGITN TAGFKPPQSFRGKG\PPFPLISPKEPV I\SFLKNFGPCTIGKKKKPHPPAKNGGP LQ/RPPTQGGGRGKKKGKNNQRPLSLG GNRSPKPPF
2123	16024	A	2138	2	357	FLGSSDPPPSASPVGRATG/RVFFFFFL VEVVSHYVAQNGLELLDTSNPPAVASQS VRITCVSHRTWLLSPLYKIIQVCVSK/S PELEQSEDKSLKK
2124	16025	A	2139	379	16	LLQVRCFVSTVNRGSSCKTIQVYVQE AIPPSFLLSPFLM/PYTKINSRWIKDSN VKPKTIK\TLEENLGMPNIFFTYQLLW LYLHPESQLEICNSFRALQEGNLIIFI GRVGRPGTTGL
2125	16026	A	2140	73	411	NYLLNNLFFFFFFLERGLTFAPRAGGWGG NLTSWNLGGPPGNKPPPPPPKRP\GTPK PTLKEGLFGFFKTTFGPPGAQKGPELPG LRGPPGLAPPRGNGKGNPPPGPLKTFN G
2126	16027	A	2141	46	421	AGVSWRDHSSLQPCLTSRARAV\SHLSF LSSRDYGMPPPPPKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKQ
2127	16028	A	2142	26	479	LAYLLSPVMYKPNWRTILQSTISNKG LCRIYKETLQLNHKKTNPIFFKWVKS KHFRGAIQVANK\HIKMKLNIISVYGN AQKNTMRYHHTPIKMKKMGCALWLPVM CQEAGYILKMPGWTPYPGRVVGRTAP ALPPRGTFPRD
2128	16029	A	2143	9	166	QNRLLARLTKKKRGKNQAH/IKNDKGD ITADPTEIQASIREYHKH
2129	16030	A	2144	1	328	LEKESRPPPPPPPPPPPPSP/PHPGS LPKPLGLQPLPRPEVSFLTEYLPKLKAC EGGGVEIAAASFPRYILMGMCQRDRIQ KDIDVVIQKSRAEDCLFAGVKAILKA
2130	16031	A	2145	1	440	KTFLRLSLWQLVE/CYISSGLIDHRRPM ALTPRHPRSGITAPRPRPQPPGRVGPIE PTALSPSPGPPPPCSTPGRCQVPSLER RRKEGREPPSVGRGCGGHGISPSSDIFF HLNFCLAHPPDLFVFCVSIQNQLYIFHE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKGR
2131	16032	A	2146	23	422	IASGRPFFFFWGAPGGEGKKNNFFWGPR GGKKKIRGAPTTPRGKGNPPPKPWGKKGG APPKNLGLFGKKGAQRGPPGWFKTPGKK KSPPPGPKKGGKKNRGRP\GPPPIFFKP FFSTGEKNPLGKKTNNRLLPW
2132	16033	A	2147	3	372	KKNTFFFLTPRGPPPPPRGPLSPPPKRA TPPPPPFKKKKPGFPKKKNFFPPPGGG PEPP/LPGEKKGGYF/WW
2133	16034	A	2148	363	1	FNCRWFEKSHSVPOAGEQWHSFGPLQP LPPGFK\EFSCLSL
2134	16035	A	2149	2	361	FFFLVETGFHQVGGGLEHLTSDDPPTF GLP\GGWDYR
2135	16036	A	2150	387	2	KKSFFLVSPARVQWGDPPNPPIPGSNMF PFSTPPKTVIRGPPPPARKIFVFFIKTG \FPQLGRGVLSLPQ/CDSPPPAAPPKGG VSGGNPPAPPPFFFFFEMBSHVSQVGV QWRNLGSLQPPSPGFKQF
2136	16037	A	2151	23	421	IASGRPFFFFFFFFFFFFFLGGRGVFFYP PGGGGGPNFFKKTFFPGKKKFFPPSP KGGFLTPPPPPFFFFFLKKKGVINGGG GGVKISPPGGTTPFLPQKGG/NKKGGPP PPRKKKIFLFFPGAIRKQPP
2137	16038	A	2152	3	366	VIWAHCIFHLGYTDRCLKKKKKGFPG GEKMGKLNFFPPLGKKPPPPQIPNFWSV IEKPPRGFYLGAAPPKKFFLLKP\GPP FFKEPPPPKKKGGASPLKKKFFKGKKS PPFFFSDDPTS
2138	16039	A	2153	423	253	FFWGGGAPIFPPPKKGFPPKNPPGVFFS PKKKKKIFFFP/HPVNFPGPKDFKRRP P
2139	16040	A	2154	287	1	KEMNKKKNPKKKKVKKISTAFYNKTLN NINFF\FAFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFRFLFNKQTA QLMQHSAPTRP
2140	16041	A	2155	433	2	RRVLFIFPPL/HFFSPPLPFSPPPPPP PMKFFSPPTFFFYFKSPHPP/HPPQV VFSPTTPMPFITPPPPHTSPSPSFF FFFFFFFFFFFFSFFFFFFFFFFFFFFF FFFFFFFFFFFFFHIIISIKGEIGRSSVVR VMSRTRG
2141	16042	A	2156	69	606	LWWPPLSRHAAYRQWPGTAPRGLGHKV KGPGASPA\PCGAAAGSTAQG\GGGAAC LPGPAAGAVTVVPAGPGGGRATGPVLQR PAGAGOPTQQGQHDHAGRVLWQHIGIRP GAHRPGPCAP/DSAPRAPGGRCG
2142	16043	A	2157	449	0	SSPGSSSSCSPPPPGGGVGFFL/YKPPQ KKPPPPVGGPGFFPQKLLKSFPLPPP FPLGGGGPPPPPPKISFYPPPKVVF PPPPKAFLLPPPPPLPPPPSPQPPP LF
2143	16044	A	2158	241	5	KKFSFFPPGGSQGGFFGSLQNPFGFTF FFCLNLGKKWQGRGPPPRPNF/SFFFF FFFFLVETGFHHISQDGLDLLTS
2144	16045	A	2159	434	2	LGSASQLGCSGVRDPLEEAVCFPSDLQL CARRTTALFKAVRQGHLSLQRLLSF\V CLCPVPRSGAYRQASLSCGGLHPVQA SRLCLPKQAWAMAGAP/PPASLQPCSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ISDCCASNQRDSVGVGPSEPRAGYNLLVRCFLSP
2145	16046	A	2160	448	84	FLGGFFFFFWFPPSPPPQKEAL\QKKIFFVFFSPESNQKNFFFSFSERGGPPNPLFKGGGR\FSPWFLFFFFFFFWFFLVVFFFFFFFFF\FFFFFFFF\FFLLGKCLPKYT
2146	16047	A	2161	3	156	RGCSEPLRHCTPAWVT\KETVSQKKKKKFLTLGGKTFKNFFFNAPGTFP
2147	16048	A	2162	412	37	FFHSPPPPPPAGGAVFPKPKKKKSPPPPTPLLL/RGGGGPPPPPKRGPPQKP KRGFFSPKPKKKKFFPGPGPPPPQKT PPPPPPPFFFFFFF\FFFFFFFSLFFF FLRTLWRKGRGRI
2148	16049	A	2163	5	370	QSSCVQLVPVPTIQEAEAGGFLEPRS ERLQ/CSHCTPAWA
2149	16050	A	2164	437	36	FFFFFFSEAESCSVAQAGVQWHARSLPQLPPG/SSDSCLSLSSYMCLSPRTRGS
2150	16051	A	2165	3	623	RQGFTLVAVAGVQWYDLGSLQPPPTGFK RFSCLSLPSSWNYRHAPPCPANFVFLEE TGFLHVGQAGLELPTSGDLPASASQSAG ITGMSHCA/RPKVCSYHLFF
2151	16052	A	2166	337	0	PPPPPPSPPPPS/PSPPPPSPPPS\PS PPP
2152	16053	A	2167	350	156	AEATSKIRCQKCYIMIAGHSGTRLQFQL LQRLRQENHLNPPRA/RGCNEPRSHRTW PTWYISKSFLA
2153	16054	A	2168	1	337	DERLSQRSRSWSYNGYSDLSTARHSG HHKKRTKKKK/IKKKKKKKRGPFKKKG PLKTRKKPRGGLLKAHPFWGGPPPGFFL TGEGAPPPVFFKKKKKPPGLGKGGFLW G
2154	16055	A	2169	2	606	RVLRAVAHEEPDKEGKEKPHAGVSPRG VKRQRRSSSGGSQEKGRPSQEPPLAPP HRRRSQPP\HPGPLPTNAAPTVPGPVE PLLLP PPPPSLAPAGPAVAAPLPAPST SALFTFSPLTVSAAGPKKHGKHKRHH HH\PAPMVIPAPAEPI
2155	16056	A	2170	311	2	GLQPLGLGSVKQCMDLACVPETVCVCVC VCVCARAHTPVCTQGCVPPESTQCVCMHV C/VCVWACTCVPCMHTCVGVGASVCMQ RNELGRWAWENDAIRQRC
2156	16057	A	2171	78	337	NTPNSTYKAMSLKGPITGTFLPNYPGHK VCVCDTYLCVYQHTHTHTHTHTQAFP HI/HIYHT
2157	16058	A	2172	2	278	KNRLNPGGGGCSKLSCHCTLAWAT\SE TPSQKKKEKRRKGRKRKKKIVYTKI EKGNAKMTGESFIHFCKSSSVQVALS AEYRCSST
2158	16059	A	2173	2	365	FYHVGQAGLKLTTSSDEPALGLPKWDY RRE\DCAQPNVKS
2159	16060	A	2174	195	389	FRVFSKLKYYYDFFRGRISLSCPGWSTT PGFKRLSCLSLPSSWDYRRPPPCPAN\F CIFSRDGVSP
2160	16061	A	2175	23	374	IASGRPLIFFFFFFFFLLFCRGGGPPF NPRGKERGGFLIKGPPPGGKKNFWAPP PGGGEIKRTPPPGVFFFLKKKGFSFG GGGGKK/PPPPGEPPPPPPQGGKKKKK



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TRGPLF
2161	16062	A	2176	2	158	FFFLKQSLSVTQAGVQW/PVDSLQPLPP RFKRFSCSLSPSSWDYRCVPQCPAN
2162	16063	A	2177	340	120	PRFHFLASPSEMSQMTVKAKTTVPASEC AYPKIEPFFPF\DPGRSES\FDKLGVHH HPLFPLSGEPLMILHKNTH
2163	16064	A	2178	3	256	YLKKDLNVNQKTLTLE/EKQKG/HLHD MRLCKEFLNKTSKAQYILKKISQY/LIK VQNFNAVKDPVKRMKROASD/WENIFT
2164	16065	A	2179	95	1	GRVDAILAHCKLR/LPGFTLFSCLSLPS SWDC
2165	16066	A	2180	1	143	ARGERERERERERERERERERERERE RERVFV/RERAALSREGRDKCERSGLF
2166	16067	A	2181	1	304	ARGQGHLSLQRLLSF/VCLCPGPTGGA YRGRQASLSCGGLHPVRASWLLCLPNQA WAIAGAPPAALLPPCSLISDCCASNQRD SVGVGPSKPCVGYNLLVW
2167	16068	A	2182	3	163	FQRRSTESCGWDKARSQSRSPPRQQA GHHS/HTHTHTHAHTHTHAHTHAWTRP
2168	16069	A	2183	3	205	NFKLFCKGFFFLRQSL/DSVSQAGVQRH NLGSLQPLPAGFQLFLQPPPPGSKDTHP GVQRHDHNSLQP
2169	16070	A	2184	228	88	WFFRIYDSFPLVFLVFVFFFFFFFFFFFF FFCVFTFPFVYFIQYVVYI
2170	16071	A	2185	287	3	SLFLAIPQWEFQKRIYLRKQKIVLLACQ PSKGLSIVQVVRGQLNSPVLKSQDPTP\ PRFKRFLCINFLSRWSYRHVPPRPDSFV FLVETGFLHLV
2171	16072	A	2186	252	105	VSISCHPQ\PCLITYTCY/HIDGYSNIHL CTHTHTHTHTHTHTRVELQGPA
2172	16073	A	2187	267	459	KHVPGSSYTWL/IFFFRGNFLKKGANFV PQGVLLKGGNLSLYPPPPRLKQYSCITL LRIGNYRHA
2173	16074	A	2188	170	15	RSVMKDLNSHFSKENIQMANKRTKECSA LVVFREIK/TMRCHLTPIRMATIKK
2174	16075	A	2189	2	504	DVTISTCHASAKVGTRLVFDHYGKI IQK TPYPHPRGMTVSVKQLFSTLPVRHKEFQ RNIKKGLG\RRSCFCFDF
2175	16076	A	2190	1	565	FFETESLSRLECSGATSAHCNHLHFGS SDSPASASRVAGTTGACHHTWV/IFFVF PVETRHHVSQDGLDFL/NLVIRPPRPP KVLG
2176	16077	A	2191	142	382	NTPPLLFFFVIRDRVSLCCPRWSGVAQF WLSATYASRV\KRFSCSLSP/SNWDYRC VP
2177	16078	A	2192	138	365	KHQYHHCC/LLKKKKKKKKKKKKKKKK KKKKIKKKKHGGPFKKNFV/EGQPRNWA GGV
2178	16079	A	2193	385	21	RGEIFFFKTRKKFSPQGGRGVFPFSP PKNFFFPQGGKFFGG/EGGPKVPPPKKG GFPKKPQGGFKVPPKKKKKIISPVGIG GPPCNFLKCAPPPPPPPPPPPPPPPPP FFFLVRAVKLS
2179	16080	A	2194	415	56	PPPTTAPVFSPPPPPPRFFFSPPPPVFF FRSFPPAPPPPLFFFPSP\PSFPP PPPTRPCPPPPPTIPPPPPFSPPPPPF FFFFFFFFFSLLPFFFFFFFFFFFFSFL FLFFPSRLW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2180	16081	A	2195	35	369	MKRPSPPPPTPPPPPPHLLPPFPPEK KTGPP/RGFFKGGGERGPPPKKKDPPP QKQKKKKKWGGGGGGGQKKKHPPQKNP PPPPGRGGGKNFLWGRPRGPPPPQGGGK K
2181	16082	A	2196	2	266	SKPRSCHCTPAWATQ\ETPSYKKKKKKK KGLPLGGPGEKTIFFSLKPGQKAQPKNK IFPKKKIPFFSTPKGKKKKNFQGGGKKK KKEI
2182	16083	A	2197	1	277	ARGERERERERERERERERERERERE RERERRHP/RPRERE
2183	16084	A	2198	1	285	ARGERERERERERERERERERERERE REREREREREREREREREREREGGAPP PRLYRERVLKKQGRFLPPVRERKK/RS PVQTLPGY
2184	16085	A	2199	346	1	VPRHGLPCFCFPHQLQPPKRKKFNNRKR ALTSTHTQFFVFETESCSVA/RECSGATS AHCHL\CIMRSSNSPASGGAGSSELRFR HCTPVGQQTEIWSPKNKPIKKEEGCPYC QFLSC
2185	16086	A	2200	3	389	HEGMILAHCSLNLPGSGD/ASHVARTTC VHHVQLILFIFVETK/FSHYAVQAG/L ELLSSSDP/PTSQSSRTGMSSH
2186	16087	A	2201	3	204	HECHCTPAWAT\SETLSQKKKKKKKKK IFPGEKTWGGWNKKKFLNKRKFFLGKG LFHLKRGPLKLF
2187	16088	A	2202	69	379	KKKRVPFFWPGGSKPPT/SGNPPWPFPK GGGLRGLPPPPGPRGVIFKNFGKRGPFP PPGLKSWGPRDFFGLALQRGGISGLNNG APFFFFGVLLKLPPLFFVSKG
2188	16089	A	2203	81	379	KKKKKPPPPKKKNPGPKQEGGPLRGPP TFSGGGGKKTCPPQKKAAGG/SKKAPG PPPGAEEKNPALGGEKKTLPNGRGPKR LRGLAKKGNPSSFFGGK
2189	16090	A	2204	1	341	GQSLPVSRLQLSNGNRTLTLSSVTRND VGPECEIQNPASANFSDPVTINVLCEY LLF\PVAQATSPNPRSQRPGLSVPLSSK NADSPPTPRNPARHDFLQANMGRPSLD QE
2190	16091	A	2205	2	370	DAPPRPANFVFLVKTGFPPVQAGFKLP PGDPPPLASQITGKG/HCAQPPF
2191	16092	A	2206	362	24	PRGSSSSASSSSSSSSPPSSSSSSSSSS SSSPF\PPPPVLKPPPPPKKSPPPKKK NPPPPKKKTFFFFFFFLLRRGLCPFR GKRAKPPFQKKKKKKRESSFYQQVIH M
2192	16093	A	2207	357	3	AGQALWLARVIPVLWEARSYYVRISWYR NIVAMDSDSLDSGSHSKLSFRKGFPVL YAIKKTTHDSWEGVS\MSALIVWKS LIPS CVDAFEELTSSAEVAQVVG IATDLEL LVGCARA
2193	16094	A	2208	280	411	GNDVYFLVFLF/CLFEKESCSVAQAGVQ WHDLSLQALPPRMA
2194	16095	A	2209	3	392	PIIYEKYTQQINEMPRKLQHQLALVSR NGPILLHDNAQLHITQC/LQKLNELGYR VLPPLPYSLDLSPTDYFFKHLDNF/LQ GKHFNQEDAENVSQKFVKSQSMDFYAT /GNKLISHWPNCVDCN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2195	16096	A	2210	248	417	GILANCASTKDLISRIYKKLKQIN/KQK TNDPLKKWAKDMNRYFSQEETIQGVNKH KK
2196	16097	A	2211	213	493	GKRFYFACPGKIGALQGFPGGGPFFFF FFFLTTPPNTNYLTNKLKISPLCTFYF SNILGFYPSITHRTIPDAWVTA/SQSGP VLMRSIS
2197	16098	A	2212	159	413	LAPRVIFGPPKKPPERPPLFFFFFETES SSVTQAGVQWHLSS\PPRFKRFY/CLS LPSNRDYKRP\PHPANFCTFSRDGVS
2198	16099	A	2213	455	60	NPRREVGPICPPPKIRVPPQNPQVGFYS PPLKEKTFTSPAPVNLGPPRDPFKRPPP FFFFFFFLDFFFYFTIYKTSAAACPRSP AQPRVARPLVPSS\PLPSLCLAPAPR GPGSLCPRGSLEGDNSSPG
2199	16100	A	2214	2	243	LTLSPRLKCNMVSACNFCLLSSSDS/ RLR/QENCLNLGGGGCSELRLRHCTPAW TTERDSVSKTNKNSLKIFTCTFFVDA
2200	16101	A	2215	1	286	FSQLRLRLFC/SQGGRLCCESCPSFH PECLSIEMPEGCWNCDCKAGKKLHYKQ IVVWKLGNVROVFPRTKRKYSIIIVQTSF ILWIQSDLEIDR
2201	16102	A	2216	173	2	ITIFFFVRQGLTQAGVQR\DLSETLV ILPPEAPCSLQSSWDYRRVLPPLNFC IV
2202	16103	A	2217	216	4	VYPPSFMVFSQVFLSSSTHISLSFSFFWN YLFYLYFIYLYLRWSL/DSVTQAGVK WHNLGSLQPLLPFGK
2203	16104	A	2218	14	228	KRSSHLFTDDIILYMENTKHSTK/NLLE LIKEISKVTG/YQKSVAFLYVNNKQAIK KTIPLTIASKRIKNSGQA
2204	16105	A	2219	244	3	EVLNQNGLPRWPNIIRAKASLRVPROC SRGVVFSANGAGTTRYLYAKEWGLGGG GCSKLRSCHCTPVWAT\SETLSQKK
2205	16106	A	2220	162	2	INMVGNLFFFGDRVSLCHAGWSAVAPSW PTVASTSL/VKQSSFLSLPSSWNHRH
2206	16107	A	2221	146	3	GRVDGVPWRNPGSLQPPSP\GSSDEPTS ASQESGTTGAHHHTRLIFVF
2207	16108	A	2222	239	2	SYISKPKDFPHDSSPEIKPVTNWRNSF SFIFPFFFLFPEKESHVSVTQAGVQRNL GVSSYWP\AGLKLTSGDPPALAS
2208	16109	A	2223	2	159	LNRDLGGGGCSELRSCHCTPAWAT\SES PSQKKKKKKKKKKKKGGGRNSKI
2209	16110	A	2224	3	345	RFKLFSCSLSPSSWDYRRVPPRPA/NFF VFLIET\GFAILTSSKTERQSRLECIFG FYGLPCREKRASERRSVGE/HERKILFS FDDFFLGGTESCFVTQAGVQGCYLGSFP PPPPG
2210	16111	A	2225	103	319	FSEERYNVTNFMMLTMSCLTLVE/C/ WSEGYMATPCTILLLLFFORHCLTSPG GVQWCSSSLQPTPGIK
2211	16112	A	2226	2	110	FHHVGQAGLELLTQWSTHLSLPKCWDF\ RHEPPHPA
2212	16113	A	2227	2	178	IFLIFTFLEMSSSHYVAQAGLEFPG/FKL TSRLSLLSSWDYRRPPRLANFFAFLAK GDAA
2213	16114	A	2228	173	3	FIFIFISLFFIFFLRQSVLSPSAVQSR LQPPPPRFKQFS\CLSLLSSWDYKRVPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2214	16115	A	2229	333	1	HTPPPPPTFHSCLCTEGAPPPQNT/PNP PRNPFIIPLSRSHTRANEPSSLSTPRTHP HSPRPPLLTHPHNPTRASAPPGSRYP ARHRERPRERPTQRRERERERESVCCV
2215	16116	A	2230	350	3	KKKDIPPVNIYAPNTGAHKYIKQILDL NRDGP\HTITAGDFTTPLSVLNSSAESR CSRPFIIISPSLVVGLRE
2216	16117	A	2231	277	1	QMHPARGHLPQALIPVQKPAISQGMSA SGSTQVSPFLSPCFWVEVNCNKTVLT\ PFCGAGTGSHSFAQAGAHWCNRGSLQPH PPGFKRL
2217	16118	A	2232	3	335	ETRFHHVGOAGLEPLTSDPPASASQSV /GITGVSLRARPGE/GSWKTVCCNNMS EPT
2218	16119	A	2233	29	448	CPSLRQAWHEAAIDEVTRGTYRQLFHPE QLITGKEDAANNYARGHYTIGKEIIDLV LDRIRKLADQCTGLQ\GFLVFHSGGGT GSGFTSLMERLSVDYGKSKLEFSIYP APQVFTAVVEPYNFILTHTTTLEHSDCA
2219	16120	A	2234	1	365	GARLILVFLEETGFHYVGOAGLELLTSS DPPASA/FPKCW
2220	16121	A	2235	28	460	DRILIDHISKLGTRGLQGLVFHSCGNLG \TGFGFTSLMERLSLDYGGKAKLEFSI YPAPQVSTAGVEPYNSILTHTTTLEHSD CAFMDVNEAIYDICKNLDIERPTYTNL NRVISQIVSSITASLRFDGALNVDLTFE QTNLV
2221	16122	A	2236	614	84	LAASLAACAQLSALAASHRMWALQRLRK LLTTEFGQSININRLLGENDGETRALS TGSALAALVKGLPEALQRQFEYEDP\IV RGGKQLLH/SPHFFKVLVASRLVTLEAG HFCPCCAETHKW\AWFRRYCMASRVAVA LDKRTPLPRVFLDEVAARVCGHILQLG DTELQQHICHL
2222	16123	A	2237	1	393	GPMLAQLSVFRCGSTSAPNDLWYHFIEL PYHGESTMLIALPTESSTPLSAIIPHM STKTIDRWMSIMVPKKVQVILPKFTAVA QTDLKEPLKDLGITDIDVSSQGHFCQIT KAENLLV/SHILQKQK
2223	16124	A	2238	3	402	HVGOAGVQIGKACWELWLEHGIQPEGQ MPSDKTIGGGNDSFNTPFSETGAGKHVP RAVFVDLEPTVIDEGRTGTYRQLFHPEQ LITGKEDAANNYARGHYTIGKEIIDLV \DRIRKLA\DQCTGSQGLGFP
2224	16125	A	2239	2	478	GRGGLHRIPVVTPLTPSFARGLVPSLAR GVEARNAGAPIKSYPRPGSRLKMONGSK GSGLQNKTFHWEICDAHVNSKIQLKQ\H ISSRRHKDRVAGKPLPKYRPYNKLQRS PSILAAKLAFOKDMNPLAPFLSSPLA AAEAVSSALTLPFRPFV
2225	16126	A	2240	255	2	FLFVKPHQISCPTKKGKISFLVLCPINF FLFWRQDLAHPGWSAVTQSWLTAASN\Y GLKQSSYFSLSSWDYRCIPPHLGKRP L
2226	16127	A	2241	365	11	EPFPPGGEKKRGKPPPKKTPKKDGPQK KSAAFFGG\GKIKKKKGAFRKKKKGGG PPKKKPPRKKKKKKNFSPLPKHTP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLFQKPPTKIFLFSPPLFLNLFFFPLSPFFIF
2227	16128	A	2242	3	143	PNFLSPRLDCRGITIRGHCGLYLPGSCDPS/CLSPSSWNRYRSTPP
2228	16129	A	2243	132	2	MSAHCNLHLPSSSDSPASVSQVAGIMGACHIF\VFVQTKPHHI
2229	16130	A	2244	334	43	TSKHKMRCSTISLATREMQNKTITIGGHFVPTRLANIKPENAKYRQGLMC/WCWCNLASPLWKTIVHYLVKCLPYSSAIFTLG\ITYPEEVCLASSVPGT
2230	16131	A	2245	312	2	PESKLPEKNFFFFFLRQSL/SSVAHSVVQWRDLGPLKPPPPESKQFSCPTLLSIWETQTALSQDCATALHPGGQRETLSHKICVCVCVCVCVCVCAVCIYIN
2231	16132	A	2246	3	230	RAQAMVETSRERCLLRPPQIETR\HVAQAGLKLASSDPPTSASQSAGITGVSHHTWPQPLTFPCPHAKSLPFTNQI
2232	16133	A	2247	2	214	GRVDLVIQAGVQWHDLSLHPPLP\GSSDLP/ASDSQVAGTAGRFHYAWLIFF\VFVETGS/HTQVSN SYDVL
2233	16134	A	2248	3	139	EGVQGCCHHNSLQPPTPG\SSDPPTSASIEAGTAGSHYHVWLIIFLLF
2234	16135	A	2249	3	160	EGVQGCCHHNSLQPPTPG\SSDPPTSASIVAGTAGSHYHVWLIIFLLFCFEGDAA
2235	16136	A	2250	319	3	GQKRYKIFLCFFFLGWLFLRWSLTLSPRLERESVSKPKSKPKPIKPKFTPREFKEVLAKYGTKFFFVFFGLFVWFFLRWSL/NSVAQAGVQWRDPGSLQASPRP
2236	16137	A	2251	15	394	FVSFSFFPSFPHLFFSSSSFPFLPSFHFSFLPSDRPSVVP/FLPSFLP
2237	16138	A	2252	60	306	GRERILEETMAEDFLNLMKDLNISIQVAQQIPSKMNSKRPHRYQHFRSQSRILKATREKQLATYKSSVT/VSPSPGPQTVNS
2238	16139	A	2253	3	351	GFHHVDQANLKLTLSSDLPASTSQSTGTGTGI\DHCTQPNFPI
2239	16140	A	2254	150	2	RPRRPDHSRLGAGDQPGQHSKTPS\HQKTKTTSQAWRHAPAIAGTRQAEA
2240	16141	A	2255	357	1	LNLNLSLTLYAKINLKWITGTNVKHKTTFKFLGGKNGANLMDTRLDNAFLDLTSKAQLTKEKIDKLNFIKIQT/CSIKDLGNLKRQAPEEKILRNHISNKLVSRIHKEVPKLNNKK
2241	16142	A	2256	397	1	FSLFPPVGGQGGFFSSCKSPPPRFRAFFCPNPFRKGNRGPPPHPGKGTGLGFFFFFRQSFALSPRVEYNLCPLGSSDPPASASQVGCAPGLPPPAWVNFGIFFF/CFFLRQSRVAQARMQWRHLGSLQAMP
2242	16143	A	2257	2	132	TLTLTPRLECSGTIS/AHCKLHLPSSRHSPASAPRVAGCGGGHL
2243	16144	A	2258	214	347	KISLILGVHKICCEF/CFFEMKSRSVTQAGVQGHDLSSLQPPPPGL
2244	16145	A	2259	347	2	FFSFFFFFSEAESRVA\RLCSDTVSAHCTLHLPSS
2245	16146	A	2260	333	1	SDQRWTENAFVELRDEGFACPSFSEL/RSTPSTSGEEVENFEKKLDECITRITNTEKCLKELMELKAKAREPREECRLRSRHNQLEERVSVMEDQMNEKREGKFKREKRT
2246	16147	A	2261	2	357	SPRSCSVYGIALLFLYFLYKLAPALLY

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2247	16148	A	2262	355	0	GLALNSFLHEIQEP/SLASGSGPLSRNS PELPSPSPPLSLSFSLPPPPPPPPPP PLF/CPSFSFFFPSPFPF
2248	16149	A	2263	348	35	YFLKKGFSFFPRGEGRGKDSRSLKQLTF GPKKP/SCPSFLRKW\ETRLCPPAQKIF FFFFFLLEMGFCYIAQGLDKGSSQSSGI TGVSYHIWPTFIGHLTMCLAKC
2249	16150	A	2264	270	92	DRPARRKMFFTYSSRLFFFFFFFFFFFF FFFFR\FFFFFFFFFKFFFLFSRWSLM IFIS
2250	16151	A	2265	1	417	FRPPAGVQWRNLISLQSLPPGFKRFLYL SLPSS/WDYRCMPPLA/NFFVVFVVDV VVVVVVVLVEMRLRHVLARLDIVVLICI SLMANGMEYLFCLCSFAIHLPSLLKCRFT YFAHCLFLYFLETGSHSVTETGWQWCI I
2251	16152	A	2266	344	427	LIGLCEDTNLGAIAHAKRVTLIAQDLQLA
2252	16153	A	2267	310	417	RVPYGTLGSGPLATMAGFDDKLKPHMEG AAPILVR
2253	16154	A	2268	186	464	NSCLSHNQRLFRLEKMGPISAQEKL VLHTLSGFSGLV\VGWLVFEMESCSVVQ AGVQWRVHPPPRFKQFSWLSFPSSWDYG HVPPCPANF
2254	16155	A	2269	1	427	PEPPSLPPDGAKKQKTQSKKWRICFLR KKKKKKKKKKQKKKKKKRGGSQKKSR GPKLTETNIILIKGGLKKNYREIEK KLLFGGGVIGPTPTQDIKREEINYLE AVGREKQRFISLVK/TNVA/HEATRDTI FRGYL
2255	16156	A	2270	399	44	ISFQLLLPITVLPGHVRVLMEMYKEVHV VFVP\STTFMQLSMGQGVTLTFKSY\Y LRTNFNKAVAALTSDESSESGSQLKPV WAAFSSLNASKNI/RDSWEAVKIPALKG VWKKWSLKM
2256	16157	A	2271	19	420	AAGIRHEERERERERE/QRERERERE RERERERARNIYHYRPPRVFFFFF FFFFKKRRGFLVPTPPGGGAQKKTS LEGGKGVFFKGGGKKTPLKNPGGWGEPP QKKNGGGPPPRDPPPPRPLF
2257	16158	A	2272	463	20	SYNIPLSQSLIQ/SRALTFDSTKAERN RRGK\RSGLQWEGSRGWLMRFKERSHL HNIKVD EAVSYPEDLDKMDALNTKQQI FSVHKIALYSKMPSRIFIAVERESMPG FQASKDRL/LLG/ATAAGDLKLKPMIL YNSKNPRVPRAEF
2258	16159	A	2273	474	82	VGWADFLKNTSQAQATKAKMDKWDPIK LKSFCTAKETISKAKRQPTGEKEIFANY TSDKGLI/SRIDKELKQPYRKNPNPVL KWAKGWAQWLTPVILALWEAKAGRTQGO EIEATLALFSGLFCQVFLC
2259	16160	A	2274	152	3	AEGRNGDGIQKSSI\RTLLSNDKNPON IHRPTRLTMLYQQNLCHLGL
2260	16161	A	2275	32	361	LGASARYEKPTVNLIINGERLNIFFPIR/ SKTRLGYLLSLLFNIGLAILASAINQK KEIQIIQIVKKKIQTQRKKKKNKTKKKK ALFKFKGGPEKEKGPKNPFKTPPVVF
2261	16162	A	2276	329	487	EFVNITIKIATSLHYKAIVIK/AMVIW YWHKNRHIDQWNRIESLEINPHICNK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2262	16163	A	2277	2	466	AHHSCHLLTTAAHSCSPQLLTTAAH TYSPPQLLTPAHHHSCSHLLTTTAAHHS CSPPQVLTAAHH\GAHTCSPQLLTPAHH SSPQLLTPAHHSCPHLLTTTAAHHS CSP PQLANSYRG\SPYCSSWSQTPGFRKSSH VGLPEPWIFHGLQVV
2263	16164	A	2278	4	467	KNVTQQGKIHIRDKLDEMWNSTSVFCTN HMKHQTNFNKCKNVFKBCGK\TACNFFQ LTQYQISHANQKPYECQICGKPRKRAH LTQHNRIHTGGKPYECKECGKVFICCS T LIQHKRTHTEKPYECLECRKTFRRSAH LIRHQRHTGEEKPYK
2264	16165	A	2279	383	3	FLCVCACVCVYVCMCMCACAC\CMCMCG CVCVCVCVGLRGLGWAVVCRSWGPP LCFLLGILPLKSRLLWLPRTTISICTL PSAQGPLPAPGFGKYASNTTGVKSSSV FSLLSRITALSHLHW
2265	16166	A	2280	47	219	VCSSELKSCHTPAWAT\SVTLSSQKQNT KQRRTLGSIFFQHTFMHLKKEKSLILQK W
2266	16167	A	2281	294	160	NKTFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFLFLF
2267	16168	A	2282	68	490	RTFAYPKPPVFGSHSGKTTIPKNARGSF PS/PPLPFPSPSPSPGSPVSCLPRLP SPSPSPSLSPISRLPSP/SRSPSPSL
2268	16169	A	2283	3	454	CQSAPLGGASQLGYSVGRDTEEA VCPF SDIWLCAGRTTTTLFAVRQGHLSLQFR LPFVWLCAPRGGVYRGRQASLSCGGLH QVRASRPLCLPTQASAMAGAPPASLPP CSLISDCCASNERGSTGMGP/SEPGTG
2269	16170	A	2285	1	452	LKDSGRDYSQFEGCALGKQLNLKLLDN WDETSSTFSKLREQLPVTQEFWDNLEK DTEGLRQEMSKDLEEEKAKVQPYLDDFQ KKWQEEMLYRQKEEPLRAELQEGARQK LHEL/QEELSP/LGQEMLDRAHVDAL RTHMAPYSDELRO
2270	16171	A	2286	3	266	NSSPPSSGHSTPRLAPPSPAREGTDKAV SALKSPQPNRGMGRGQR/PGLPS/DTAT ITPHTSGFPKQPQLSLKVQTPQRAKGRLS HWDLEP
2271	16172	A	2287	274	453	IYTFVKSSSKTLRPRHIDQWNRIENPEI KP/EYSQLIFDKANKNIKWEKDTLLNKW CWDN
2272	16173	A	2288	81	487	TVYFKPTVETY\CWDKKKIPFKGLLRD NTPCYPKSLLEMCEKINIVFAPATTTSS /LKPMQGVIVTFKSNYLKNTF\RLGEG RKKKKKKGRKKSPHKALAAINSDSSDGA GQSKQKT/FWKGFSPNAIKNIQDPWE
2273	16174	A	2289	75	469	SRGVAGAPPKSPSPSTPSPGPLDVTGPH SSHHAASPGP\PPPPEPTASSMASAP\P PAPQPTPL\PPATLGPPSAGPE/PSPGS CTSTGWGYSFCCPRCRRWMRWQPPQGGP AWHWWPREFP/PPPRVSGS
2274	16175	A	2290	256	55	PTQPLRVELTTVTLRCDINKWDYIKLKS FCTA\KKRQPTEREKIFPNHVS NKRLIS KIYKELI HRI
2275	16176	A	2291	497	29	SLTHRVAGGA AVTFLAHACARQIFFLGD PHPTSSLLGWGPAWDPCAFOVSDHPASS

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						RVGKTLTSCPGGGRLPWVTCPPGGGQLSC LTQMHLTPAGMCSPCVCVCVCVCV GMCPRCMCVCVCPCRDVY/ICVCVCVCV CVCMLCPCWDVFTTEL
2276	16177	A	2292	141	392	SCSTEVKQPKIGVREDFVAAPGIAPSS PQKKQTTTSSLKSLRLSKVRFLFNIV LDVLAREIRQEKEIKGIQ/LGKEE
2277	16178	A	2293	14	291	YVGTEGISFTSFMRVTNVMTRHLATRE S\CYSR\VYPRFIEFLRFDIQSTGQ/RI TSRQHPPR/DLRDALLYLNRRITLVRTR CKSVAKRPPGSP
2278	16179	A	2294	110	293	LLSNRSLAIASLCGGCNELRSCHWTPA\ WRQRET VKKKKKKKKKPGWGFLNPPPPQR GKLCF
2279	16180	A	2295	96	313	WNGCYLLSNRSLAIASLCGGCNELRSCH WTPA\WRQRET VKKKKKKKKKPGWGFLN PTPQREKLGFLKRGPGF
2280	16181	A	2296	234	2	CCLETTRSLFDKGT KENTQWGKDSPSNK RCWKNWISTCKRMKLDPLYIP/YTNINV KY/IKDLNLRPEITKLEENLREK
2281	16182	A	2297	334	6	KLFSPPGGGGGPPPPPKKGWVPPETP\ KRGGGAPNPPPPKGGGAPKPPPKKNPS PKKKKKIFCPPPKKKKGPVFLRGPRGP YRVFLKGPPLFFFFLKKSWRPLAMXA
2282	16183	A	2298	467	8	LPGFKASTDRDN\VAGDFKLKQMLIYHS ESSSALKNDTKSTLPVLYRNKEAN/VTA HLLIPWCTEYFKLIAETCCSERKISFKI LLLI\DNAPSYPRALMKMFKINVMSDN TTSIVYSTDQGVILTCNSYYLRNTFYKA ITAIDS DSCRMPQEGN
2283	16184	A	2299	1	449	SIYLSIP/FNLSINLSIYLSIPIYLSIY /HISVYIYL/SIYLSIHLSAIICLSIF QSISSLINLSIYLSIHLSSIIYS SIIYHLSIH/LSYYLS
2284	16185	A	2300	1	445	QAGLQLLTSGDPRTSGLPQCWDYRC\DH RSWQT
2285	16186	A	2301	241	22	KWVLGTCACVHVFCVVMCLYVCANV/C VSMCLYVCACVMNQCVTVCMCVCVCV CRFVCVGIPPHSKWISIG
2286	16187	A	2302	3	478	GGQTETLLTSQRKGGWPEALLTSQMGRP GRGAPHIPDDEQPGRDAPHLPDGAAGQ\ SAPHLPDGE\PGRGAPHIPDGAAGQRRS PLPRWGG/ELGRGAPHIPDGAAGQRRSS HPR/PGRPGRGAPHFPDGATG/Q/DGAP HFPGIPPDGT
2287	16188	A	2303	440	41	KSHHLSFLSFLFFFP/TKSHSVAQ/CW SAISAHCNLCPLGSSSHSALASRAVTT GVYRI
2288	16189	A	2304	2	395	FFLVKTRFLHVGQAGLKLFTSGGPPALA SQ/SL/RTGMSHRTQPE
2289	16190	A	2305	184	2	SIKKPKPLVNLNRH/NT/WQAVTPACN SSTLGGRGGRITRSGVQDQSGQRRESEF LRLGYGLD
2290	16191	A	2306	86	472	I IKLCWKQNK/RFEAGSLVPENGFYYVT QAGLELLFSRDPHTSASQSAGITGAAPH QRWSVGTVLLQVDRGTPPVGDCGSRTPO WPGQAFRLTALKSEAHPPHSSTDVTPVL WSEGS PCLLSPPSLSFTG



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2291	16192	A	2307	133	2	RVIHVVRSHPAIP\TTREAEAGESPEP GGGGCNEPRSCHCTPAW
2292	16193	A	2308	3	369	LTTAFDPDFPGSTHPLTSASQVAWATGAH HHSWLIFVFFVETGFHL/SELLSSSSPL ASASQSAGITG/REPPCLTSPFFFF
2293	16194	A	2309	253	365	TDYFYLFIYLRQSL/SSVAQAGVQWQDL GSLQPPPSGFK
2294	16195	A	2310	362	0	TKAQCCVHENHFKLKDANTLNKIVWRNI CHSSPNQKKYGLAILNLKSGFRSRKDT GDEE/HFIKIKKSVIQEAI I I NIYA
2295	16196	A	2311	167	2	LCYCVIFVFFIFWRQSLTSLSQGMQWCD HGSLOPLPP/GLKRSSHLSLPNSWDYRR
2296	16197	A	2312	67	482	DHLTPGGGGCSELQSHPCPTPAWVA/ET LSQKKKKKREK
2297	16198	A	2313	188	437	AGFFPPENQLTNMKVRKANESDPWGVKP ESDESETHGSLSLSLSLFFLFI FLRQSL /NSVIQAGVQWRNLSSLQRISP
2298	16199	A	2314	41	325	TTTLFXRVRGYSSLLMFLLPFVCLCPA GRGGVYRGQSSSLSCSRHPVRASRPLC LPTQASAIAGAPPPALLPPCSLISVCCA SNEQGSVG*DP
2299	16200	A	2315	417	0	SEPRNWDYRCVPPRANFVFLVEMGF/Y HVARPEFGLLELPTSGEPPTLA/FSKCWD YR
2300	16201	A	2316	98	288	LMAVVPATWEAEAEQESLEPGWGGGEEG CSELRSCHCTPAWVT\SETLSHTHTKKK KKNGAAL
2301	16202	A	2317	1	410	LNHIPNLSLTKRKPSPHSLNLKKKKKKK KKKKKKKKKKRGGGVKKKPRGGQKKK GGEKKNFPSKGGKKKKRGEFGKNFFG GGKKREKTPQKKSPKGGKKNLR/BERG EKNPKRGGEKKRSSSPRNNLERGEK
2302	16203	A	2318	249	3	PLKASSPPKAENFCREVGPICPPPKKV P\PKIPKLVFIPPPIRKLLPCPPPLTL AEPVPLKRPP
2303	16204	A	2319	2	393	AHLGLPKCWDYRHEPPRPAPLFLINSYF GLDLLT/S/GDPPALASQSAEITGVSHC AQ/PEYVY
2304	16205	A	2320	389	2	RGNSNIGGPGPLRGKKFSPPPPLKNWGT KLGPPIPPPPPPPPPP\GKPGFSIFFKPI LKFKGPKKPPRAPKNGGSPGPGWFFFF FLSNFTQLPGIKLSKGGKKNFASPPPPF FFFVHYKTGYPSATPDW
2305	16206	A	2321	389	206	FQWRWGF/NHVGQANLELLTSDNDPPASA SRSAGTTGMSHHAQLKNYFLMVRMWRNW IAVGM
2306	16207	A	2322	371	42	SFFPQSGFFSPPPPHEFFPPPPPSFFSW VGVRQIPPPKIFSSFPFGGFFSPPE R/VDFFSPPPPPPPPSFFLSPPPPFF FFFFFFFFFFFFFFFFSFFGVKKRK
2307	16208	A	2323	82	386	PFLTQKYFFTPPEEGFLKKPNRREGPPS PITDPTLWPNMMKGIVKAPPIIFMGGG INMTFSGFVTTKAPFPRPLRFNPMLRQG FDLLTLKAS\WGSSASWY
2308	16209	A	2324	1	413	RSGDNRHGPPCRVNFVLVETGFLHVG RSGLELPTSPALASQSVGITGVSC/RPP PQASY
2309	16210	A	2325	58	400	SETLVSKKKKKKKKTPPPPKNPKKKKNP

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						PPPPPGAKKGPGGKF/PPPPIFQKKRGG FKK/SPPKKPPKKKTPPPLGKKGPPPP RGGPLGGFPPPPQKKNPPPPKKKPPF FFPPK
2310	16211	A	2326	462	306	AHNLRLPGSSDSPASASGVAGTT/GMC HHARPILYLSGDASALLHCFSSAQLF
2311	16212	A	2327	1	393	SRPPSRTEKIRNFFVFETGSCYVAQAAL KLLDSSDPPTSASQSAG/ITGMSHRAQP TS
2312	16213	A	2328	391	2	AWFKETKAGWIIPRSWDRGSWSVQPYSA LTSSPESGFHSVTNGDSMTCLEDGKHS L VAPHGIPQRGSSLDGVSFCPAPT MKPY LASTKM\RLHEARELGFFSFLSLRQGLA LSPQLECSGAILAHCSLNL
2313	16214	A	2329	2	115	GCSELRSRFTCPAWAT\SKTASQKKKRG KKKKGGVFYF
2314	16215	A	2330	2	406	AAAPSALALRDGWAVRPELDLLPPCGEE VAPGAHCLGCGPSPCLFLSPSHTRQSP APTSSPGLSTSPPLVPTHVSAPHSSKGP PSIPGAQALRGCGLGWDR\PSSPSLP/ PDVSPKPLNFAP
2315	16216	A	2332	226	377	KRKSKHITFLFKTLSPDTPVAHACNPST LGCQGGRI/TPRSGVRDQPDQHG
2316	16217	A	2333	3	191	CLSPGGGGCGGLRLCYCMAWVT\NETV SQERKKERRKEREKEIKERKKRKKERK KEKKKKK
2317	16218	A	2334	295	81	FFKPPFPKKKTCPEFS\FFEWKRGFPPP PLRSFFQNPDPKGGPPILLKGPPPPPSL GWPPPPPLFFFFFFL
2318	16219	A	2335	375	8	TQIVPLPSNLGNKTRLRLLKKKKRNEQGN IPTDTIDNRKQIIQ/TYYEQLCANK\N LDKMDKALESHNFPKLKQRESLNI/HSA KRIHFI/ILNISTKKTDPDTGFTGKFLQ IFKEKKMAGHSGSHL
2319	16220	A	2336	399	97	FFFFFFFFKQNLA/SVTQVGVGQYFRSL QPLPPRVKPFSPNPLSNRGYRGPPILGR VRQENCPKLKSKRFQNLKIPRLGKKKL RFPKKKKKEKKKIVKT
2320	16221	A	2337	411	57	KKPRSFSSSSSPFFFFFSPPPKKKIF PPPQIFWGPPFFPPPPFFKPPPPPPFFS PQKKKKI\SPPPKKKFFFKTPPPPPFF FFFFFFFFFFFFFFFFFFFFFFFF
2321	16222	A	2338	97	354	AKAPSLSLVLSFSTFFLGIQGLALLPM LECRGATAYCSLNLDPSSGPPTSAPSP TPY/RIAGATGTHNALLLFKFFSRDGL PL
2322	16223	A	2339	391	45	LMFFHLSHKHRSGEAPSIHWSIYLSIHP SIHPSLYHSSIHLSTIYPSTCLSIH /CISIHPSTIYPSICPSVHLLAHFSFIHST ICPSMHLPIHVSIOHFLSAQILPVSVFG EVSDI
2323	16224	A	2340	506	0	RDHEQLGTVRADKKKKKKKKKKKKKKK KKSSSSSSSPGTFFRG/VPLKDPVG
2324	16225	A	2341	203	1	VELRVRATEPGFNFLKGIYCTSMVDWIK KMWYIYTMEYHAAIKG/DRIMSFVATWM ELEAIFLSKLMQ
2325	16226	A	2342	402	40	PYPKKKASPTDA\FSSSSSSPPPPFF SPPPKGFFSKPFFFFSPRFFSFPFLK

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						PPPPQFFFFGGLKKNFFPPPPALKFFFFFK SPPPLFFFFFFFFFFFVEAGVLLCYSG
2326	16227	A	2343	181	1	QLKDQASDLLGKNGDEVKETIPSFLLPSS LPPF\LPLFLHQFLPSFLPSFFPPSLLP FLS
2327	16228	A	2344	2	407	FVASQLGCSGV\RVRDPLBBAVCPFSDL QLRAGR'TTALFKAVRQGHLSLQRLLSF \VFLCPAPRGGAYRGRQAFLLSCGGLHPV GASRLCLCPKQAWAMAGAPPPASLPFCS LISDCCASNQRDSVGARPEPGAGH
2328	16229	A	2345	405	178	IIKFIYEKATA/LLNG/EKLKAFPLKLG TRQGC LHSLLVCNTVLEVLTTGLRQEKE IKGIIIEKKEVELSLFADRIL
2329	16230	A	2346	2	412	FKASKASLSPLLGANTAGDFKLKPLGIY HSLH\LKNYADSILLVLCQWNNKAWMIA HLFTAWFTEYFSPPLRPAQKKISFKMLL FIDSAPSQPGVLMEMKYKEINVVFMPANT TSILOPMDQGVILTLSYWLDRDTFH
2330	16231	A	2347	2	397	ESLEPGRRRLQGARIIMPLHSSLDNRVRL CLKKERKKEIGVLIRCWQECKIVQPLWE IVWYFLKKN\ESPYEPAVPLLNIPRE MKIHVYTNCTQIFIVALFTIAKSGKWW GTVACACKPSSE/WLRWDYL
2331	16232	A	2348	3	423	EGCSELGSHHCTPAWAT/AESVSQKKKK PKKK
2332	16233	A	2349	49	262	QMCKGSNRRRGKRVGSRQISKKTNAPI KKWAKDMNREF/DIQMANKHMEKCSL IIREMQIKSTMRYHLY
2333	16234	A	2350	356	2	FVTAPLHSSLGNRARSYCKEKKKQVAA KAVLRGKFI IAYTVFKRKISININLSIS LKTLEKEEHTETKADGAQYVTKI\RAKI NKIETANETKRSLEKTSKTVEGKCLRD ILLSAQI
2334	16235	A	2351	360	19	LDAQFLEVGLGELLFRSTVPTLQPPGCG ASFPVLNTLPF\SLSPSQSSSSPASLVR PWVAPPFLCPHGEPPDGGPDSTSLPFP PAATGPAARLIQHPASRQPRPASHTHCG V
2335	16236	A	2352	360	0	NTFLAARLVFCQMTSYSLALLSHKLAL MPLNLSDLLTRWTHCMGELFFLDILAIQ NPFHTVFFLGHPWGMESRFVQAVVQW PDLRQLQPS\PPGSMRFSCLSLPNSWNS PSYGR
2336	16237	A	2353	34	474	EGWRPCKELAARQVGCPSFCSPHWQLL QKQEKTAGAVSVCVCTSTLCVCVCVCVC VCAQAMCVCAGA/CFCVCVCAGA/CLCV CVGA/CLCVCAEAVSVCVQ/VAVSMCVC RS/VSLCVCMQGQSLCVCAGA/CLCVCV CGIPPPVLCN
2337	16238	A	2354	297	16	KFFFLKSFFFFSFFFLTTPRFFFFFPKK KKIFFFPKRKIFFFLIPPPXFFFFF FFFFFFFFFFFFFFFFFFFFFXRHGG WFEEITILTV
2338	16239	A	2355	3	315	PVTPATRETEAGETL\HDLGEPGGRGCG ELRSCHCTPAWVTEQDSVSKKKKKRGA RFKESNFTTGPLQRNIFFLGALKLISGA GVLRKRDGKTLGFPQFNRPWG
2339	16240	A	2356	399	154	PGQRGETPSLPKIQ/ELAGCG/GHLNPG

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						GRIFGEPRSRHCTPAWATEQDSICKSHS RSLWCYKSSSVYLSTRGVWVRGIASV
2340	16241	A	2357	416	2	FFFFFSETESRSVAQAGLRT\QWRNLGS LQAPPPGFPTF
2341	16242	A	2358	209	2	KKNLVPWPRGGYFKSLQPPPPGV/SCPN PPKKLEYRVLFPQPSNPPFFFCIFSRDG VSPCCPGWSRTPD
2342	16243	A	2359	279	380	RGYNP/WPGAHAHTCNPSTLGGRGRQIT RSGDQDH
2343	16244	A	2360	415	224	FFFVFFFLLITFILMLNLLPCHKFLFL QFLLGYLFLLYL\CAFFLLVALNIFITS FQQLDYTF
2344	16245	A	2361	278	2	ISDPFRFwniYRIHTGLISLIQISENCV SCQKFQILEHFRFQIRDAQSVLRK\RA WTGAVAHACNPSPGLGGRGWISRSGLDV HPGQHSETP
2345	16246	A	2362	139	282	KKKKGGRGGGGGGGGGGXWGGTKKKKK GGEKKNLWGGGKGGGKGGGS
2346	16247	A	2363	19	409	PKPPSVLGGGPARYPSPGLGGPNRPVPL GPGVGAPPGPPGKTPFFLKIKKIYPARG GPPVIPASPGGEGKKSPLPPRPRVPLTQ IFPP/PPPPGPNQG
2347	16248	A	2364	159	383	HSHFKNLSSIIKKLHRNNTFTEHFSLS SLNQCFNLTLTVFYSHLGNFKNSN/SWPG AVAHTCNPNTLGGRGGQITR
2348	16249	A	2365	400	221	GRLRQENCLNSGGRECEPR/S/HLHCAP AWAT\EQDSVSKNKKQNKQKQTHIYTVL LCARH
2349	16250	A	2366	383	14	GGRGCNAPRSCHCTPAWVTERASQKTK KQKNTHTKKRISCCYKMEDPLRQA\TF LQCPRAEGPSQKAARMELMEKQEKNOGP ARHRRQEQPLTSRCPDHLCVVLSQVSS TPAQGLSLICK
2350	16251	A	2367	274	1	PRKILKARGKEHLASRGTMIRMTSDFYL QTMQARREWSKIL/NVLEEKIHQHRIL/ PVKSSFKEEIEIKTFSDKQKLRGLVTSR SDLGKDVK
2351	16252	A	2368	161	2	FFFFFSETESCC\VTQARVQWRHLGSLP GSSDSPASASQVAWITGRHYAWLIF
2352	16253	A	2369	361	198	NGRLIFVFLVEMGF\TMLARLASCDPPA SASQSTGIRGMSHNSQLKCFTEFDSFC
2353	16254	A	2370	116	300	HLNGDAVEERDFMCKTVSGIIIVAHCNLE FLG/SSDPSASAPRVAGTTGMCHHIWLI FVILVEM
2354	16255	A	2371	2	192	MKLDPHLSPYTKVNSRWIKDLNLRPKTI KILEPNIR/ITLLGIGLGKDSMTRNPKA IAIKTKLAR
2355	16256	A	2372	1	133	AGELLEPG\GRGCSKPRSCHCTTAWATE QDSSPEKKKKKKGGF
2356	16257	A	2373	43	403	LHDSFALASQAGTTGVSHHARPAAGIN SRIGQAEDRISELEDWLSEIR\ROSGRN MDKRMKMNKQNLQEIRDYVETKSM/NTR LIGVPERVGENSNLENIFQDLIHENYK GKPIRLMVDL
2357	16258	A	2374	404	215	GOGGRITRAQKFETSLGNVVRPGSEAE LLE\PDGRGCSEPRSCHSTPAWTTEQDS VSKRRKCC
2358	16259	A	2375	3	397	SKQLEFTQLYTKLNQINKTKISDLKKEK

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						YPIRLFSKENTQMASRYRTKYSTWLIIR EMQIKTTFRHKLAALASSRCLLGLG\AT SAHCCTVGAPLW
2359	16260	A	2376	413	1	PKKGLFPKPIIWVTPGFFPPPRFKKPPP KKIFGAPKKKKSPPPAKKFFFFKGAP PPFFFFFFFFFFFSGDSQERVREAM PVAGGP\PRPHLSAPHAPGGTAWTPMH PVQTHKAQSPKLPASECPPTTPLS
2360	16261	A	2377	398	247	RRFHAGQAGLELLTSSDLPALASQ\SA GITGMSHHAQPSATHFQKHLVS
2361	16262	A	2378	2	143	QENRLNPGGGGSELRSCHCTS\AVWTT AKLCLKKKKKKFFGKGGG
2362	16263	A	2379	417	90	FFFFFFFFPGGGRLQVCPPIILFCFLY KGGSPGGSTIFPPPPPEVGPFGPPPP GGFFFFFFLE/QGGVSPDGPFGFFVLPTK KPPPPAPQKGGEPKFKPQVWGPWPPTF
2363	16264	A	2380	36	427	VHPLNHHDQKGQASSTQKKKKKKKKKK KKKKKKKKG/WKGGGAF
2364	16265	A	2381	402	2	NFFLKGRGWGLPPFPLRGPFPGRGPQK /RGLGGPPPPFFGSKTPPAGSRTPMG QKKKGPPLEGPFGGAGQAPFLPPVP RGGVPSPKKKKG/APPPPPPPPPPPPP PPFFFFFFLRYNLALLPLGCSGT
2365	16266	A	2382	166	5	THGHVIYVDQEMQMMIENM/WPGTVAHA CNRSTLGSRGWITRSGDLMVKPRLY
2366	16267	A	2383	2	457	TSQPSLLSSWDYRSTSPRIANF\ILFYF IYFFFAFSVETGFHRVSQDGLNLLTS/S /IPSIPRIPKHWDYRHDP\RTWP
2367	16268	A	2384	2	417	GRVGFSQSNNGNPSSLSFTLLKVD FEVTI PGEGKDRIFKVSIKWLAI VSWRMLHEAL VSGQIPVPLESV/QALDVAMRHLASMR Y
2368	16269	A	2385	318	32	TMEIMLDKKQIQVIF/FEFKMGREAVET THNINYTSGPETVQWWFKCKCKGDESLE DEECGRPEVGNQDLRAI IAHASADAWV DRDSGRCCACAP
2369	16270	A	2386	409	3	ISQAPSTPPRKRGR/PPQKTSFLGPPF YAAFYQEKKFLFFSSDPPRETGDKGKQK GFPKPVAPKKKGFFKGPFGKKKDPP SFFKHKSQTRPPRAPALEGPRSR/SAA LQPGDRRR/PPSQKPTRPPTRPPTRP
2370	16271	A	2387	415	10	KKGFFPFGPFIPLFPFGFLPPPPPIF WFSGFPPPPPLFYFFFRGGPK/HILVF PLFFLPPPPFFFIIFAKESPPKKGPGP LNFFFGPKKN/SPPPPPFFFCMEFEH SCRPGWSAKWHDLGSLQPPPPVFK
2371	16272	A	2388	410	95	KATMDKSDHIKLSFYPAKETPTKVKTQ PPEWEKVFANYP SDKGLPIIYKELKQP YG\KKSNNISIKKAKDLNRYFSKDIQMA NRCMKRCSRPGAVAHTYNPST
2372	16273	A	2389	362	92	RFLFFSPPPKGGFFKFFFSRVPFP PPFFLNPPPKLIF\GPPKKKIFFPAPGG KKIFFLKGPPIFFFFFFFFFFF PVENTFY
2373	16274	A	2390	131	487	ATEHEKTEKSSLSFFSISKRRKKMEKLH DIGFSSNFLG\RPKAQATKGKTDWTS AK LKICSSRDITSRMKRQPKWAKTFANKS CNNKKPEKIDKNKKKKKKFLGGALLKK TNLKPRG

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2374	16275	A	2391	408	145	RWSLALSPRLCSGVSSAPCKVPPPGVT PFSLSLPSNWEDRCESPPPAQ/IVFIG EGFYILHGFF/RRGPKIRCFISGCPPPV LSEPT
2375	16276	A	2392	1	203	LFFFAFSVETGFLHVQGAGLEPPTSGDP PVSA/FPMCWDYRHD
2376	16277	A	2393	386	16	TPSAGGRHIELSLSTCPSCAQHQKEHL EGGEGGGAQSLTAPSSATSSQDPISAH AVEDKLSIRLETDLKTKS/WPGAUGHT CNPSTLGRRRQANHLRPGVRDQGPLVIC RFRPPKVMGLQA
2377	16278	A	2394	3	396	QLLERLKQEDRLSTGSQGCSELRSHHCT PAWATEP\DSVSK
2378	16279	A	2395	273	416	FFYSFLIKIRWKKQPGMVAQACNPSTLG GQGGRI/TLRTGVRDQPGQHG
2379	16280	A	2396	329	76	FIPIESACSQECLKPNLRQEW/YIFGTL KLIFFETESHVPTQ/DWSAGELL\DRPG RGCSSELRSCHCTPAWATRAKLCLKHHTK IKK
2380	16281	A	2397	210	7	GGKKMYCRKPGGGGFFAAVWSPKGLFS/ RIWKEAPILSPQKKKKKTNNPIKKWAND ANRHFSKEGTQQ
2381	16282	A	2398	48	393	SILKTRKPLKKGRRRKEKESVRTHV PFSYQSNAPPSKPLNNMTLGRLLSFSF FLVHFFFTDGIILLCCPGWSRTPGLKGS SHLSFPKCWDYIHEPPHPAYHS/LFCR
2382	16283	A	2399	128	383	EEAPKHFPKPNLH/QKKVLVTAWWAAAG LIHCSFLNPWETITPEKYAQQTNEHQK LQCLQLALVNRKGPILLHHNVRLHITH AS
2383	16284	A	2400	54	384	LFTFILNSVFHTYMCLYFWTLFFSVNPF VSMPIQCLDSSFIISLDSEINPNIYS QLIFDKKTQRGKNSLPDRWCWENCIFTY KRMKWDPYL/SPYTKIISNWMKDLNIK
2384	16285	A	2401	393	1	HRGENTHQGGGLSRWRHRSRQRTSRW IRHTRQWGPSRWITPSRQRGSSRWKR RAGDIEVEKTQQSEGALEVRIRSRQRT SRWRSFSRQVRSFRWRICSRQRCSS/KV RRRSRQRTSRWRHRSRQRT
2385	16286	A	2402	1	330	RPPPPPHCWDYR/HEPPR\QPTLWVIFK LSVETRLCYVAQIGLELLGSSKESSRLD LPKCWDYRHLLCWMVIFQEKLV\SGFL FKIPRFFKAGMEIFKQIBGFWSHPLAT
2386	16287	A	2403	3	407	ADAWGLRGTHGPWEQAGISGISPSNSFL FVCFRQSVLVSQAGEQWRLGSLQPPP PGCGRESC\PSFQGGITPSCFFVLEKM GLHRVGQAGLQLMSGEPALCSQRRGI TGVSHHARPPSKGFIWHTGAPAM
2387	16288	A	2404	239	573	VCFGVFSLSHFFSEFSSITQAGVQWLN LGSLLQPPSRGFKQFLCLSLSS\YWF TPPLVGGGSAGLRGG
2388	16289	A	2405	1	122	PTRPGRGCGELRSCHSTLAW/VNSETTS QKKQRKEKKLPLL
2389	16290	A	2406	417	130	QALRVKHVQLVPSSDFAKTRAQSVNNL LRHSSSSSSSSSSSS/SSSSSSSSSSSS SSSSSSSSSSSSSSSS\SSSSSSSSSS SSSSSSSSSSSSSSSSSFLFLFFFFG LRGAFLGRFCPIRR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2390	16291	A	2407	327	3	RQSQSLRYMAHQPVCCFTCSILIRAEIN EI/ETKNKKIEKINET/RKSWFFEKINK MGAITPDATERQNI IQGYEQLYMQNLE NLEYMDKFLGRFKPPSLNQEELDTLNR
2391	16292	A	2408	178	404	AAyrINSLQEVQHPTKRHSQPRKQSKLR EGNAQRNNIRRGPGMVAHACNPSTLGGQ GGQV/TLRSGVRDQPGQHG
2392	16293	A	2409	94	386	TSFALVALGGRSCSEPRSCHCFPAWVS\ SETLSQWKRKTPTLNNAKYWGGRLRFF FLTRGGGGRRFFFGGKTKSLGAGFKKG GGGKPGGPPNKGLG
2393	16294	A	2410	1	384	PTRQVRIKLFPPRIYVHTRKRLKNIYGNT ETFITQPFKNHNSVWQLIRNNRNAXKQEN VAHNEEKNNKQSIETN\QKYTHKNLDT TKKKKKKKKKGGGGLKKTIFKARGGEN NFFFLGPQKLN SGAGF
2394	16295	A	2411	423	2	FFFFFFPQKKS LFPFFFCGPKIFSSPP VFLTPPQKIFFC PPKKKKYFP PPRGKIF FFLK\PPPPFFFFFFFFFFF FFFFFF FIF FFFFLGFLLSLLIGVPFLLLNAN IMILLQKKILKDEVQI ISSFPSTKNRNV L
2395	16296	A	2412	218	112	LKKENNTKCYYGWGTGTGLIHC\WW\KL IQVLWKT D
2396	16297	A	2413	64	403	LKNFFFFFFFKKKGPPGAPGGSKPRGLG EPPPPPPQRRGNTGGGPGARPKNNGGGF FFFWRGEP/PPPPAKGGGQDLGPGPFG REETNNFPAPAPPKPKNKLGPRAQKIL CF
2397	16298	A	2414	217	409	VKYLVS VLLTIICTVQACYQELRPGAM AHTCNPSTLGGHGGRI/TLRSGVRDQPD QHG
2398	16299	A	2415	416	0	ERPPSSFFPPLAPGQVGQFFYGKGPWP EKSKKKNRFWGTKPFPEGGGPPPPNS PPGGGEKSP LFFFGGKGNPTWSPGPKFL KKRVIKGPLHPGGKGYKKTREGLKPGP PPPKFFLGGG/PGFQWKEKPPQP
2399	16300	A	2416	277	0	PFVLLSSSSSSSSSSSSSSSSSSSSCS LLVRYLCKVKHKSSLCAHPGTVPFLELI HDTDSFAH/VFPADLL
2400	16301	A	2417	205	486	RHGYGFGFWKNTCMQHRHSYRRVYIHRH IHLTFLAYVHRESPEAMSALLTQILLFF KL LSF LRRCLA/SVTQAVVQWCSLGLSR PRPPGFKR FWC
2401	16302	A	2418	364	1	KESLGDVPKDTVILFATRNPMQMGSNYQ FFIYLC LTHLSRSYCWFGCKMLQ/PLW KTVWQFLKKNLNAEPYDPAIPL\DICIP VFTASLFIIAQRWEQPKCASTDEWINQM WHMHTIEHYPR
2402	16303	A	2419	281	492	LFPPSLPASHPKLSTQQPERSH SVTHCG /VDRRGSD LGLLQPRPRLPKSSRLSLW SSWDYRPAPRPANSC
2403	16304	A	2420	63	465	RLQRFLLSF\VC LCPAIGGAYRGRQAS LSCGGLRPVRASLLCLPKQAWAMAGAP PPASLP CSLISDCCASNQRDSVGVGPS NPGAGYLVARRFLSPLEKRSIQGVVTL FSRCRLSPLSLTRKGNSLTPCAS
2404	16305	A	2421	61	482	QRARITGVSHHAQ/LRFCLFDMRSHSVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QAGVQWCDNSSLQPPPSGLKML/STSAFQSL/WDYRCEPQHPIHY
2405	16306	A	2422	90	444	YCFSSSECKRCPCPGHDLQLSPGLCHHG VSGLAKEPLLCFWPWIWKQPLCSPTTSL PFLPLPPFSQCPQGPAPWLELEGRPSLWK QGGLQSLAKR/REGSRAQWLTPVIPAL WEAEAGG
2406	16307	A	2423	1	444	PGPGPGCGPVATLGSPSRPARTDSPSLP PHSQLREAEARNRDIEAHVRQLQERMEL LQAEAGATGESLMCLPLPRT/WEEVGRLL
2407	16308	A	2424	189	418	SRRAEPGSFRGCLRVGVPSTCV/SLWV CVCVCWG/VVCVCVCVCARA/CLCLCA NFSL/CSHVSLLCLSLSL
2408	16309	A	2425	30	895	LDEQCTSEIHRGEATARPRAPEHPAPP ATAVRGRDAASQNLKRRPGSGTDGLRLQ GAEPSSLRLTYAGGAVIPRGTPERAQPP PEQDPLGRRRWLSRNTWGPWPGTTQPPS PQLLRNDWGS CGFMVPEAARGKVFQDSQ EGAHIRRET VSKSVCAEPWRHQARDPA PTNFPLKCKQKRGASTSSGQHGDRVNLV FFIDDDYSPPSKR/PKTNEPPQPPVPEP ANAGERKMRFNNSGPHNVEETKLICLC PSGHASCQVHLWTGAMLLGFQSWRKLPG SGLKARILQ
2409	16310	A	2426	494	154	SSRVRCQCA\LLGGASQLGCSGVDRDPLE EAVCPFSDLQPRAGRTTALFKAQMEMQK SPVFCVAHAGSCRLELFLFGLHSSSLHG LWN
2410	16311	A	2427	416	1	PQRGPLLALEPGRQGAAPVEDLQPGPD KPPPPPLPQPFRTVTAAPVPRHPPV ACHPPQPLAASKPWP/SVAGDDLPLPG PERPVHAFFIGFI FVHLGLGGVSGRGAV APARSGPVPPRPPSSSTRFSLFLHE
2411	16312	A	2428	84	409	DYKHAPTMPRIONFVYHSPQQPRCENRI NFTPKKKKKKKKKKKKKKKKKKK/KIF WGG
2412	16313	A	2429	1	389	LRDLSSDRSNPGRFLSTSNSSLY/EKDK RNKAYFTK/RPSPVNDIIST
2413	16314	A	2430	456	0	PGWPGRGAP\PSQTGWPGRGAPHIPDDG QPGRGAP\PSQTGWPGRGAP\PSQTGW GRGAPHLPDNGWPGRGAPYIPDDGQPR GTP\PSQTGRPGRGAPHIPDDGRPRD/ GSSLP RRGSRAEALLTSQTGWPGRGAP P
2414	16315	A	2431	3	344	CRERRSCHCTPAWAT\SETPSQKKKKKI FFGNGPPGGPQAGLKLRAWGFFQXRGTM GGGTKNHPGQGEPPLLQKKQKITRPGG GGPGAPPQGGGAGKSFNPGGGMFQGGGE IP
2415	16316	A	2432	1	109	RPLRRLRQENRLNRSGRCSEPKLC/HL CTPAWAT
2416	16317	A	2433	1	239	QSFVLPRLVSNWAKVICL/PSVSQNA EIT
2417	16318	A	2434	3	464	DWLQLEMQGEIVALVSHHGGPLWLSSES ARRLQVQSDLPWWLVCRGTIHKFRCVPH LTGRRFEHGVTDCTYLFDAYHLAGIEM PDFHRENDWWRNGQNL YLDILQAPGLYP VPLSAAQPGDVIMCCFGSSVPNHAAT/Y



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CGDGELLPHIPK
2418	16319	A	2435	3	427	EGARTSSERHPCNKYLLHLSLAHLFTNA LNLVLKGLSPSPFPALPISFPFFSPH FLGTPTLEGGRADLPFLQPPGAPG/QPA PLNYGPGPYRNPCP/RLPQLKPAGPGHG LLKSPPPNPGRNWPLLGSLFDFFKRTS IPLP
2419	16320	A	2436	238	400	QFRWKRGKALFFFFFLRQSPSVTHAGMQ WSNLSSVQPPPPGFKQFLC\PSVSS
2420	16321	A	2437	11	442	LGTRPRATDWGVRLELSRACPVLGHPAK HPRPQRWCKVNFSYSPEQADELKLQAGE IVEMIKEA/CGNPDMPSPVSPGQRPCKT TEDKGWWECECQRRRGVFPDNFVLPPPP IKDAQPLLLFGIDQEAGPTESGISGIRF RRLSC
2421	16322	A	2438	411	80	PQAEAGAPTSGSENFNPPPPRGGGAPPP PQKNFFPPRGVNPGGGGQKRPPPKKGG /SPKKNPGGDKNPPPKKKKNIGEGGFI GAPRGTPKKTTPPRDGYFQVFFIVSLK
2422	16323	A	2439	290	1	QLNKIKKTPLLFLPWANEKVPKIPPNYP PGPKKKGYPPSIFFFFFLROGL/NSVTR AGVQWRDLSSLQPPPPGFKRFSCKPNS AFPHASADAWDP
2423	16324	A	2440	440	213	PFSRPLFFFSPPPKKRASPPPPFFCFPR VFFPPPPF/SKPPPKFFPPPKKKKIS PPPPKKIFFFSPPP
2424	16325	A	2441	131	408	GCVPEPAFLCFVLEIVSSVAQAGVQWR NLSSLQSPPPGLKRFYRPLPSS/QDYR RAPPLA
2425	16326	A	2442	102	351	QASSSVLKLVCVVRARLCV/CACVCACV CVC/VCVCECVCVC
2426	16327	A	2443	190	3	PQGAREKSHRPGPIGRRLKL/DPPFLSP HVKINPRWIKDLNVKPTTIKTLEGNLGN TLDDTCPG
2427	16328	A	2444	410	30	VCVAPPLCVCIGTLCVRHTQFCVCVHT HSLCVCV/CQFLCVCVQ/VAVSVCVRA SLCVCV\ALCVCVCV\TVCVCVHGTVCV CVCRDSCMVCAGAVCVCVCVCV\C LCVCVSAQQLGRGFCSSVNIKGAGP
2428	16329	A	2445	243	1	KVMVQNKGPFSNLFFFGPTINFFTPQFK QGGGQNPFPFLFFFFFMRQGL/DSVTQA GMQWCHAGSLQHLPPGLKQFSCLLP
2429	16330	A	2446	276	408	MLKNCAFWPGTVAHACNPSTLGGQGGRI /TLRSGVRDQPDQHG
2430	16331	A	2447	24	405	LGDVCAFFFFFYLNQNLNPGGKLLILPVG PAGENQRWEQFDKLQKGGIKMNPLRGGI SVPLTKKKNQ/WARGE
2431	16332	A	2448	239	3	SPLCGNNVYKPTVEKTNQVEKMPPSKQ IWELCVELLWQ/SNRGIAGSGAHACNPG TLGGQGWIRMSGDRDHPGQHGETP
2432	16333	A	2449	406	144	GCSEPRSRPCTPAWVTSETLS/RKKRKR RKKKSCLLRAILSTSPELTHFTLTPLF SRYNDYPHFRDEKTEARRVYATCSGSHS WKRLG
2433	16334	A	2450	349	1	GGAIFLTTPRPKVPLTPTPLAFNPGHQE BIPLPKKKKIVRAIYDKPTANIILHGQ KVEVFPLKTSTRQGCPLSSLLYQHKTRM PSL\PLLFNIVLDVLAIRAIKEKEIKGI

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						QIR
2434	16335	A	2451	382	19	DLGRMTAGSGDQRCAGVKLLSFSLGAA GKGPKHSEAEASLPRNPGSYNRQAQWPQ SSLHLKGTIPDTSNLNTPWKMLSSSLKVP SWQGAHAHDCNHSTLGG\RGGWITRSRV RDQPGQHG
2435	16336	A	2452	3	396	FKLKLMLIYHSENPRALKNYTKSTLSML YKWNNAWMAHVFTTWFTYFKPIAET YFWGKKKITLKLPLVDNAPGHPRALME MYKEINV/VQICILQPMQGVISTLRSY R\KNTFCKDIAAIDGSDSDRT
2436	16337	A	2453	115	411	KGCNFPFPPGGGGEKKIW/PNGGPPPRGK RKPPPPPPGGGGKGGHPPPGPIFFFEK KKKGLFGG/PGGAPNSHPKRNPPWPFE GGELTNPTFFFEFGAF
2437	16338	A	2454	3	114	HHV/GQAGLELLTSDPPASVFQSAGIT GVSHRIRSVS
2438	16339	A	2455	397	1	WSWQK\NRRIDQRSNIESPEMNPRMYGQ VIFDKIAKNTWEKDSLNNKWCWNWI/ LKRMLDHPHLTP\KQSKWMDLIRPE TEKLPEETGGNPHDIGLSNDF\LDLTPK AQGAKVNTDKWDNIKLNFPTRP
2439	16340	A	2456	424	3	PKKKKIFFPPPGFKIFFFLRAPPPFFFL CLSHFLLNRSRSLSCSTSCCVSTIPTSL CNKSSGV\CGLHCSLLAI/CSLIHLTLC PFCVLLVCMCDTVCVCVCVCVCDTVCVC PCPYGTLDIAFKHFFSRWSLTLVAQAGV QR
2440	16341	A	2457	266	379	HWPGAMAHTCNPSTLRGQSGRI/TLRSG VRDQPDQHG
2441	16342	A	2458	10	409	SRTGPNPRAQTDRPVVCVAFACFELPLW RSVDSATREAEAGGL\DPGGRGCSELQ LCHCTPAWV/TSETL
2442	16343	A	2459	184	387	IVHFQMHKMINVAYIIPQFYSFILEIQS HSVTQAQVQWHSLSLLEPLPPGLKQSSH /LSLPSSWDY
2443	16344	A	2460	110	1	KNRVSFFF/CSFETESRSVTQAGVQWCN LGSLQPPTP
2444	16345	A	2461	380	2	FFFFFFSETESRSVAQAGLRT\QWCNLSS LQAPLPG
2445	16346	A	2462	382	29	NGPGHGGPPVIPGTWGGGGGFFPRF/GS KPGFTWGNPPFLKNHKNYPGGGPPPVIP NFLGGKPGNFFYPGGGGFQ/SGPGAVFP PPPGQRRSIFLPKKKKERKLILFFSLEQ RLQNCDA
2446	16347	A	2463	228	1	KKGTLFKPPPPGGRFFFFFFFETQSRSA VTQATVQ/WMP SRLTANPTFRTQGILLP PGLKGSSCLSLPSSWDYRHV
2447	16348	A	2464	395	1	RLRRENHLNPGGGGCSEPRS/HPAQQS ETTSQKTKTKKQKALASDTVLSPROSS EERFHLSLFHSSFVTPFGIFSFLTTSPL PILPVWLAPQLPAICYGDSVIKSNFQL WLSKELQESLSRLLWTQAFS
2448	16349	A	2465	29	299	ETPNEASPKTSWDYRHVLPCLANFFIFF VKTGL/HRAGLELLTSSDLLCFPKCWDY RH\DRSTWPLSSVFGSIFLVYWPYLI ETNMLTTL
2449	16350	A	2466	1266	1473	YFVPQSTQNHA AVFRVGSLLQEGCGKIS

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						KLYGDLKHLKT\FDRGMVWNTDLVETLE LQNLMLCALQTVNG
2450	16351	A	2467	49	356	VQVILLPQLRRRLRQENCLNPGGGGCSE PRWSHCCP/PAWVTEQDSISKTKK
2451	16352	A	2468	115	3	LSHTKWSAWPGAVA/STLGGRGRQITRS GVQDQPDQHGE
2452	16353	A	2469	3	404	FVAPGGGQGTFFGSLQWPFRPGPGASGS PSRAPLIFGFFGGKGVSPVPGGFLLP SRD/SGPPGPPKGWGS/GLGPAPGP
2453	16354	A	2470	404	218	FAQVVIKYGALSSPKPPFPFGKLFGRPS PPSYWDYR/RRPRPRLFFFFFFLQGLA LLPRLE
2454	16355	A	2471	386	258	AGGLSPGVQGYNKLLSCPCKPAWTT/S ETLSQKKKKKKLPFY
2455	16356	A	2472	2	364	HHTQIIFVFLVETGFHHVGOAGVELLTS GDPPASWDYGR\GHRTWPYSHIFNNL
2456	16357	A	2473	1	292	DRGCSEPTSCHCTPVWAT\SETVSQKKK KKKKKTPLLRGPEKKNPNPPFRGFRKN PGFKRKKGGAPPPGLFKIGRKKSPVGGH RHTFILGGPLPRF
2457	16358	A	2474	1	307	SLSCSSIVRRACFPFTFYHDCKFPEA/S PVMLPVKPVEL
2458	16359	A	2475	2	596	MKNAEDILTMEVLKSTMKQEELEAA\QKK HSLWELLRIPNICKRICFLSFVSSSSSS SSSSSSSSSSSSSSSSSTKITAW/LP PLEASFYRSTCLMPARALLFASTIPFWG LTLHLQHLGNNVFLQLTFLGAVTLLANC VAPWALNHMSRRLSQMLLMFLLATCLLA IIFVPQGEKSSQVEERKCLSLFSQGLPW SHLS
2459	16360	A	2476	367	44	YQEDITIMN/TYALNIGVPTYLANI/DL NREIESNIIIVEYFNNTLSKMDRYRSSR QNIDKETVDLKYSI/HINQMDLTDYRT FHPTATERDSISKRIKIKIKINKSLT
2460	16361	A	2477	12	362	HHEPG\GGGCSELRLCHCTPAWVTELD VSKKKKKKKSQKKK
2461	16362	A	2478	401	1	FFFFFSETRSHPVA\RLCSCGAISAHCN QCI
2462	16363	A	2479	3	353	YMCVCVCACVCICVLPWMCLCVC/CYCV CVCWYLCVCLCVSLCGHQHLAVSGKRSQ PPSHESFKTSLLLWVFNLPPLLCWVP QVSQNMPDGTRTLNNVSLPDEKVHDL LPLTAA
2463	16364	A	2480	57	361	MNESLLSCKRWSLLAFSHI/CVFCLICS TDISALCVTVACAMHVCGRVCVMCLCV CLCLCVCRCMYGRVCAPMCLCVCVHCVL ARMCACGCGCVYKAECP
2464	16365	A	2481	3	381	YMCACGYICMHA/CVPVCMCVCTCLCAH VCL/CCMCVCTFVPVCMCVCTCLCVC TPIITLPLFSQERISFCTDLRSFRATAK RSHEEVKNVCVYLQTIWNQYLIIFYLQNP NFGWAQWMLLVIPAVWE
2465	16366	A	2482	2	380	IHVLGNCLYFSEPQFPHWQQRITRSFLE GYGENLMRLHMSYIHMCLHICAYICT/C /LCVYICVLLCAYICVCVYLCVICMCI FVYLCTHICVFVCLVCIYLCV/C/VCV CICVCI
2466	16367	A	2483	296	1	NGTTIRMLPIFSRYRPGMPGLVQCTIQ

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						SCTANSVPYSHGFIYFFIYLLRDRVWLC YSGWSAVAPSWLTITSN\YRLKPSSCLD LLGSWNYRQMPPCI
2467	16368	A	2484	1	319	NTVGLCVCV/CLFVCVLSLCV/CLSCLV /CLCVCVSLCVC/VSLCM/CVSHCVCL CVYLWLCVSVCSLCVSLCVCVYECVIS STKRSLGAPSAEAAKLPRNWPAPAKQSH
2468	16369	A	2485	3	334	NHFIIISIDI/DKHFRKIHQPFVPAKAITK LGIKGNFLNLLRGTSVKSTGNINM\NGE KPNLPLRLVIQGDVLFHLLLEVLASAV KKKKKKKKKKKKKKKKKKKKKKKKKKKK KK
2469	16370	A	2486	17	409	CLDNKKPRKEYCQKTHLIKKNPLLSRIC KELLKLYDKRMINPIKKWAEALYRCLSK GDV/HEMASKHMKRCSIS/L/SIRKMQM KMTL
2470	16371	A	2487	410	165	LECNVTIMAHCNLRNLGSSDPPTSAS\Q TAGIHHSLOHFFFLFFVETGFCYTQAGL ELGSSDLPTLASQSVGVTGTGHGTWP
2471	16372	A	2488	142	417	VEQLLEGYRTKSLYLRSFFLFVCMFLRW SL/DSVSPGLTNCHHLGSLYP PPPGPKQ FSCIS\LWAWRTP
2472	16373	A	2489	1	404	KAGAOMGIKHPQHSSRLRLRRSPRLPS SQKPLNTHYFSPSFSFCAHRHTHTHTHTH THTHTHTGV/HLHPHT
2473	16374	A	2490	373	146	YGLERKISFKIL/LFVGKSPSYPRALME MCKINVVFMHANTTPTLPIDQEVILGP GTVAHACNPGNLRGQSGRNA
2474	16375	A	2491	427	85	KTPPPP\RGPPFFYFFFFFKKAKNFFPP PPTPPLGKKKNP\PPPEKKISPPPGFPP PPFKKGPPKTLFKTPLKKKKGPGAPQKK PFFFKTPPPFFFFFFF
2475	16376	A	2492	443	240	FLFFFFFFXXPXXFFFFFFFXXFFFFFFXFF FFFFFFXXXXXXXXXXXXXXXXXXXXFFFFF FFXGCLFIYLF
2476	16377	A	2493	3	135	ISAHCNR\LLPGSSNSTASASPVAEIT GACNNNRQDFSFIILQI
2477	16378	A	2494	37	420	AHVCVCTCVVCICLSRRVVCAHSHVC AGIFLHLINQFTTTHL/CVCKVMALRVT PSPCLQGA\QTQLAGQCMCAKVCNMFM YIFIEGHICPQTCSCLGEPIRGGLSPLVC IC/MCAGFFVSFC
2478	16379	A	2495	402	178	RQNKTPFGVKKQITGGGGRGRVSYFLRG VSQENPLNPGGGGCSEP\RPPGWGTKNP LFQKKKKSSKQQEGRGED
2479	16380	A	2496	138	439	RTFILGDHHHPSAVHFHLPRRKLCTHE TGAAPPPPALGATVPPSVSVCLTGGGPQ ITPPPPALGARDLPSVSVRLTMGGPQIT PPHPDQQPL/SPPSVSVC
2480	16381	A	2497	118	382	VKSFCASMRACVCECYMCMVCMCVVCV CVSACLICVCLCQ/CDLINKCV
2481	16382	A	2498	164	439	VKSFCASMRACVCECYMCMVCMCVVCV CVSACLICVCLCQ/CDLINKCV
2482	16383	A	2499	1	411	ISTSFYTDITNRTALHFAVGRNHLSAVD FLLKHKARVDVADKDGMMALHFATQSNH VRIVEYLIQDLHLKDLNQPDEPKESPLH LVVINNHITVNVNLSAQHDIDIL\IRS SKPPLHVAADRGNVKLVE/LLKAGCD

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2483	16384	A	2500	80	404	RTAAAVSTVSFPQDFEQSPKCTQGVRE ALRQIK/RLVPTGSLRH/WPAGSLA/LC QPLSDEKDLTQLFMFARNAFTALAMMDY PYPTDFLGPLPANPVKGRRRLPRRRERP
2484	16385	A	2501	215	1	AATQOQSLACSHSVPPATTPRAYTPVPP QLLVNRNF\YPKTLELRSQLRCARRFPRE TGADCRHAGAGRQTK
2485	16386	A	2502	423	214	WQAQVGGLLEP\GGRGCCELRSCHCTPA WVT\GEILSQNNPKRQNKTKQKMGPV PGSWGSPRAGGLTV
2486	16387	A	2503	294	1	LHWNQRQRCPPPPPPPLPPPPPLPPPPPL PLR\HRIAGAGQTGAKIRVVGRVVRVGA GLGVAAA/DSRESCPDGAAAGGEGGGGD SAATAGPGGGGGGGTK
2487	16388	A	2504	331	411	PFLKTGNKGAPPPTKIFFLFFKKKGG/W PGAVAHACNPSTLGGRGGRITRSGDRER
2488	16389	A	2505	407	195	GGRGCSLELRSCPCTPAWVT\GEVLSQKK RKSSNKKSRCLDQAEVGGERQLVQVSV PSTCQRRVGAWFIYL
2489	16390	A	2506	1	468	RQGS MNKLETERQIKKAPARNPERERER ERESKKGEDRHTDICTP/RERERQNYRD RQ
2490	16391	A	2507	27	380	FVCLCPAPRGGAYRGRQASLSCGGLHPV RASWLLCLPNQAWAMAGAPPASLLPCS LISDCCASNQRDSVGVGPSEPGVGVNLM VRRFLSRSEKRNIRVGVTRFSRCVCHPF L*LGKG
2491	16392	A	2508	396	234	RQENCLNPGGGASSEPRSLCTPAWATE RDSISN/QNKQTNKSHILRAAFSRPSCY
2492	16393	A	2509	1	421	AKKIKPPFPLKKKKKPGRGPPPPPPP/ AKFGRETPLNPGGKGSIKPKLGPPPPPP GGPPNLPKKKKKKAIK/PLVP SHVKS TGFPFPCS/RSALLRAFTQ
2493	16394	A	2510	197	3	TGPPDFNFFFLEMKSHSVAQAGVQWRD LGSLOPPSPQFKQFYWGLQGA/LPPCL NKICIFSRGGV
2494	16395	A	2511	114	454	QGPLEKKGAPFKNKFFKTGVLFFGSQNI PPWWFKKGFSRTPF EIKKNPPGILGGS PKKFFFFFFFEMVLLHHPGSALAQSL TTASDF/LRLKQSSHLSS
2495	16396	A	2512	3	495	FFLSRGLFIHLESAPAIQCLLFVVFV FVATGSHYVPQAGLKLASNEPPASNSP KCWVYRHEYPAKCLCFGLCLF/AFLP
2496	16397	A	2513	25	437	PLLFSPAGHAMEEDILPPAPSF LFYFF FYWL VVWKIYLYVLAQAATTNYHRLSG LNNKHLFTILEPRMP/SIKVPA
2497	16398	A	2514	2	256	QAPSAEGEMTSYVLLAYLTAQPATSED LTSATNIAKWITKHS\NAQGGFYNNQDN LPYSLCSGRNESTAFGTNGQDIHPVHS S
2498	16399	A	2515	2	284	KCQCDELCSYYQSCCTDYTAECKPQVTR GDVFTMPDEYTDYDDGEENNNAIRHEQ A\GFTSVISDLQAQIIWSEQKHMSFV EEMTVLEVIL
2499	16400	A	2516	2	432	RDCERESSRAAEYASLKASCWMGDLAE SPSLDPQVAMGTPPAGPCGWSVGTRSQP FPRGSPSRGPCCVSPSWTPEPGTGQ/CG EGGGRWSPQVPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2500	16401	A	2517	401	2	GGEAAIRGQTKPQLEGKAPECSECEKKT VRS\PRILRRQRTPTGKPYECECEGKS FSRRYRLAQHQ\TRAGEKTYECNECGR GFSERSDLINHYRVHTGERPYKCECGK NFSQNSDLVRHHRHTGKPC
2501	16402	A	2518	398	1	ETFGK\SGGRSIVPGQFLAVGPKGRAVM ISAIEKQKLVIILNRDAAARLTISSPVE AHKASALVYHVGVGVDFENPMFACLEM DYEEADNGSTGEAAGNTQOTLTLYELDL GLNHVVRKYKEPLEEHNCI
2502	16403	A	2519	384	3	GGGID/SDASLVIAGVRLEDEGRYCEL INGIEDESVALTSLSEGEALPLPHSCV AAGPPRLGLPGLLPSISSAPLGTAPASP RPRRPSSPSAPIRWSPSPSPPPRCGVS VPTQPGPVVQLLRGVY
2503	16404	A	2520	1	426	GDRQMITALLRKLKQSRSESVENRPRIL LKALKELGDFYLELHWFQSWVPLLSRI LPDACKIYKQGINIRLDTTIDFTDMK CQRGDLSEIFNGDAAPSESVVLDNEPK VYQRLRHEES/QEKNRTQVDCLETP
2504	16405	A	2521	2	425	ALPIGRMPIMVRSSR\CVLTGKTAEFA KLNECPDPGGYFIVKGVKVLIEQEL SKNRIIVADRGAVGASVTSSTHEKKS RTNMAVKQGRFYLRHNTLSEDIPIVVIS KPMGVESAQEKIQTVPQEPPEWR
2505	16406	A	2522	2	376	IQSFSVVYGYHLCSQGISERVSASKFP LLFFFFFKKGGPPFMP/QGGKTGKPLKP GDPQSPGIKGFPCLPNKGKGGPPPP RGNFLGFKKKRFPQVGGGSKPPREGK PPPLAPQGGGNRGG
2506	16407	A	2523	403	3	GAPRSLSEKERQLMGMINQLSSFREQLL HAHYEQKLAASQIEKQRQHMKGKQ/Q QEQIARQQRLIQQHKINLLQQQIQVQ GHLPLMIPVFPDRQQLDALAQGGFLL PPGFSYKAGCSDPYVPVQVIPLY
2507	16408	A	2524	2	369	NARCLILRAAEYMAACVYVCISVFACMC FCVRVCVPVCVSGCLCVCSMNVHLSLC /VEQCACLWMCVSLHVCLYICACLCVSV CEAVCLHLESHCRGGRPPFPVVGPAFSL SSCLILAPPSVT
2508	16409	A	2525	59	380	RNRNFKNSFFFFFKKGPWGGGPGGK GPKQRQGE\NHWGQKNFPGQTRKPRKP TPGPPPPKKIFFFKPLEKKGPGQPGGG QKPGGQKKPPGGAPQKRKTGGET
2509	16410	A	2526	1	371	VMPLSRKHPKGGFFSNHTLVLHVARSEMD KERVQATRKSPP/CFVPLLPWPT
2510	16411	A	2527	445	3	RWLGLALIALKRELKKGDL\PEMRWWD SIIPNG\FDLTEETPKREDYFGIANLVE HPAQLNPPVDNDTPVTLGVTLKKEQKK LRRQTRREAQKELQEKVRLGLMPPPEPK VRISNLMRVLGTEAVQDPTKVEAHVRAQ MAKRQAHV
2511	16412	A	2528	1	478	RPTRPKRKLKSHRLQSRQESKKVRVL/T NAEDNEMEEETDDGPLLVPVKVAEDGS IILDEESLTVEVLRTKGPCVVEENDPIF ERGSTTYSSFRKNYYSKPWSNKETDMF FLAISMVGTDFSMIGQLFPHRARIEIKN KFKREVYASAIEDQATSVHT

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2512	16413	A	2529	385	1	QKKCEDLK\DQDNPIVRPPPTPGSCGHG GVVNISKPYVVQLNWRGFFYYLYGAWGRD YSPQHPNKGLYWVAPLNTDGRLLLEYRL CNTLDDFLLYINAREIRITYVQSGSIAV NYYNKYVSMYNTVNV
2513	16414	A	2530	1	1228	FRATLRPETMFGQTNCWVRPDMKYIGFE TVNGDIFICTQKAARNMSYQGFTKDNV VPVVKELMGEEILGASLSAPLTSYKVIY VLPMLTIKEDKGTGVVTSVPSDSPDDIA ALRDLKKKQALRAKYGIRDDMVLPFEPV PVIEIPGFGNLSAVTICDELKIQSQNDR EKLAEAKEKIYLGKFYEGIMLVDFKQ KVQDVKKTIQKKMIDAGDALIYM\EPEK QVMSRSSDECVALCDQWYLDYGEENWK KQTSQCLKNLETFCEETRRNFEATLGWL QEHACSRTYGLGTHLPWDEQWLIESLSD STIYMAFYTVAHLLQGGNLHGQAESPLG IRPQOMTKEVWG\YVFFKEAPFPKTQIA KEKLDQLKQEFEFWYPVDLRVSGKDLVP NHLSYLYNVHVMWPEQR
2514	16415	A	2531	335	2	KKKALFFIHPPPFVNGRPHKNPKIKSLG SPTPFSLIFLKKKFCFVNQDGVRLYFG SLQSLPSRFPFFCLNLLSSWEYRGLPP RPGKYFFPFIFFYFLVEM\GFTVLARMY
2515	16416	A	2532	3	380	AINSYIRGDDPSSYPEVVQSASRSSK\W SPLPRALHLTDAK
2516	16417	A	2533	3	2083	SSEGYLRGNMSENEEEISQQEGSGDYE VEEIPFGLEPQSPGFEPQSPFEFEPQSPR FEPESPGFESRSPGLVPPSPFAPRSPE SDSQSPFESQSPRYEPQSPGYEPRSPG YEPRSPGYESESRRYESQNTLKTQSP FEAQSSKFQEGAEMLLNPEEKSPLNISV GVHPLDSFTQGFGEQPTGDLPIGPPFEM PTGALLSTPQFEMLQNPGLTGALRGPG RRGGRARGGQGP RPNICIGKSFGRGS TLIQHQRIHTGEKPYKCEVCSKAFSQSS DLIKHQRTHTGERPYKPCRCGKAFADSS YLLRHQRTHSQGKPYKPCRCGKAFADSS YLLRHQRTHSHERPYSCTECGKCYQNS SLRSHQRVHTGQRPFSGICGKSFQSR ALIPHARSHAREKPFKCECGKRFQSS VLAIHARTHLPGRTYSCPCGKTFRNSS TLIQHQRSHTGERPYRCVCGKGFCSR TLLQHHRVH\SGERPYKCDGCKAFS\R ASDLIRHQRTH
2517	16418	A	2534	434	3	APLHSGKRSPTKCN\ECG\GAWNRSLL DRHKIIHSEENPNKCECGKAFKQASRL TIHKIIHAGEKPYKYEECGKVFSQSSHL TTQKILHSGENLYKCKEKGKACNLFNL TNHKRIHAGEKPYKCKEGRFANISSNL NKQECI
2518	16419	A	2535	46	454	PSTFSSKVMQKQTLCSQATSNTRYAA ALYRQGSYIPKEMKTCVHTKPYTVVHSS IFMIAKKWKQPRCPSA\DSWRNRMWSIH AMGCYLTMEKNEAVMLPRR\WLENIVL SERSH
2519	16420	A	2536	13	476	ALKTYKYSHKAFNPVKVYGKCSQKDPF PINHCLPTEKLHLCDKIGEGVFGKVFQT

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						TADHTPVAIKIIAIEGPDLVNGSHQKTF EEILPEIIISKELSLLSGEVCNRTGFI GLNSVHCVQGSYPPLLLKAWDHYNSTKG SANDRP/DFPKDDQLY
2520	16421	A	2537	162	296	YVCQRYKL\NFFLPSTYTKINCKWVTDIN VKPTSVKLLQEKRRKSL
2521	16422	A	2538	495	348	FGW\HAFIVKEPRVEKLCKASARAKPQP PAIIAKTFKAGGITGQYQAAL
2522	16423	A	2539	480	63	ARSEAWISTADAYMASPGDRIAQLLLLP YIKVGNSEIKRTGGFGSTDPTGKAAYWA SRVSENRPACKAIIQKQFEGLVDTGAD VSIIALNQW/PKNWPKLKAVTGLVSVGT ASEVYQSTVILHCLGPDNRDSTSHYSKT R
2523	16424	A	2540	2	509	NVDADDVRLAIQCRADQSFTSPPPRDFL LDIARQKNQTPPLIKPYAGPRLPPDRY CLTAPNYRLKSLIKKGPNOGRVLPRLSV GAVSSKPTTPTIATPQTVSPNKKVATPM SVTSQRFTVQIPPSQSTPVKVPATTA QNVLINPSMIGHKNILI/TNMVSSQNT A
2524	16425	A	2541	501	1	QWQVVEDPGGPRPREEASSYKCELREQ \LPQYVRDFFRKKAESGMDSSRNLEKL AERFLAKTCSTKDDQFKKDONVLSFVNC CHILLTQVKRESRAHTLSDIYLNIIIP RFVQVSEDSGSLFKKVQRYFFTEVRGWS NDTIFKILLDIMLITWVTQLSVHQTEPV
2525	16426	A	2542	473	287	EKDFNLPPKDLRL/KTSDV/TSTKENEF EDYCLKRELLMGICEMGWEKPSPIQVC
2526	16427	A	2543	268	482	KKKKAAGLQRGGKNFPAKALPTHGIQI NSCSVRL/VDIKKEKPFSLKVEGQAQA RTHLNRAFDIIVLTRGG
2527	16428	A	2544	407	1	CKKICYLIHYWWEYKMIQPLWKTVMQFL \KKLNILYDPAVILYDIYPEELY
2528	16429	A	2545	28	399	FRHSSFQRSGRGSQMLVHFLSL/SVMPK IGSVAGINYLVAAPPATTGETLDVQM/K GEADTENH
2529	16430	A	2546	2	365	FVVNVDEVGGEALGRLLVVPWTQRFYE SFGDLSTPDVAMGNHKKVKAHKKVLGAF SDGLALLDNLKGFSATLSELHCDKLHVD PENFRLLGNVLVCVLAHH/FDKEFAPP
2530	16431	A	2547	375	1	GFACRRMQRVREVSHAEESAASKKVR ANGSGKQNEGMNVTWTATLALSQAVISS ATYTQMOPHSLIQQQQIHLQQKQVVIQ QQIAIHHQQQFQHRQSLLHTATHLQGA \QKQKQQQHEWR
2531	16432	A	2548	3	376	ELGSDVA\GAEALVDRRQERKGEIDAHE DSFKSADESGQALLAAGQYASDEVREKL AVLSEERAALLELWELRRQQYEQCMDLQ LFFRDTEQVDNWMKSQEAFLNEDLGDA VDS/IKEILKKHE
2532	16433	A	2549	360	1	RGEMLWTV\NNRFLKNFVPGKIEPFKSH SLYPCCYVHDVSFWIDQKKGDFDEFHT VGRAVSQDTIISIQLSRFQHPKTQQVS LCYRLTCQTCDKALTQQQVASMRSQIRK EIQQHGY
2533	16434	A	2550	2	403	VVAERDTELRLDLLVQTLNLSGVNLRIKA ELRAGVFLALEEQEKVENKTPLVNESLK



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						KFLNTKD\LOGLEGRENLARDLGITAE CTVGGPPLLEVIIRRCQKKGPTTGEA LDLSDVHSPPKSPEGKTSAQTT
2534	16435	A	2551	1	409	VERNPTPLGGPGGPILRSREGGPPGLPR EPPSVLKKREPPTRGGRPPGFPLPRR RPEKWNPGGQTFPEPKLRPRG/HHPGG QTKNPFPPKKK
2535	16436	A	2552	256	1	HEMDGTLGFPFPPPGSSKGPSLTGPPIL FQSPGP/APHTPSSSPANLKT/CTPVCP SHLPW/CCPLCLPMRLPWSVPVPSKSS PPALY
2536	16437	A	2553	398	3	ARQQQLLQQQHKI/NWLQQQIQVQGL PELMI PVFPDQRPAAAAQQGFLLPFG FSYKAGCSDPYPVQMIFTTMAGAAAATP GLGPLQLQLYAAQLAAMQVSPGGKLP IPQGNLGAASPTSHTDKRCI
2537	16438	A	2554	20	517	DRPPSTKRRTDTPQLRGADLSRGPAPV PECPEH/SPRKTSACRPPLPLRPSHSS PLE/SPQPSHSTPQASCLPEALSPAP FRSPQSYLRAPSWPVVPEEHSSFAPDS SAFPATPRTEFPEAWGTDTPPATHRSS WPMRPSPD
2538	16439	A	2555	361	3	KSSQEALEALRQRLEELKKLCLEGE PGKLPVEYRLDPGEDPPIVRRRIGP\AF KLDEQKILPKGEEAELERLEREFQSQ ITEADRRLASDPNVSKLKKQRKTKYIN AVKKLQVY
2539	16440	A	2556	470	2	LKAAVTAGLEVPSDVSDRAFE\WLSAFP L\DSPYSIHHPRRIQVSSEKEAAPDAGA ERITADSDLAYSSKVLLSSPGLEELYR CCMLFVDDTAEPRETPEHPVKQIKFLLG RKKEEPVLVGGEWSPSLDGLGPQADEQV KVSNAIRCAQAQTGTV
2540	16441	A	2557	2	315	VVAEEDTELRDLLVQTLNENSGVLNRIKA ELRAAVFLALEEQEKENKTPLVNESLK KFLNTKDGMFSLFLFYI\EFNLDTI WEKSGISGLFFVFNCYRSSF
2541	16442	A	2558	372	3	CNISHFANKKCQDVIVAARNVMTSQIH HAV\KIIPGFNINVPGLPPPDETELEV QKVSNPQYHEVMNLELENTLDQHSYSLP TCRISEYVKLMELAYHSLLEAASSDQ CADQLFYSVRCI
2542	16443	A	2559	64	435	WGDASCTGRAQLGIAHKSVLPTLTDKFN TIPAKTPMSFFKEPKLTPKFT/WKNRT PRTVK
2543	16444	A	2560	113	375	VGPARDSTORRAVKNDKKELMSIPGIP GPVQVPGGLST\GMRGFPSSGLFTI PGGALIPFSPAFFSRVGGDLSPRNTGPG QKPG
2544	16445	A	2561	431	51	RKIYRVYERENFRVEIMFRSHTSKKVC KGNV/DVAKFIKLHRDGHVNLNVQCACH QKGGIYWFRSIHVELIGYPPPRSSHIK IGDKVRVKASVTTPKYKWSVTHQSVGV VKNIIWIKFLMLTFH
2545	16446	A	2562	1	455	PEGIALEVVTSTGKEREHTFQPGDNVE VCEGELINLQKILSDGNKITIMHKHE DLKDMLEFPAQELRKYFKMGDHSVVIAG RFEGDTGLIVRVEENFVILFSGLAMHGL

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						KVLPPPLQLCSETAS/SIN/VGGQHEW
2546	16447	A	2563	407	1	KWDHPLSKCEVPCGGSTISSNGPVSYPG FSPPY\TSSQDCVWMITVPSGHGVRNLN SLLQTEPSGDFIAIWDGEPQQTAPRLGVF LRSMVKKSVQSSSIQVLLKFHRDAATGG IFAIALSAYPNTKCPPTIHPCT
2547	16448	A	2564	382	1	TQEEVAVSLDRAPAFQSGCQSETLSQN SNSSNKTWILDHFGLSDFLDQRFSACTV FTPREQVSSHTRMFIAALFTIAKTWSQP /KYPPVIGWIKK\MWHLYTMEYYAAIKK DEFMSFAGTWMKLEAMY
2548	16449	A	2565	429	0	PLQSSCQTSCHQNC SRKTSLHFPDVL TPEQVGGSPAQVPIPYLDDDIPLLEVEQ EPVSLELGDVSLVSVREGLQPASITGS RGHLIVQLQELLHHWVLSAVKSRWVIV GLFVSLILSLVFAIRLR\SASRAPVLL RP
2549	16450	A	2566	464	1	VIHGVI\NPFVHGDQYKKKFPLK\FYQE IYESPFVTETGEYYKQEASNLLQESNCS QYMEKVLGRLKDEEIRCQKYLHPSSYTK VIHECHQRMVADHLQFLHAECHNIIRQE KKNDMANMPVLLRAVSKGLLHMIQEHVL RALGRIPTSYVRMQS
2550	16451	A	2567	3	178	YNPGGGVCSDLISSHCTPVWVT\SETLS QKKKKKKKKKNFLPETRERALPGKKKG GGG
2551	16452	A	2568	215	411	IHLIFIHLVFDYLSVRHSSKILGYISE QIRKRS/WLYVVAHTCNPSTLGGGGGQ ITRSGVQDQPG
2552	16453	A	2569	170	430	TSSQLAPQCLAV/VSGPLAACPELTSAT SPWLQVRTNAMASPLLKFSADLLFKAA LSQFCVIMLNKLSVQKYEK\LISAFSD SR
2553	16454	A	2570	3	463	CRFFGYSTAAAPMTPSSGGSTLSGITAP AVPNIPSPIGVNGFTGLPPQANGQPAAE AVFANGMHPYPAQSPTVADPLQAYAGV QQYAGPAAYPAAYGQISQAFPPQPPAMIP QQREWPEGCNLSIYHLPQEFGDS\ELM QMVLPPFGNVISSKV
2554	16455	A	2571	3	424	LKTMKGGTGNGLEIMLDIQDEYLPVWG ETGTSPTSGAPLHGSRPQP/PARGFLGF TVRPG
2555	16456	A	2572	1667	2046	YIFFFTAFLWAALTFQVTTTLAPLALLV RSKMMRASHDKPTANITLN\GKTGRAS KORREERNRQEVKLSLFTDDMFLYLESP IVLAPKLLLLINFSKVLAYKINVQKLLA VLYIKSSRESNEEHN
2556	16457	A	2573	1	399	FAISQDHPALPSRPPSLHHPKPGT\TFH PDLPHQATCSRPIRQRTWPEDAPLAKA DTVSPAETHPPAAATKAP/TR/PAPDKPG GTSDPQTGPAP\PASPPCSGP/APQVPV RKPSRAAPSKVSVTVPRRVPRTFPP
2557	16458	A	2574	2	452	AKVNEMKSPMRKGHTLLKNKEEKLNOLE SSLWEEASDEGSLGGSPTKKAVTFDLSD MDSLSESESSESFPPLDSTPSLTSRKI HGLSHSLRQISSQSSVLSILDSINPQS PTPLASMPAQLPP\RDPKSTPTP/SYC GRCRGFSLTS

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2558	16459	A	2575	2	369	TLVYPATITPILLSICICYWIVTAVFLTT SGVPVYKVIAPGGHCIEHNQTCDPETFN TPEIAKACPGALCNFAFYGEKSLYHQYI PTFFVYNLFVFLWLINFVIALGQCALA\ GAFATYYWA
2559	16460	A	2576	406	1	RQEGTGPSYLLLVGITPRSFWGFSPPLG PSGKNPIKTFGGPLQGFFFRVQMGVLLP LPGPSGN/CSIKVSALNSSPSPSGVNP EASLPWF/CFFEMESRSVAQAGVQWQPP PPGFKRFSCLSLGSGWYRRPPLV
2560	16461	A	2577	3	410	YISPFYITHMRAHTNLPGPF/KLNQRAD ALVSAAFADAQTFHSLTHLNAAGLRKRY GLSWKQVKEIVKHFSAGEVLHLPHQCAG VNPRGLSPNSIWQMDITHIPTFGKLSFV HVSVDIYSHFIWATYQTGEATAHVK
2561	16462	A	2578	386	1	TERIRQRQYQRETEKDKRYTERQRKTER IRESDRDRERQNIERDRRAT\RERDRE KQRESDRETYRERENQIETERDRKRQSD RDRETQRETGRIRYRERERQHQTESDRD RERESDRETQRHRECI
2562	16463	A	2579	2	432	LLYFAKRYGAAFGECCQAADKAACLLPK LDELDRDEGKASSAKQRLKASLQKFGER AFKAWAAARLSQRFPKA*FAEVSKLVTD LT*VHTECCHGDLLECADDRSDLAMYIC ENQDSNFSKLNCECKPLLEKFHCIAEV END
2563	16464	A	2580	3	426	NLLNDALAIREKTLGKDHPAGAATLNNL AVLYGKRKYKEAKPMSKRALEIRKKVL GKDHPDVKQLNNLALLCQNGKTEQGE YYYPRALHIYHTKLGPDDFNAANTKNDL VACYLKHGTVKQA*SLNKENLTSAREWD V
2564	16465	A	2581	10	389	KLAG*GLWGHTLITNPLTEPLTYPFLGL YL*SIITSSICLLQTDI*ALIAYSSII HIALVITAILIQTP*SFTGAVILIIAHG LTSSLLFCLTNSNYERTHSRIIILFQGL QTLRPLIAL**LLA
2565	16466	A	2582	1	192	LIPTLAIITR*GGQPERLNAGTYFLFYT LVGSLPLLIALIYTHNTLGSLNILLTL TAQELSNS*ANNLI*LAYTIAFIVKIPL YGLHL*LPKAHVEAPIAGSIVLAAVLLK LGGYGIIRLTLIILNPLTKHIAYPFLGLS L*GGQPERLNAGTYFLFYTLVGSPLLI ALIYTHNTLGSLNILLTLTAQELSNS
2566	16467	A	2583	2	438	QAHGPLAGCRLRPRSPSPVLWRRRRWW RQRRKWKTKTATAAAGMYASWTACRGL EELINLTRLNVSYNHIDDLGLIPLHGI KHKLRYIDLHSNRIDSIHLL*CMVGLH FLTNLILEKDGDNDPVCRLPGYRASIFQ TFAQL
2567	16468	A	2584	3	415	GRAILLLEEAIQYLSGIEIDLIDTDRGE WDSLTPQARR*KEAGLQMFVQLARFHN VCKEAFGTLAFLTSEIKSLFGHPFLAER IISMLNYFLQHLIGPKMGALVDFSEF DF*PQQHVSDSGAIYLDLGDEENFC
2568	16469	A	2585	2	453	DAKMYLSYKYATVIRNLRGTCPEAPSD ECKPEKRCALSHQRLKDEWSDISVGK IKCVSAETTEYCIA*IMNG*ADAMSLDG

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						GFVYISGKCGLMPVLAENYNKSDNCEDT PEAGYFAVAVVKKASADLTWDNLKGGKS CHTAVGRNAC
2569	16470	A	2586	3	413	MAVESRVTQEEIGKEP*KPIDR*KTCPL MLRVFTTNNGRHHRMDEYSR*NVPSSSEL QIYTWMDATLKELTSLVREVYP*ARKKG THFNFAIDFTDVKRPGYRVKEIGSTMSG RKGTTDDSMTLQSQKFQIGDYLDIAI
2570	16471	A	2587	1	798	LEVMLMLVKAGADQRAKNQDGMNALHFA TQSNHVRIVEYLIQDLHLKDLNQPDEKG RKPFLAAERGHVEMIEKLTFLNLHTSE KDKGGNTALHLAAKHGHS PAVQVLLAQW QDINEMNELNISSLQIATRNGHASLVNF LSENVDLHQAEPKESPLHLVDINNI TVVNSLLSAQHDIDILNQKQOTPLHVAA DRGNVELVETLLKAGCDLKAVDKQG*TA LAVASRSNHSVLVVDMLIKAERYAWREE HHESIRDPSTGFTL
2571	16472	A	2588	2	285	AWSIAPSHPHSKVPPGPRRGKAEGRPGA AAQAAEQAEVHPSSGSPLPARQPPVW QIPPTPSLKTTRRGAQPQHSRKRLA*S RSVSVLFRKM
2572	16473	A	2589	11	438	AYYGLNWHLGATLSQKKKKKKKKKNFP RGGGPPRNPFWGIGGRPGTGPPRGEKN GLKNQKKEKFLAPR*KKSTGKPLKPPQG KGWGGGPKFPKKKRPPRAGGSLKPKGK NREPFLLALKSLPGVFLGGFGGNPGMGLK NQ
2573	16474	A	2590	313	391	VHLVRVKLGL*SRIYKELLQLNNTT*DN PI*KWATDLDRHFSKYTQMVDRLMEKCS TS
2574	16475	A	2591	62	616	EVHQGTEVRDSEVRRRPQARGPLMPAER ACRQRWLVPALQPRRGGLRR*RGAVRQH GAHPHGLLLQDQKI PALPGRKQAGSLHA PGTEGEPDHGGDPVLDAGIQHHRQQRHP TADHLNPGEHRRGEAHVRAAV*PAAGAE GAAKERRAHQANTALQVHRR*LGSAEL RLLRKPGRTSVWPSPM
2575	16476	A	2592	345	438	HKRWLPVPILYQHLLF*VFGHPEVYILIL PGF
2576	16477	A	2593	479	313	QDGLDLLTS*STRFSLPKCWDYRREPPL KLINLQSSGVGLHVQLFPFSFCFDQLL
2577	16478	A	2594	3	419	LTLHSNTLPPPEMSGLT*PPATNAYWTF LPSAIRLFPFIFFIIVLLSVSLFDETER LSDAHSWRLTFKYERDANYHLLMSAQER LERLFGHLGGTIPIVPTADFHDSISGAS DTDIAHSGLAYTMERSARQIMRTAMKY
2578	16479	A	2595	1	419	HKCEGRYRGKTYGGYWSLCATVNKALDE RIPITSASYATVTLDHVRNIIIGSDTDV SMPLL*ERHRILNETGKFLVDKFGGSPFI NCVR*RDNIAHKLMLLVESFPSYRDVT LFEGN*VAFYTRAQILVTDGTGVLEGGK
2579	16480	A	2596	199	397	SPTALNTDDVNPFGSSSRGHHRRQFQTG IVSDHPAEAGPIS*DEQELPYAVLHFFHK VQPLEPKVTD
2580	16481	A	2597	154	3	MLSLRGFFCLFVCFETGS*YAAQAGLKL LGSGSPPISSFQSARITGVSHL
2581	16482	A	2598	425	223	QITGHGGKCL*SQLLGKFGQENFLNLGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RSFN*PKLLPGTSGWVTMLNSLGKKKKV TAYLNKWMPTP
2582	16483	A	2599	3	441	QGFSRDLVSELYQINAFDTPESLLMIGK DHSDPIHHTFDHMRWRTKEHNEAGWLLLR SVDKVMKENDELGDSISQLQKQILSLKY AKIALTERLISCPV*TEIVLNYT*SLIM LLTDLL*KVHAQSHHAHQASNCNVMT LIGLQH
2583	16484	A	2600	131	423	GPAPMVLFLHLTGFLLAFLPLSHLLTSY LVPWILSGTDGHTFRSACLPRWLEAEWI FGGVKYQYGGNQEGK*CFFTG*SYVYNG SSGKVPWETFSRT
2584	16485	A	2601	222	447	SGIPSFGL*VVEQNRPGRLNAQILKDLG VSPGSDYGLKNGISSGLDNGVTTSDHD VLKMAIVGRKIWILGDWSG
2585	16486	A	2602	2	457	FICDPLIKAIGTEGDTDLVSEIMNSFAK STIEVMGDGCLNDEHLEELGGILKAKLEG HFKNQELRQVKRQEDNYDQQVEMSLQDE DECDVYILTKVSDILHSLESTYKEQILP WFEQLLPLIVNLICSSRPWPY*QWGLCI FDDIVKHCSFSL
2586	16487	A	2603	1	297	DHRQKLYAHTCEGKALLWKSVCVHQKI LEEEKPCEGTKYDNI FSNRGCPVPRMV HAVEIPCK*TECEKATGVHGRGASEFL PERPTGMNMAKCESR
2587	16488	A	2604	1	405	RFDVSDGLELRPKYNGIAHRLTTIWL GLRGLYKGVTPIIWSAGLSWGLYFVFN AIKSYITEGSSERLKASEYLASTAEFGP MTLCITNPLWVTKTGLMLQYDAVNSPH *QYKGMSDLVVKIYKHGGVQGLY
2588	16489	A	2605	165	3	PEELLLVFFPVLKNTGIRPGAVAHTCNP STLGGRIITRGD*DHPGQHGETLSL
2589	16490	A	2606	3	455	KRYGCFSKRMNKR SATNVFFCARKEVL GLLGHNAGKSSSIKVITGDT*PTAGQV LLKSGSGWDALEFLGYCPHENALWPNLT VRQHL*VYAAVKGLRKGDAEVATR LVD ALKLHDQLNSPVKTLSQLKIKLGFCLS ILGKPCGILA
2590	16491	A	2607	1	429	VDYTVRKFCIQQEGDMTRNRPQRLITQF HFTSWPDLGVPIPIGMLKILQKEKACN PQYAGAIVDHCKA*VGRGTGTFGDIEAML DMMHT*RKVDVNGFESNRNRAQSCQKVQT DMQYVFIYQALLEHYLYGDTELEVTCLE TPW
2591	16492	A	2608	166	435	KFLSNNYVHFQNFKKVLKFIKHLVLNY FKNIVLGQV*RATPGIPALWEAETGESL EPRSSRPTWAMWRNSISTKNAQIKNIVL RILDPG
2592	16493	A	2609	228	431	IFSKICIFNGFNYPFIVGHIGRIYLFIE TGSHCVTQAGVQWCDYGSQLP*TPGLK* SSHLRLPSSWDH
2593	16494	A	2610	439	175	RNGGLHLWSQLLRRLRWYHFSFGSQGC SKS*SYHCTPAWVTQGDSSLKKQKRKIS TYTSLSVLNETVYIIIVYTKKLDTSFK RKKL
2594	16495	A	2611	1	439	LLGSILSSMQKPRGLVDQETLRKAR*QA ARLNKLQEHKQKQVEFRIRMEKEVSHV V*DSGHITT*VQSMNSIERSILHEVVEV

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						DGLTSFYFGEDDDCRYGMIFTKDAAPSD EELDSYRRAEEDWPHMADDKRKLTELAQ RPDDDA
2595	16496	A	2612	1	439	VIRKVTGTGESSSTVLDTIPSSSTGMP VRKSEDQTDTKRTVIKTMEDYNNNDTAP AEDVIIIMIQVPQSIWDQDDFESEDQDDK STQPISSVGKPATVIKNVRTKPSAIVKY PEKESEPFKILKFTMDVSHEVIPHEVK SS*YSA
2596	16497	A	2613	2	453	EKPEKEECNLWTEMWQENVPGSFGGIRL YLQELMTITQKALHSQPWKMKQAQAIAM ASMALQTNLSLPPYLGMLTALVEGLAG RTWALKEELLKAIACVETARSael*KSV PNQPSTHEI IQADLKECKENGPKYI*P VICAADILHA
2597	16498	A	2614	2	441	LEPALPGRWGCRSAESPSPSGSVRKTRQN KQKTPGNGDGGSTS*APQPPRKKRARAD PTVESEEAFFKNIMEVKVKIPEELKPWLD EDWDLVTRQQLFQLPAKKNVDAIL*EY ANCKKSHGNVDNTEYAVNEDVAGIKEYF NEMLGT
2598	16499	A	2615	1	430	RGDRDLHCTESQSEASTEEGHDSLSVGI FEEDSQLEFILDPPKSKPPAWLNGIMTC *DFELLNPRRVRFLLEVKDLALTRRQIL LHKGLSDYEKSTTLQELVLKSSRSRSGPP LSIEDLGLNFQL*PSSRVYGFTAELKLP SGE
2599	16500	A	2616	373	552	ICKIKYKLFNSALLFFROGLALLPRMEC SGAIKVHCSLDPLGSSNPL*RKIKESTL NLEKSLCTRGIPLCKYEEVPKQFLKICF QIFLETGSRSVSQAEVQWHDQNSLQPR PGLKSFSCNLNLPKCWDYRCEPPRRALCS
2600	16501	A	2617	498	157	QLIGSSTHQALRSRLPPPAGPGTFHF HYQGKAWVVKGGTSPDSLPSLLGRGVSV QLHPRGKEQRGASDT*HKCPVKLWTIGG KYRVSETSRIFSLPPTLQRLAGLDSGSG SL
2601	16502	A	2618	255	389	LSEFYTYEGPSIRPPIGS*GTNLPLPLS YIPRSPSAVDENLLDE
2602	16503	A	2619	3	207	QHSSLIIRATAIKLGIAPFHF*VP*VA QGTPLTSGLLLLT*HKLAPISIIYQISP SLNVSLLLSGT
2603	16504	A	2620	3	207	QYSSLIIMGVGIRKLGIAFHF*VPEVA QGTPLTSGLLLYT*QTLTPISMIYQISA SLNVSLLLSGT
2604	16505	A	2621	45	447	WRRIDCRNLNLCVTTASLKHFFSIAHKFH LHNGSHLQSQHSCEAQLRRTARFIICCL PYGESGQSWPTLTLEARNLNLTVYFNN WKDWEYDSQYMSNFRSSEMNIIVW* RSIDNLPHIICSTLINTKNSFL
2605	16506	A	2622	3	142	GNQATPKTAPATMSTPTILVATAVHAYR **VAEKEHPLKFGGRACS
2606	16507	A	2623	2	453	HGPGGLLDYIDKERIRDFLNGECMCEVP DGGLVPKSLYRTA*DENEDLKLWTDTI YQSASVFKGAPHEILIQIVDASTVITWD YHVCKGDIVFNIYHSKRSPLPPNKDYLI AHSITFPDGNNVHLNNKVWMLGPDYIMW ITTLITNNEN

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2607	16508	A	2624	1	315	EEKQAPGFTTGRGKLTPLFCAHAVRFIT STSLIYKGAYP*ALKGKEY*LAVFWVY NKKGLNNNNLFLDGVHLCFVPEVRKYLA GKGLPFSLGLYHLILLLLEFFF
2608	16509	A	2625	232	478	LDCGNYFTV*MYIKTSHCTP*IIYIILNF HLYNFRYNLGDYNGEIVSEVMAQRQPMK PTYAIPPIIPITNSSQFKHQEAMDVKE
2609	16510	A	2626	3	430	TSTPNVHMGSTSLPGDSTTIEDAIQSHS ESASPSALSSHPNNLSPTGWSQPKTPVP AQRERAPVSGTDPDRDKLRPCGQRD*GY WEIEASEVMLATRIVSGSFGTVYQGWK GDVALAILQVVDSTPEQFQGFNDVAGL RI
2610	16511	A	2627	2	341	ALQKHEDTDCPCVVVSCPHKCSVQTLR SE*SAHLSERVIA PSTCSFKRYGCVFKG TYQQIKAHEASFVVQHVNLKKEWSNLK KKGSSFDKECVDKNKSIHCWHIQCSSV I
2611	16512	A	2628	2	179	RHTGLWVTS LPAVFPQVRRTLFITGLP RDARKETVESHFRAHWLVGDFSPCCIS RTGEADPVHHRTPQRCQEGDCGEPLFVS RWVGSFLIH YIQEHCL
2612	16513	A	2629	1	418	GFSFCHPVPVKWRHRDSPQD*TPGLK*S CLGLPKCWDYRHEPLRPANISY
2613	16514	A	2630	3	442	FTCGTIIIAIPNGVKEPT*LATLHGSNM K*SAAVL*ALGYIFLFTVGGLTGIVLSN SSLDIVLHDTYYMVAHFHYALSIRAVFA IEGFIH*FPLFSGYTLHQAYA*IHFTI IFIGVNLTLFPQHFGVGLFGMPRQYSDYP DAYTTR
2614	16515	A	2631	2	454	AAPMELICWSSGGWGLPSVDLDSLAVLTY ARFTGAPLKVKHIIINPW*SPSGTLPALR TSHGEVISVPHKIIITHLLKEKYNADYDL SARQGADTLAFMSLLEKLLPGLVHTFW IDTKNYLEVTRKWYAEAMPFSLNFFLPG RMQRQYM*RLP
2615	16516	A	2632	131	410	WMWSSKAPHCFRLPSIGDADTVHQCAM FQKGHSALEGVHLVFKPDLVYQTLQ PPRKCCWPGAVTHACNSMTLGGRSR*F TRSGVQDQP
2616	16517	A	2633	2	230	FFSETSSLEIQGIARHGGTWRRLRQENN LNPGGGGCSELRSCSCAPAWVTVRDLR KKRNRNP*KILKNYLKIFVI
2617	16518	A	2634	2	370	GTSSSDPAQPGDDKEFIDASRLVYDGI DIRKAVLMIRTPPEELDDSDFETEDFV RRTSVQTEDDQLIAGQSARAIMAQLPQE QKAKIAEQVASFQEE*SKLDAEVSQWDD SGNDIIVLAKQ
2618	16519	A	2635	2	376	MTDTDALY*RELFDPADKDKMDHSRRGI ALVFNHERFFWHLSPERRCTCSDRDNL TRRFSDLGFEGKCFNDLKAELLKIHE VSTVIHSDADCFCVFLSHGERNH YAY DAKIEIQTLTALF
2619	16520	A	2636	1	461	DMAFLILTERKILGYGQGRIGPNVACP GLLQPFDAI*LFTKEPLKPVSTITLY ITAPTLALTIALLL*TPLPINPLGNLN LGLLFILATSSLA VYSIL*SR*ASNSNY ALIGALRAVAQTISYEVTLTIIILSTLL

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2620	16521	A	2637	2	384	IKGSFNLRSLITT ENFKALAMIAFGQYRQKRPFDHVHKLAN D*LNFATKCVADESAENCDKSLHTLFGD KLFPIATLRETYLELADCCAKQ*PDIEH CFLQLKYDNPYLPRLVKPNVDVMCTAFH DTEETFLK*YLYEIA
2621	16522	A	2638	1	373	TFIYLLFLFSSAYSRGVFRDAHKSEVA HRFKDLGDENFKALVLI AFAQYLQQCP EDHVKLANEVTEFAKTCVADESPEN*DK SLYTLFGDKLCTVATLRETYGEMADCCA KQEPDRNECFLQ
2622	16523	A	2639	2	375	KGPCYRLVSTGTQRRHPGAVYLNKHLK* CNVGKA*GPHCEKCTLPCTFNEEPLKAL TFFREHGP*VSDPEVATAPTEKEIPSLD QETTKLEPGQQLSPGISTIHLPQFPV VIEKTSPPVPVEI
2623	16524	A	2640	215	478	KYFLASHTSLFII CYTAHLTCTIAEPKQ IESHFGKRLDADLVF*KSDDSTVVDVIP SKPV*TSGLFSGKCL*HIVEGIIRAVDP RKLY
2624	16525	A	2641	208	376	ILRNLIKHFHFWPGVVAHACDPNTLEAM* GQITRSRDWDHPDRHGEAPSVLRIHRLA
2625	16526	A	2642	424	2	KGEPLPPLGGWKT*GPRAFPQAQIPHAG FKTRGCPFPLPQGRNKAQVPNPFPRER FLPGKSGRVPAPLKNAGLGGPPFYPHP FGGPSRPVPLGFGVQTHLGNKPKPPFP KKKKGGTGC SVGNWGP KSSQTLPS PQAS
2626	16527	A	2643	190	3	ELSTRGFQGP HRR IAGLQCLVMFP ELE RSGGLSEH*HLHLP GSSDSRASAS* IAG ITSVCH
2627	16528	A	2644	2	339	CCEKPLLEKSHCIAEVENDEMPADLPSL AADFVESKDVRRNYAEAKDVFLGMFLYE YARRHPDYSVLLRLAKTY*TTLEKCC AAADPHECYAKEFHEFKPLVEEPQNLIK
2628	16529	A	2645	81	369	VEVTGQPQNASFVKRNRLWLLPLIAALA SGSFVVRTPDG*TSVVR* IHNHMTQLI NNHLRA*YSVYRDIYFLWIAI**SS*PA SVLLFTADYCPE
2629	16530	A	2646	1	348	DMDMNPLRPQNYRFG*ELKADIDYHFKE DNEDDHQLSLRTVSLWAGAKDD*HIVE SEAMNYEGCPIKVTTLATLKMSVQATVTL GGFEITPPGDLRMKCGSGPVHIMGLHLV AGEE
2630	16531	A	2647	1	178	GYTDTILDVRSQRVRSLLGLSNSEPNGS VETKNL*QILNGGESPKQKGQEI KRYDL YLT
2631	16532	A	2648	181	244	TIKRYKNVMIFYFNF*F*RLNSLAQA AAQWCNHSGLNQPPGLKGSSCLSLPCS *GYTIFYLSIHQLIDIWVSTFSLFLH VSAYSSIKMS
2632	16533	A	2649	2	369	KWITFISLLFLFRSVYGFKEFLLDAPKN DVAHRFIDFGEQHFKA LAEIAFDHYFLH CPFEDLVTLVNE*TEFA*TC LADESA*N CDKSLHTLFGDKLCTVATLR*TYGEMAD CCAKLEPERI
2633	16534	A	2650	1	349	VTFISLLFLFSSGYSRGVFRDLDAHKSEV AHRFKDLGEENFKALVLI AFAHYLQQCP FEDHVKL VNEVTEFA*TCVADESAENCD



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						RSLHTLFGDTLCTVATLRETYGETADCCAKQD
2634	16535	A	2651	21	403	CVCCVCVRESRTESLPGDNEDFNVKNASVKDVRCVHFDCDSQNDPPMEATGFTAQV TIYSLINLLHRLKYFETLDLH*IAIFFS KVSILNHPGQIADYAPALDCHTCHAC KYAELKEMIDRRSVK
2635	16536	A	2652	1	355	ARMSITDTYGQHLIAGGLMTQEDVSEIK SSYYAKSNDHLNNMAHYRPTALNLQAHW HGLAQAEAQITTWSSGVFPDLLLMVGMM TVQVP*ELQMHSLLKTHDQSRMENMMY GIKLDW
2636	16537	A	2653	2	360	LFEHLG*YKFNALLRLRYTMKVPQVLTP TLVKVSRNL*KVGIKCKHPEAKRMPCA QDYL SVVLNQLCVLHEKTPVSDRVAKCC TESLVNRRPCFSALEVDETYVPKEFNAE TFTFHAD
2637	16538	A	2654	360	314	YTCAIVPCKLFWWCCRDRVSLCCLYWSQ TPELK*SSCLSFPPKC*NYGHEHTWPARI IFLNLYNKSG*TATRKCPPTKVTPSSHQ Q*HCTWPFYFK
2638	16539	A	2655	1	353	NWTL*TLKKIFSLKDAIKRIKIQSVRWK KIFAKHTSDKGVESKYI*RTLINQ*ENN SIKNWSKNLNRFTKDIQKANKHMLSAT SLVH*ESKLK*Q*YHYTSIRVAKMKKTD YVTSW
2639	16540	A	2656	340	10	GREDKSEKCYLKPGRSQPDGAPKSSPG VP*PPAPPALPGPGRSSPFPQGSAGKD LRPRQPSQPGGPGELIFPVKTKKKKIKE RKTLLAWTRSNERPEIAGREGGCLRQ
2640	16541	A	2657	509	261	IPYFKIHCLHSALGVAETEKETAELDL AGASSRPKDSQRNSPFPQIPPPSPDSKKK SRGIMKLF GK*VKQ*TSGMGPVLHVA
2641	16542	A	2658	345	3	SAHLSHPKCDYRREPLHLARISFLKA SSPLYGRATFYLPSTPPLMDGRWVASIFW LL*IVLP*AWVYKYLSETPLSIF*KTGS LSVAQAAVQWHNHGSLQPQTPLKRSSH L
2642	16543	A	2659	271	56	VILYIVMPIPRPCPHPHYIHTHTHTHT HTHTHTRLGKREF*LYSW*LPGYSTNGN KIFLEIYLLPILLKM
2643	16544	A	2660	366	68	PGQOSKIMPQTERKKGRKEEREEREKE EREGRKEGRKNEGTEETVIEGGSSKTQEQ TRIKAS*LNSLYTTVKPQRRLKGGKKHP KDSNFKD*RNISPHR
2644	16545	A	2661	351	199	LLRRLRQENLLNPEGRGFSEPRSHYSP DWATE*DFWSNKKIK*QKVQYSKY
2645	16546	A	2662	1	160	ERAWLHLSPGDGVCEPRSHHCTPTWVT E*DSVANQPGWDRVRLCLKPTWVTE
2646	16547	A	2663	233	3	GRDNWLKTVAKPESLSGRGPSLLRKVF NPFPVYILFLPQAPKGNLSPFPFPFFF FFFLRGSLAM*PGCSAVAQS
2647	16548	A	2664	96	349	QMPSSVLTRVANAYYSGFFFWFLKQKFC FVTQAEVQGRSIS*PGLVPGFKRFLGL TLLSTWNCRRAPPGLVIACGFKMSLLTL
2648	16549	A	2665	322	74	DTYTLPRLNQVESLNRPTIGSEIEA INRPPTKKSPPDRFKAKFYQRYKEELVSF LLKLFQ*IEKGGIGWARWMLPVI PVL

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2649	16550	A	2666	2	228	NLALSPRLECKSQGFTMLIRLVSVS*PC DLPASASQSAGIMGVSHHAQPFLLHSYLR PLILIKGDQFKYAFNLFSC
2650	16551	A	2667	129	301	VRPLAGLGSPLIFFFFFEKSLAFVAQAG GQRHNLG*LLPLPPGLKGFSCNLNPSTW D
2651	16552	A	2668	318	21	FSLLVKDFQNDLAVNSSSIFPSTFLFLV RS*LDFVNLNFFNFYLFDFEFLCCPGW TRIPRLKQSSRLRLSSWGKYKCVPLHPA INRFL*CDFISISGY
2652	16553	A	2669	2	322	QDGLDLLTS*STRGLPKCWDYRREPPR PAPINKCLLSIYHGPGPSLGTEGEKQD YIPAIEQLTDQWRRLTWGTCYCAVAED SMGVVWPLLPGYEAEKEAGRFH
2653	16554	A	2670	29	261	EFNTLSKCVWIY*LFSLSLSLCVCVC VCVCVCVCLCVSVCLFYGSPICLHFHMP DTLSEESFHFLQIISKELLKC
2654	16555	A	2671	5	224	GSAWWLTPVIPALWECKAGRSPEVGSRLR PA*PRDPPALASESAGITGVKKNLIAEL WEVKSCILLIFISLDKV
2655	16556	A	2672	126	321	WGRRGARARRDSHRALRVSPELALLELR PSTMAHICNPALGGRGGWIT*DQEFET NLANLEKPC
2656	16557	A	2673	360	74	SRLRLKLRQEVGLNLGGRGCSGPRLLHHC TLAWATERDPDSKNKTNQKNKQRR**TL PETNSLLAWEPDCVCKTNKLATRLA QKSCSQRPQYH
2657	16558	A	2674	192	357	RIRKWLYYYYYLLRWSLALSPRLECRG TILAQC�FHL*SSSRSPASAPVAGIT
2658	16559	A	2675	236	375	EEVLYSRKDRHVASYSRK*W*RSGBAAH ACNPSTLGGRGGWITRSG
2659	16560	A	2676	236	2	ATKVSINSIGTLGVKVGGLLEGRRRLRPG PKQSSCLGLQSSWDHR*VQPHGNNFTL FVETRSMRLARLVSNWPQAIFQ
2660	16561	A	2677	164	389	LTVQHGLRLRLKLTVMVSEGGQASHLLH KAAGRRESECQGNQCMLIKSSYQPCAEA HACNPSTVGG*GERITRSG
2661	16562	A	2678	208	1	CSVYEGSCFCILRVRRVCVCVCVCVCVC VCARSCIYVRSENH*KQLPSSSILT*RF *IQSTFRSNKRLR
2662	16563	A	2679	159	382	RWLKHNPTQARIQVRGLLDRDCQTQTW LWESGVQPLATTPRRHSEMGWPGAVAH ACNPSTLGGRGG*ITPPRPESKLEDCLT GTARHRLGCGSQGCSLWLPPIPGGIQKWG VGRAQWLTPVIPALWVAEAGRSLEVR
2663	16564	A	2680	29	367	DCQSEQLRKLRLWEHHSQGV*GCSQP*S HHWTPAWVTEQDPVQNKQTKNYNTHQRA GEVWREINCLSTEQLTELYSEITQILAL SVRN*KLL*YVKSSVISAETQISGGKIF
2664	16565	A	2681	256	1	ENIVPVRFLCIHRFLFALIMVQ*LKRKR DHIVIHNLTLTETVYLKKWQTRPNAVAH ACNPSTLGCGRRITRSRARDYPGQHGE T
2665	16566	A	2682	1	395	LLIEHILIAMALLILTERKILGCTQLRK GPNVVGPPYGLLRPFDAIKLFAREPLQP VTSTITLYMTAPTAVTMAVLL*TPLRI PNPLVNHDGLLCLLATSSSLADY*IL*S R*ASHSNYALIGALRACPH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2666	16567	A	2683	3	349	VRIDNAAVCLLY*AWAEFIWALANLITR PDLDPGNLGNLNDHIYNVIVTAHAFV FFIGIPIIYGGFGN*LVPLIIGAPDMAF ARITNIRF*LLPPSLLLLLASAIVEAGA AGT
2667	16568	A	2684	99	2	LTVAHACNPSTLGGQSG*ITRSGVREQP GQHG
2668	16569	A	2685	325	4	SSFPMSEFIINSFIIIFLYTTIFLIFYDV VYSPEFKP*VCFCLTECDYRREFQCSF LPCKRV*VLAPFIKNFFFFFLRWNF FVAQAGVQWRHLGSLQPPPPNF
2669	16570	A	2686	382	269	MGFHHVAQADLELLGTNDPPALASQSAG ITGVSHHAQPKLTF*TFSY*ACVGGSSP QFILVVQHGLAGNSFCCF
2670	16571	A	2687	3	381	GHLIALTFEFSQICLFPRITYKTCKKSF WLPFLNLVSLCAIEGYKTKKVPNSV*KG IFIHHQTGFILRMQGWLN*TSINGIYH ISRIEDKNHKTMFIDAEKWFHNI*HPFI IENIRPGVVAHICN
2671	16572	A	2688	289	91	IKYKELGVACSKTSRNVSYCYHHHHHH RCHHYHHHS*RLAALCEESGWRKALGST SMGRVAFHRH
2672	16573	A	2689	3	211	LHHVGQDGLDLLTL*SAPLGLPKCWDYR TEPPFPAPNEFLLHSLSKHYALGRPH TPRRKKASGILR
2673	16574	A	2690	2	197	DLLTS*SAHFGLEPCWDYRREPPRPASY AFIKYFCPALSCFWCIETGPYLIFAYLR EESFVRSRT
2674	16575	A	2691	253	356	AVPVKMAIVKKTRNNRCW*GCGEIGTFL HCWVEC
2675	16576	A	2692	211	339	PGHPLSII LQWIWGEDTRRGPMHEALH* PCCSELRSCHCTPAWTE*NSIF*KKKK KWLGELEKEQKNMACANDP*PGHPLSII LQWIWGEDTRRGPMHEALHGKSGDGVYA VRLLTAY
2676	16577	A	2693	1	175	RHEGLNLGGRGCGEPSSCHCTPAWTE* DSVSKKKRKGKKKSALILIFSNGLVFC LG
2677	16578	A	2694	234	13	KTSREPWFSEFLSIKGEQQCSFGLLYVFC FQMESHYAAQAGV*WCNLG*LQPPPTGF KQFSCLSLSPSSPASAS
2678	16579	A	2695	149	2	SQGEDFTKTRALQWRRRSVVAHACNPS TLGGRGWIT*GQEFKTSIAN
2679	16580	A	2696	2	194	CIGLGVVAGACSSRLRQENDMNLGGGAC SETRSHHCTPAWTE*DSISKKRKRNR WGGTRFSN
2680	16581	A	2697	338	357	YLIRKKISNSKS*FSWPGVVAYACNPS TLGGRGRRTTRSAVRNQPGQHGDPKFFL VSS
2681	16582	A	2698	53	293	TISIKSKWKKNQGEYNKWCMENWLAIC RRLKLCPIVLVHSCIAIKNYLRLGNL*R KEV*LAHSSTGCTGNMAEKPHGRR
2682	16583	A	2699	2	335	LYAAKVPLQKACIRTFYSYISFFIFFFFF FFGKQSSFPGPLKARGGTPLIGTPPLG VKRNFLPQFSGKPGITGCPPLQKFWFF KKKRGLIF*PGGVPNSDPKGIGPPNPP
2683	16584	A	2700	166	3	DYRRVPPRLVKR*GFTVV*AGV*WRNHG SLQTQTIGLKQSSHLSLATCWDYRYE

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2684	16585	A	2701	209	340	YRMTVFPPARHGGSHTCNPSTLGGRGGWM T*CHEIETTTLGNMVKP
2685	16586	A	2702	78	341	EVACNCLLPAGCFASVTYV*SSVLL*F EL*VLNENSS*NFIIH*FF*NRVLICCP DWSVMA*S*FTEALTSQITRSSHVSLS PS SWDY
2686	16587	A	2703	258	185	TMIAPVHSSSLGDRARPYLFKQKR*GLAL SPRLEWTGAIIVHRNLEFLCSSNPPTS A SGVTGITEMEVEVERHGWIQETFWK
2687	16588	A	2704	361	41	NFGPVYKTNPGPSRPGWGLGKPPGPQK FFFPGVPPSPFPKKGVSFSPGGGQGP FKGVFWGFP*PRGKKTPTQQPGSPKVP NWDFPKGGFPKKKKKKRILRN
2688	16589	A	2705	12	329	SCTQLTTPRLK*SSRPSLPNN*DYRHV PPHPASFP*FSEMF*DSQIFLNSLKFS S*YLLVIFFFKMEPCSIQDGVQWCDLS SLQPLPPRFKRFSCLSLPSTRP
2689	16590	A	2706	232	1	KRKRKSFKTYKKFFLNSSFKNQCPYAI GHIFRSIIFFFLRQSFGLVA*AGVQWQ DLGSPQPPPPGFKPFSHLRLR
2690	16591	A	2707	135	1	CFFLIFFFFSSDTQAGV*WPQPPGIKRS SQLSSPRSWDYRRISPR
2691	16592	A	2708	1	157	LDLLTS*SARLHHPKCWDYRREPPRAD KYFLKEVASLIVKLYLPCKLNFE
2692	16593	A	2709	88	344	MQEHYYFIKRGNKMIIRKYVQLHANKLD SLDKIDKFQVKNHQN*L*KK*KSWPGAV AHACNPSTLGGRGGWITKS*DRDHPWLTC
2693	16594	A	2710	1	383	LHKVTTVLRFLSKFHILVLYFYTCVHV SVSDMWCWFLY*IFTDMYNAVFQ*LDEF KLSIKFLRCIC*CVY*IFIPVFIYCPFL YLICLFLSYFLFNIVMLLFYILCIYF YVIFSSSSIF
2694	16595	A	2711	227	1	IFFFSNSFLKISLGFFLNFAFF*KPKEFP PFLSFKINQNFFFGFPFNFLKIFKFFP NKFFKF*IYLTFFKKT KPK
2695	16596	A	2712	1	136	KNTKISQGWPTPVIPATQPEAGGSLE RGRQLQ*RNLGSLQPLPPTFKRSSCLR LLSSWDYRRRPPPLANFCIF
2696	16597	A	2713	3	349	LIPRGQGSTVVLPPYNPATSI FGNDLNEI KMYGHAKTCIWMFMTSSFIIDRTRKQ* CSSVREWINKQ*CIQTMELVFGRNFFFF FFFFFFFF FFGPPPKIQIFKEI NPQ
2697	16598	A	2714	181	342	TSQLNLPLPIIKA*AIROEKEIKGIQL GKREVKLFLFAHDTIVYP
2698	16599	A	2715	3	205	FRHVAQAGLELLSASSLPTLASRSAGIT GVSHCVQP*TVSSLRLGFYDTSFKIADI QSCFSWVLYYCLQSAEL
2699	16600	A	2716	388	23	ASNQSKNSFEKGEKNQQSVMKTSQQAL NKRAFFDMIRSVYQKTYK*RNA**ERQS FSLKVENKKEYPSLLLENIVLKVLVNT GHKEK*KAHRFDRNIIQFANDMIVYVEN PKDSTKRLS
2700	16601	A	2717	4	194	FSCLSLSSWDYRSMPPHPANFLYF**R RGFTMLARLVLSWPHSAGITGVSHHAQ PFNYFFI
2701	16602	A	2718	1	212	LCCPGWETARLKRSSRLSLPKCWDYRH

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						ESLHLAFGFLL*YFGPYLMVYVFSFNL YDFSLVSLYGTSTI
2702	16603	A	2719	53	299	KAVHVNIFFITKVHLMETQIVSLSLFP FPSFLHPSLSLSSFL*RDRVLLCYPG*S AVVQS*FTWPQIPGLR*ASCISLVSS
2703	16604	A	2720	139	320	QPTMRHSFSF*KQEISIFLKVSSSLHHT LRFLFFFFLLDRVSLCHPGWSTVALS*L TVAW
2704	16605	A	2721	1	99	IIILAYSSITHIG*IIAVLPYNPNITILN LTIYM
2705	16606	A	2722	215	361	LTFFFFFERRSNFVTQAEHQGGNLV*L KPRPPGLKHFFYYLSLQSTGNY
2706	16607	A	2723	335	24	AIPLRPEF*THPGQNGTRFPLKPNLT GVGGNARYSQFPKRLRLKIPLNPEVGPS INPNFHPGIPFWAQENFFPKKKKKKEI IMLNFSLICYNLFFLYICY
2707	16608	A	2724	27	314	WKQLKYPSPSEWINKMNCIHAMEYLAIK RNKVQLCVT*RWRWLMDDTKKK
2708	16609	A	2726	1	112	GFHHVSQDGLNLLTL*STHLSLPKCWDY RHEPLCQAR
2709	16610	A	2727	271	3	RSPMLKNQAIKSVIMVYIGTIWRSAGPF AIFFFIAEYTNIIIIITLTITIFLGTTYD ALSHELYTTYFVTKAVLLTSLFL*IRTA YPRFR
2710	16611	A	2728	121	1	ENKYRPGAVAQAYIPNTLGG*GGWIT*G REFETSLTNVEK
2711	16612	A	2729	2	290	NRHFTKENIQMPTRHKKRDPQSSLVIRE MQTKTKVRYFFILTRMAKVKKIDNTTC* *GYEKLNSPKLQTTKCPFEWVNKLWHS QIVEYFSGIQHA
2712	16613	A	2730	98	264	LVSSE***IYQILFFFPMECHSVSQVV VRGSNLC*LHPLPPDFKRFSCFSYWEQ
2713	16614	A	2731	2	286	PFIKATVIRTVWYW*KN*QIDQWRKES PEIDLHK*SLLI FAKGAKAIQWRKDSLF NKWC*NRWISTCKNESMLGVVAHTCNPS TSGGQGGRIA
2714	16615	A	2732	323	181	RDFVLLVEITMLARLVNS*PCDLPAASA AQSAIGTVSHRAPFLDL
2715	16616	A	2733	272	131	GRVDRNLNPGGGGCS*LGSCQCTPAWVKE TPSQKKKNKIICFYAFLFI
2716	16617	A	2734	227	87	AASTLTLSLIPPIITLVNPNKNSYP HYVKSIVASTFIISLFPPTIFMCLDQEV IISN*H*ATMDFT
2717	16618	A	2736	25	415	FSKYLLDHQLSAGLLVEQHRGSLCPLSL LHSDSSLSFAVSGKVS LAASIRNKLELP ET*RALMM*NHGHPLFEGGM*PWT*EP GS*RC*ELGQPGQARRLACNPSTLGGRG CWIMRSQVRDQPGQDVET
2718	16619	A	2737	390	1	KGFFLETKRKFFFTNGFFPFLGGKGVFP PGKRLGPPILGFYPPQRFVFPFKPPFFP PGPFKRQKPPGGGKNF*RGPPGPPKKG GAPTGKKKKKEERKEKEKTPRNISKP LSHPPFPNFPFCATVRGFS
2719	16620	A	2738	96	331	QFTYTHGLFPFNFNRLCVFFFS*KLVG V*LCCPGWL*TPGLQSSCLSLSTWDY KGVPPCLAEHFFFEKKSPLSL
2720	16621	A	2739	379	14	LREVFPPFPSPKIKCFSKNSPQKYFPPP VVFKTPTPTPPFFFPPLFGKNFFPFLFN

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						FCPPRGFF*RPPLFFFFFFFFFFF FFFFFFFFKFYSLLLLYFLFILK*MLTF KTSISTQCY
2721	16622	A	2740	198	38	ANPLFFFFFLLRDGVLVYRPGWSAVVQS *LTADSTPWAQVILQPQRNPIEHDF
2722	16623	A	2741	290	39	MSKVGPLLGLVLTSTFRVLLKGPETKGD LLANPLFFLFFFLRDGVLVYRPGWSAVV QS*LTADSTPWAQVILQPQRNPIEHDF
2723	16624	A	2742	1	399	ILIRKHSIDIGTLYLLFDA*TGTIGTDL VLNRTELEPDQATLLGNPDVHEVIDTAH ALGIIFIVIPIIIGGFN*LVPLIIGA PDMAFARINNISF*LLPTSLLLLLASAI EEAVPGTG*TVYPSLA*NYCR
2724	16625	A	2743	398	2	SPPPLIFFLWGFYSYIFPPPKKFFFLINP PEKFSPPPPFFKPPPPPPPPPP*EEKK NFCSPPPFSPPPPFFLLPPLFFFFFSS LKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKRARSRSRTSPTRP
2725	16626	A	2744	295	185	FFFFFFFFFFFFFFFFFFFFFFFFFLF FFLFXFFXF
2726	16627	A	2745	374	4	LKKHKSTRVP*NVKSGK*NFSPPFKIRP WAQKRAKKKGAREKKAD*EKGEFGKLK KKSFRPGKKV*G*PKGFQRNFEKKPVKS QGPVNMGVIPAFEKKPRIPPVAKIPI*G AQKKKGRPLAI
2727	16628	A	2746	2	382	QDATAPIIDELISFHDHALIIICLICFL ILDALFLTLTAKLTNTNISDAQEITV* TILPAIILDIALPSLRILYITDEVNDA SLTIKSIGHQWY*TYEYTDYGLVFNSY ILPPLFLEPRDLGLL
2728	16629	A	2747	2	374	DWPPTVKKRTNPRAQSTAADRFILEFTV RGLTGIGLANSSLDIVLHDTYYVVAHFH YVLSLGAVFAIIGGFH*FPLFSGYTLD QTYAKIHFTIIFIGVHLTFFPQHFLGLS GMPRRYSYDPA
2729	16630	A	2748	55	230	QIPAK*INKYLQ*KKKKKKKKKKKKKK KKKGACLKPKHGGAKEKSWGRQKLSFK GG
2730	16631	A	2749	161	3	NGNYTLVKKCFNTKEKIKWVK*IFFFF MRWSFTLVAQAGVQWCKLGLSLQL
2731	16632	A	2750	362	1	PEKKSFAIKGVKKAGKQCKCDAPKKGN PPKKKNPTGTPKRVLLK*PPREKKNSP QRKKKNTAKNKEKEAPQEBI*KGPPRYI FFFISFFFFFYYFFFFFSIVINLEGT FIATTLEA
2732	16633	A	2751	311	110	ITLPRHGGPHVQSOLFRLRWKDHMSLG DRGCSELSSCHCTPVWRQSKTFSKIKYG RNGTDKAATCNPGRFRSWGRKVA*GQES ETLSNSRTRL*KNKIWSKDRQGGYL
2733	16634	A	2752	223	16	KKTPQKKKNTGKGPVKSPQKFLKST PP*IFFYVCFFFFLYFIYLLFRIFSF FFILFVYYLFIIP
2734	16635	A	2753	367	10	PAPRGGVYRGRQASLSCSGLHPLRASWP LCSPTQA*AMAGAPPASLPCCGLISDC CASNERGSGVVALS*SGAGDNLVCRLL SGKCRNHPSSASLTAAVDWSCSYSAIL APPLKNS
2735	16636	A	2754	14	341	PGPNF*FGGQNSPGKNQNLSP*KGNG

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						PGNPKNGGPTVPPTPPETRGSLRLTLQG PLRPSGTPPTRRAPGTPVGNPGF*PRDF FAQKGPVREGLKQGPKNPKGLNPPP
2736	16637	A	2755	15	172	HSWWECKLVQPL*KTVRRLKLLKIDPP YYPALPLLGIYSEERKSVKQSRRG
2737	16638	A	2756	263	2	QKPLPPRNDFVFPKGPBTPRPTWGFI GGVPLGKFFTLVSPFFFFFSPSPNLFF F*NRVSLCRPGWSAVV*SWLTAASTSQA QAI
2738	16639	A	2757	311	106	FVCFRLRQLALLPLECSCVILAHCNLRL LCSSDSPG*QSETVSKKKKKRKEKET GNL*RSMDMKGR
2739	16640	A	2758	23	328	NITYYT*LFVLYFYVPGHTVVFXXFXF FFFFFFFFFFFFFFFFFXFFFFFFFFFXF FXFXFFFFFFFFFFFFFFFFFXFXFXFXFXF FXFXFXFXFXFXFXFXFXFXFXFXFXFXF
2740	16641	A	2759	1	338	DR*LFSTNHGYIGTLYLLFGA*AGALGT ALSLLMRAELGQPGNLLGLDHTYNGIDT AHAFAILFMSLAIIRSFGN*LVTLII GAPVLAAPRITDISW*L*PHSVLLLLA
2741	16642	A	2760	120	2	INKYAWLGTVAHACNPSTLGGRWTA*GQ EFTKSLANMVK
2742	16643	A	2761	251	3	CRGQIGTPTLHYSSSSSSKWKDLNVRV KTIKLSNTGVNLRLELGDCLDDTKS KNSTRKIRK*SLKLETFFLGGTR
2743	16644	A	2762	11	303	ALVLKRSSCLDLLKCDWRHEPLHLALS EILMYRFCL*IFDIFFWYSREIDLIFV Y*FFFFFFLETGFWFLPRGDLG*WEPPP PGYKGSSCLGLPR
2744	16645	A	2763	236	356	DWLIFVFSVERGFCHVAQVGL*LLGSGD PPASASQGAGIT
2745	16646	A	2764	2	332	LTQTPGLK*SACLCLPECWNRYCEPPHP AGFLF*RHFDKGV*LLIYPGTGWS
2746	16647	A	2765	297	19	KKKSWFFFKKKKCWGGATKFKN*RGFFL KFVYFYFFFIG*GVFFFFFLISIIIFFF FFFFFFFFFFFFVFFVFFVFFVFFVFFFLF FAMKINVFY
2747	16648	A	2766	1	147	QILRRLRWENCVNLGCGGCSEPRLHHCT PAWVTV*NSVSKKKKNPLLF
2748	16649	A	2767	357	183	NWDYRPLSPRPGKFLDF*VNRGFPLTK LVSNF*PCNLPPSTSPKAGISGFNPRAQ P
2749	16650	A	2768	2	193	RWESCLNPGGGGYSEPRSCHCTPSWVTE *DSVSTTTTKEKERKQRTWSESNSLQK YKDTNHF
2750	16651	A	2769	333	173	VSQDGLDLLTS*STHLGLPKCWNRYREP PRPAQKLLMVIWLGFMSSPKSPLEL
2751	16652	A	2770	3	331	CMENCMVIPPKVKHKNYHMIQKFYFWK AVQQLSTELNIL*PYDPAITLLGIYPKE LKTSFRKTCT*MLTASLFVIKTKWQP RCPSVGE*LSNL*YVQTMECYSVLK
2752	16653	A	2771	209	55	RPGRPQVLRVRPQNRNLNPGGGGFSEPK *GPCPPAWGAQRDFISKKKKTTT
2753	16654	A	2772	213	57	RPGRPQLLRRLRLQNRNLNPGGGGCSEPR *GPCPPAWVTQRDFISKKKKTTT
2754	16655	A	2773	148	1	KATGRKTWVKSRCWVGTVAHTCNPSTLG GRGR*TARAEFKNSLRTLAK
2755	16656	A	2774	2	364	WSAVRRDWITALQPERQRETSPQKKKKK

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						KKKKKKKKKKKKGGVVRHGVKSRKP*TSGR PGRKNHWRQIQGPKTPRERAEALKNRV GLKKLFKTPGHVNGAGNPKFRNGKSGKP PEVHLNGAW
2756	16657	A	2775	121	2	HLRSGVSDQPGRHGKAPSLLKIEKLAGS GGTCL*SQLLG
2757	16658	A	2776	195	3	GRVDINTLLALLLIITF*LPQLIGYIE KSTPYECGFDPISPARVPFSIKFFLAAI PFLLFDL
2758	16659	A	2777	3	285	FLNIRNKVSLCCPS*A*TPGLKQSCCLG LPKC*DYR
2759	16660	A	2778	135	379	HWSATVKLYAILLGLLKWESGTLTCSKD VLFFL*G*SSAYSIESVMQIKAT*VKG KARVOLGAKKLKAYWQRKSPGIPAG
2760	16661	A	2779	364	1	GSFTGAVILITAHGLTSSLLFCLANSY ERTHSRIIILSQGLPTLLPLIAF**LLA SLANLPLPPTINLLGELSVLVTTFS*SN ITLLLTGLNILVTALYSLYIFTTQWGS LTHHINNIK
2761	16662	A	2780	356	1	GCLRAHIWPKGNHEGQVHLFIDKVCRO PMTEDCINEITTQVAQIFLVHFLLRQSL TLSEKRRKKRKKRKNRIESPENITHI YQQLIFNKGAKKIK*G*NSLFNKTYLDP WISTCK
2762	16663	A	2781	1	204	AQVGLQDASSPRIEELITFHDHALIITF LICFLVLVALFLTTLT*LTNTNISDAQD SETDCYSQSYIL
2763	16664	A	2782	1	522	YKNECGKVFENQQAHLAQHORVHTGEKP YKNECGKTFQSQMSNLVHHRLHSGEKP *KNECGKTFQSQMSKLVHHRLHSGEKP *KNECGNTFFHNSTLVSHKAIHTGEKL YKNECGKVFENQKTTLARHHRHHTAEKL YK*EECDKVFQCKSNLETHKKMQFSKTD SAFSLQ
2764	16665	A	2783	1	327	ENRLNSGGGCGSEPRSHCTPAWATERD SVSEKEKEQKQNFHLNAQSNQKLSKSP* KYLKHPEKTDILSKASQYNNQLTADQSI LKFKTKTFDQKKGRPKGHGMTYSNS
2765	16666	A	2784	335	128	FSLIFCRAGILPCCPGWS*TPVLKQSSC SSLPKCSDYKQEPYPYLACATLKCYQIPN FYCWPHIFKRMFY
2766	16667	A	2785	208	3	RPICPLSLWGVSLFFFFFLRDRVLICH TGYSAVAQYCNTHCYSPLRK*SSCLSL PSSWNHNLIPPR
2767	16668	A	2786	49	332	VEMGNSPINRKYVPKSYNRCLKNTEE GVLNDLGIAEFNTCSKSLLLIFFKGRI LLCCPGWIEVVQSQLTASSTLGLK*TFH LSLFGSWDHR
2768	16669	A	2787	331	187	GCSEPRSPPCNAAWATKGDVSKEKKKN KKREEKKH*HNTSGEKLNI
2769	16670	A	2788	325	34	RSQRLGLPSMSIS*I*NSRLR*LRPRRL FIFCRDRVSLCCSGWSQTPGFKQSTHRS LPKCWDYRREPSPLAQIRYLGLFFSQGL SSAFVCYVAMVSGF
2770	16671	A	2789	3	150	AASTRQLIFHTSKHHFGFEAAA*YWHF VDVV*LFLYVSIYWL
2771	16672	A	2790	86	311	NIHPLNDIFTRLKNGFKKKEISLVKNEP NKGT*SLISIKVLFHT*K*FIRPGVAH



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						T*NPSTLGGQGGWIT*SQE
2772	16673	A	2791	2	123	GGGACSEPRSHLCTPAWETE*DSISEKK EEKK*LQIYTN
2773	16674	A	2792	302	162	PLLRRLRPENCNLLGGGFN*PRSRNCP PAWATKRDSLLKKNLKNF
2774	16675	A	2793	1	258	GGCSGLRLCHCTPAWETD*DPVSKKKKK KNFTRAKLLIFGTLVLGKVKRGPPFKPR ILKLPWETWQNLVFTKKKKIFFLKNRGG GE
2775	16676	A	2794	199	3	VGPIFRHDKPPHSKQLCTYSPAFTQLFS SGKILKNHLPWGTVAHACNPSTLGG*A RWITRSGDR
2776	16677	A	2795	1	302	GGCSEPRSCHCIPAWATEPDSI*KINK* INK*K**KINRNKKGNHFLSSST**PQ VASSFLTGHRYTKL*SSQKVLLDSATL QSKSNAEVRVNRRTD
2777	16678	A	2796	228	326	NDNGQSGVVAHACNPSTLGGQGGWIT*G REFKT
2778	16679	A	2797	270	1	KFGISAPFAPSPKV*KRFFF*NFLGNP PVKIPPF*TPL*NFSKPGKNFPFF*KT RFSKIFPNGFFFFFFFFFEGVLLCCPGWS ALTRSW
2779	16680	A	2798	307	36	FKNFCCG*EVSLCCPGWSQAPGVK*PSC LGFPKCWDYRCELPCLASCSL*CDRNQT RISAVVLWIEFHLSPILPVLPLFLKKPQ AGLLCF
2780	16681	A	2799	132	5	IFEVTV*CTK*HKRNMQPGVVGHACNPS TLGGQGGWIMRSGV
2781	16682	A	2800	32	314	KQHPGNGPNPSGKGPGRASRFLKKKNFF F*KTPPKKPHTPCKPSPKGGPERLPWH FFNQKFGPLPMGPNPDQAGFCLRDP*G GGKNRSPPTL
2782	16683	A	2801	139	3	AASTFYTFETTLIPTLAIITR*GNQPE RLNAGTYFLFYTLVGE
2783	16684	A	2802	238	3	AASTSHVSSMYNIYII IQFKTFPVFFF RDKVSLCHTGWSAVAQS*LTAASAALTS CVQGILPTQPPEYHTRPLRLFL
2784	16685	A	2803	110	291	KKLGVFVGFGFGFKTKSNFIMQAKGQLPN LG*LKPLPRGFPPQFSGLSLSGTWDYKHT PATR
2785	16686	A	2804	97	2	SYNNQDSVVLEKEKTNRSVKQN*APIPE KKKKKNKVGGLTLPNCKTYKATIIKTIV WYWRKKRQIGQ*NRIESPEIDPHKY
2786	16687	A	2805	268	1	ATFLLFYVFRPQIPYYL*IFILSLF*Y RHSGPPYVGGPPQYVPVQPPGPGPFYDGP GPGDFPCRLPIRKWWLVWLMQNLNPTVW PTIIT
2787	16688	A	2806	153	3	IPLPKGLLVPLFGVFLKVFFFFFFFFF*D RVSPCRPDWSAVAQSRLTASS
2788	16689	A	2807	3	216	NAARDHTVKPSP*PLTGALSALVMTSGL AM*CHSHSISLLILSLLTSTLTIIYQ*RR NVTR*TSYQGHHTPTDQKGLRYGIIIFI TSEAFFLS*FF*AFYHSSLSPPTQLRGH WPPTGLSPLNPLEVPLLNTSELLAS*VM PLSLHIASNTKPTNQHTNHIPMKAQCNT INLIPRPHTN
2789	16690	A	2808	168	354	FLERESGFVAQAEGQGQNLNLS*WKPFPP LKHFSCLSLLRSWNYGPTSPVPAKVGGF

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						WRNKIY
2790	16691	A	2809	61	360	YVSNKSCSNHRK*SLFFFFFESSFV PQVELHGRDLG*LQLWLPFGFKFPGITP LRNGDDGPRPQPPANLGLLVKTGFSPVA HLGVNLGTLGDCPALP
2791	16692	A	2810	236	3	KMFFQMRVTMLKK*QATFGFILALKNVL KTFLAPIFFFLRRNSALVAQAGVQWRDL GELPPLPSGLKRFSCSLSPSC
2792	16693	A	2811	140	210	NAKITKC*KGYGKRGITLMHCCWQFKMQ LLWKTGYQFLKLLKLELLSNVPIPYL*I WKKGNPYALLAI
2793	16694	A	2812	230	1	VKLCPVSLKTVRPLTSSSEVIFILNCK FNIGV*LLPGSLLLLASAIVEAGAGSG *TVYPPLAGNYSHAEPYALV
2794	16695	A	2813	3	345	HEVRIDVHTRTCFTFGTIIAIPITGVKV FS*LATLHGSNMK*SAAVL*ALRFIFLF TVGGLTGIVLSNSSLDIVLHDTYYVVAH PHYVLSIGTVFAIIGGFH*FPLFSGYT LD
2795	16696	A	2814	2	184	ARVGFHHIDQAGLKLLTL*SAYFGFPKC WDYRHEPPRLALKFNNIKKKKKKKTP GEKI
2796	16697	A	2815	276	3	ARVHRIDHGLM*HQPLGLK*SLCLSLPS SWD**SMQPCPDDYGRSDQKKPTFKSP YVSQTGLEHLGSSDLPASASQRAKITGM SHHALV
2797	16698	A	2816	3	94	HENQYSSLIIMATAIKLGIAPFHF*VP EV
2798	16699	A	2817	93	1	GGGGCSEPRLHCHTPVWVTE*NPVSKKK TRA
2799	16700	A	2818	1	197	GTRAQSLLLGRLRQKNQLNLGGRGCSEP KSGHLTPAWAT*PDLVSTKSCITLIYLV TQALHITLLP
2800	16701	A	2819	109	2	GVF*GVFLAQGLTLVAQAEVQWHDLGSL QPCPPRLKRLV
2801	16702	A	2820	2	347	ARAPGFAENEVVFVSSCFVWVMPGGKGE NAELMQPSSY*ESQHFFPAPPRCSVCV* LCSLGPLLGLTIFCQFTLSELPRFRKG *FSSSLKKVFCFGDRVLLCHPGWSAVVQ TQL
2802	16703	A	2821	1	353	CTRRDVTRESTYGGHHRPPVQKGLPYGI ILFITSQVFFFT*FF*TFYHSTLTPTPQ L*GHWPPTGITPLNPLKVPLNNTSVLLP SRVSIT*AHILI*NNRNISSLLITI LLGLY
2803	16704	A	2822	261	400	VEHSNSNKENFLGQGTGCHACNLNTLGG RGGRITWRSGV*DQLDQH
2804	16705	A	2823	273	97	LNTPRMQRLTQLATVILRFHKDQGFAML PRQVSNS*AQAICHLGLPKC*DYRREPP GQK
2805	16706	A	2824	159	355	KKFFSIFFFFFFFF*DRISLCHLGSVA VQSWLTAAT
2806	16707	A	2825	67	338	LSPEL*LY*IF*KPFS*QLSLTSHSPSL FSALLLSISPPTWLHSQSDKNLHLFSF LFRDSVLLCCLGSAVT*SWFTVASNSW AQVVL
2807	16708	A	2826	3	359	HEQKYSFLHDSQTLFCF*DSIPTPSNMD ETQQKSRLELVRLISLLIEPWLEPERLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RSMVANNLVYDTSDDYHLLKDLQEGI QTLMGRLGYGSRTGQMLKQTYSKFDTN SHNHDAI
2808	16709	A	2827	3	338	LERNLDTTFLDPAGGGDPILYQHLF*FF GHPEAYILILPRFGIVSHIVSYFGRLE PSGYLRMG*PIISVGLLGFI*SHHIFS VGVDIHARAYSYFGSLVMAIPCTLEVFT
2809	16710	A	2828	1	406	RHEGEKLRRTFGPRHRGAGTAKMSASL VRATVRAVSKRKLQPTRAALTTPSAVN KIKQLLKDKPEHVGKVGVRTRGCNGLS YTLEYTKTKGDSDEEVIQDQVRVFIKK AQLTLLGTEMDYVED*LSSEFVF
2810	16711	A	2829	332	3	GIIVMQATTIATALIGYVPLGQISL*GA TVIAYILAAIPFIGTDLVQ*I*VGCSVD SPTVTGFLAFPFVLAFFIAAVALLLRF LQGTGSPNPLGGASQSDKIAFQFSC
2811	16712	A	2830	186	349	YSEREVAFFFFGNGFCF*TOAEWNGGNL G*LNLLPPR*KEFSCKIFPRTWNYS
2812	16713	A	2831	303	590	NILTTLLNKQSKSNQLQNKIHTVYTKI KIFFFFLRQSLSVTQADVQWHCLCSLQP PPPGFK*FSCCLLSSWDYKHAPLHPAN FCIFSRDGISPS
2813	16714	A	2832	1	370	EELITFRDHAVIISFLICFLVLYALFLT LTTKLTNTNILDADQDIQTV*TILPAIIL VLIGLPFLRILYITDEVDDPSLTIK*NG HQWD*TY*YTDYGGGLIFNSYILRPLLE PGE LRRLRDVN
2814	16715	A	2833	207	1	QFFIFLRHSFTLFAQAGMQWRDLGSLQP SPPGFK*FSYLSLTLRGLARKITLAQEFQ TSLGNMGGPHRA
2815	16716	A	2834	223	1	DNLAHKGKTRVYLKSRNKLKGGGAGNL VSLDSIGSRDRHRRAPPCANFVFLV*M GFPVHGQDGPPELLTSCSC
2816	16717	A	2835	1	321	GTRKPSP*PVTGALSALMTSGLTM*LH FHSITLLILGLLTNTLTIYQ*WRDVARE STYQGHHTPPVQKGLRYGILFITSEGG LEAGFF*AFYHSSLDRTPLQGGQ
2817	16718	A	2836	57	370	IWMGRVLWKDRLYGVFCRAFNRVTSRV WAEDPWRVPKTLSDVPRKLPPFS*ISVR GQIYFT*FFFFFETESHTVAQAGVQWWG DLG*LQSPSPGFKRFCLSLP
2818	16719	A	2837	2	345	ARAHRLDEP*L*RRPGERHPSW*SEET VERQRTKT*SESSQTGTSITSSRNARRR ESEKSLHLETLNKEEDCHSPTFKPSTPD HPLKVMPPAPSPKENAWVKRSSNPPARSQ SS
2819	16720	A	2838	15	376	AKIEPLYSSLGKSETPSQKGGKKKKKK KGGGGGKGGKKKKKTEGGTRGLTQETQFF GNPKGPKHLGARN*KHRAKQAKRGNQPR EYRFTEEKGKELFNPGGGRSQKPKTGQ WNSAGGKK
2820	16721	A	2839	3	336	HELLASILLY**CRDVTREIRIPLAHH TPPVQKGLRYGILFITS*VCFLAGLF* VLYHSSLPSTAQLRGHWPTGITPLNPL EVPLLITSVLLASLCSFI*AHHSLEIH
2821	16722	A	2840	338	3	KIIFYLFFLRSAFLAQIEGHNAVFSSS KLWPPGFKHFSASTFLVNRVFKGGPRAR VNFGFFIKSGFFPIF*VGF*LFFFFFFE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TESRSVAQAGVQWHDLCSLQAPPPSSC
2822	16723	A	2841	2	149	ARGCSEPTLHPCTPAWVTF*DSISKKKK KKVECSNGNVCRTMCILCCFW
2823	16724	A	2842	348	175	SACKVVSITGMHCHA*VIVSVLLV*TGS LHVGQVGLLELRTSDDMHTLASVSGGITG MS
2824	16725	A	2843	338	118	DPGGGACSEPRLRHCTPAWVTKRDFVSK KKKK*NIKC*HAKSGTVLYSFLYLFYS* YFLMRVVSVHLPGPSTK
2825	16726	A	2844	189	47	KCVALLLSLFLSCSVM*RNACFRFAFCH DCKFLEASPAMLPIQSVEL
2826	16727	A	2845	335	139	EVSPSWPG*SQTPDLKRSACLSLSCKWD YRPGVSHRARLNGSFLTQLYEMLTYPFI IWVTLQVFR
2827	16728	A	2846	3	352	HEQRLTPEWKAATAALGDVVKGAVDAD KHHSLGQYGVQGFPPTIKIPGSNKNRP* DYQGGITGEAIVDAALSALRQLVKDRLG GRSGGYRSGLQGTSYRSSKKDVIELTND SFDN
2828	16729	A	2847	2	269	ARGLFSTNHKDIGTLYGLFGA*AGVLGT ALSLIRAELEGQPGHLLGRDDISRIHVK RIIPGCGTLDGISVGRECACLWTPACSR KCARG
2829	16730	A	2848	317	28	SFLPN*KLAGHGGRL*FQVLRVRLEG CFSLEG*GCSEPWSCPCPLTWATETDPF SREKKRRRREEKAEKRRRNRVPSLSV FLEEYVELTLIL
2830	16731	A	2849	326	107	FHHVGQDGLDLLPS*SAHLGFPKCWD*R CKPPCPASRNFKTLKLYHIFSNNLIE*N *KSITRGTLTVQLPGN
2831	16732	A	2850	224	3	SILQAWLKVPSPGNPLGLLSQVDFFF *RQGLALSPGLDCSGMIMAHCSLKLLGS TDEPTLAS*VAGTPSSC
2832	16733	A	2851	27	329	VRTAAINRPGFLLPCFIGQNFFFY*RFE TYRLGV*MILTPH*YLLSSLSGLDCVIF FSFILFFYWFIVYCHVMVYLFFFLFVI LFVLCVFVVCYFLLFV
2833	16734	A	2852	351	60	NLLSSLQGGRLPRPPGLSPHPQIFTPHG GVPL*LPGPWKSRPEASLNPRS*PPPGQ PRGNPFPKKNFFFFETVLLCRPGWSAV AQFOKKKNLLIC
2834	16735	A	2853	186	365	LTQLNLNI*YQNQIEYPQPYAQCGPRSG NAQQIGHSFPNG*QVPASGMHGLPWTHQ GLKK
2835	16736	A	2854	17	239	HFTTLQISMSLLTETTLARHDSTHLWSQL L*RLRRNDLLKSGAGGCSELGLHHCPT WTTEQDPVSRPGAVASEH
2836	16737	A	2855	325	140	GFHYVSQDGLDLTS*SACLAFFPKCWDY RHKPPCLAAYIFIQSRVFLAVISISTHS SFQLL
2837	16738	A	2856	1	157	GTRGFHHVGQAGLEVLTSDNLPVSASQS AGITGESH*AHERSDGYANTNSPG
2838	16739	A	2857	157	361	LLLRIVSLFWRKSSPLGVAEMYRPDL VTKPPPPD*DKDSCSLSLITWDYRLAPP LEANLEF*I*TG
2839	16740	A	2858	3	346	HEGNHFKTIINVHLR*LNQNL*SGLEGD KVIWRNI*TSVTFLFC*MNGKMNPDLE QFTYEVGRIFFFSLKD*VWLCCGSSSTV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DLGSLQPPPLGFKQFSCLSLPSSWEPPC PA
2840	16741	A	2859	18	233	KNPTILCCKGGGAQA*KPRLGLRLRQEK GLTPGGEGCRDLKSPLGIPWPATRPKLL LKKKKKKGGKKKTLF
2841	16742	A	2860	356	3	RVNFKIFGKKGFPCPGPGGFEVLTPGDL GPLFFQKGGDSPSKPLKPPFFCFALKST TLNYFQFAFCVLRPTPN*SVTQAGMQ*H DHSSLQPQPPSLK*SSQLGFSSWVYRH APPSC
2842	16743	A	2861	115	374	IVCGKILNV*YTQ*HNKLQNKKNVD*PT IKMLISQSLGILIFIQKRDDEVNYGMI LKKRGWPGPVAYVCNSKTLGGQGGQIT
2843	16744	A	2862	163	360	LKRIWLLILHSHPHTSPhDRGVLTQLEAI GERWY*TYEYTDYGGLIFNSYILPPLFL EPGLRLLLDA
2844	16745	A	2863	1	236	GTSPFFSFFFLSFFPSFLPFLSFFNPTT LLLSLHSNIS*KKVLFSEFEMESHVNRLECSGTISAHCSPAATGTDSSIS
2845	16746	A	2864	67	364	VCVCVCVCVSVVCVCVCVYICTYICMY VCA*YRIRRYIMLPTLVNSCPEIHDSK SCALHTGATTRATR*PCLCIHIPVCLTV CLTVWLHICLSVCM
2846	16747	A	2865	2	155	ARGLTQENRLNLGGGGCSELRSHCIPA WATE*DALSQKRKKKKGTYRGII
2847	16748	A	2866	344	81	IQENSFIFLKIFISRDGALLCCPGWSPN SWAQSSRLNLPKCWDYRHEPPHLVVQF L*KHYMYKWKVHCVFVSHYNKIIFGTQK TEN
2848	16749	A	2867	217	340	RVFSDFYMNLKWSLRKRRTWPGLVAHAC NPSTLAG*RGQIT
2849	16750	A	2868	3	349	HEATSPIIQLITFHDHALIIITLICYL LLYALYLTTLTKLTITITMSDAHEIHTA* TILPAIILDLDLPCLRILYVTDEVNDP YLTITISIGHQWY*TYEDTDYGGLIFNSY ILT
2850	16751	A	2869	1	352	GTRIDVYTRAYFTSATIGIAIPTGVKVF S*LATLHGSNMK*SAAAL*ALGFIFLFT VSGLTGIVLANSGLDIVLHDTYYVVAHF HYVLSIGAVFAIIRGFH*FPLFSGYTL DQTYA
2851	16752	A	2870	2	342	ARARFRTSLLLA FALL*LPWLQEAQAQ TVPLTTLFDHTMLQDHRHQLAIDTYQE FEETYIPKQKDSFLHDSQTSFCYSDSI PTPSNMEETQQKSNLELLRIFLLIESR L
2852	16753	A	2871	254	2	YPGYQAISQSDMQSYAYRHL*LQPPGVK *SSIVSLSS*DHRPVPCLANEKNFFF *RQGLAMLQSRVLVNSWLLLYSHAEPR
2853	16754	A	2872	282	3	HTHILHYIYIHGHIST*HLSPTNIYS LCNIKILIYTPYDH*IRIPLHQEHAVH RRRLIHITHITSVCVCVCVSVACVCV CVCVWVLV
2854	16755	A	2873	278	3	LWPLKNSGPQWPQMDLGKPKVKTVPVY YKGP*KKFFRK*KNPGFFFFFLRQS HSAEAGVQWRDLGSLQPLPPGFKRFSC LNQISSC
2855	16756	A	2874	2	348	ARA*SLILVSLIIPNATSNLLGLLPYSF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TPTTQLSINLAMDIP*AGTMVIGYSSK IRHALAHFLPRGTPTHLIPILAMIESMS LLIQPIAMAVRVTDNITAGHLTMPLTGS PTV
2856	16757	A	2875	1	260	GTRENHLDPA GRGCSKSRSHHCIPAWVT D*DSLKKKKKKKPQIILGNGGTEGNQK* RGNPFRGPWGPSRQKIKELGPGGKHGKS KF
2857	16758	A	2876	176	1	EHLFCCKLLGEEKGSLSKFEFGKCWNPR *KWN SRPGVVAHTCNPSTLGGRGGQITR SG
2858	16759	A	2877	168	1	GVRVFGFSSVPEFSFDTCCAGAQWRNLGS LQPLPPGFK*FSCLSLSSWDYKRTFRA
2859	16760	A	2878	67	333	WQGLGRAVARVPRS YETWAGNLKGAA* FQQLFFFFFFFHLLFFFFFFF FFFFFFFFFLEFSFFLEFFFFFFFFF FFFFL
2860	16761	A	2879	335	1	GRKEGRREKEKERKKKKERKKERTIF KKHIPSPLEAFPRKAWKLKEIQIKLVAH* KINRQAIRGCPPNKRPHPFQNMIPGRE EGEGGLETSRDERNLWIFGPSVGPLR
2861	16762	A	2880	3	345	HERHETASTILLIAILFNILSGQ*TTT NTNQYSSLIIMAIATKLGIAPFHF*V PEVAQGTPLTSGLLLLT*QKLAPISIIY QISPSLVNLSLLTSLISIIAGS*GGLN QT
2862	16763	A	2881	347	156	WLIFVLLVEMGFFHSGQAVLKLLASSDP ASMTSQSSGITGLRHCAQPR*AFLLALC LPPSAKI
2863	16764	A	2882	338	2	IKKAL*HE*LREKKKSPRTSQSSKAP* NLPRSKKKKESNNYQLL*AHKLQKVKE MGKLLLETPNLPLLSQKVAEPLNQPTSS KIETLIKKPYHPEKSYGHDEVTAKFSRA
2864	16765	A	2883	206	1	IRTRPFTPMFIFYMFVYLATRSCTLA GVQWHNHGSLQL*PPGLKSSCLSLSS WDYYACLHAE LV
2865	16766	A	2884	341	140	DGGCREPRSRHCSPAWTE*DSKQNKTK QKQKRYTNISSPQTSPLCYSFSAYTPLH NMPGNIMFSSL
2866	16767	A	2885	360	247	FHRVSDGLDLITS*SAHLSLPKCWDYR REPPRRPKAL
2867	16768	A	2886	229	351	KLNNRPGVVAHAFNPSTL*KLNNRPGVV AHAFNPSTLGG*GGWIMRSGVRDQPNQH GETP
2868	16769	A	2887	359	2	FYSSSSSSSELVPCRQDVQVPHYLEGLF LRSCFMEIKYDT*KRKIKYTHVHTHTHT HTHTHTQREKERDFPRFTAKWKANLEAG SGYATASSIRAVLWTTITLV
2869	16770	A	2888	4	305	ADSHMWKYKAPGITKILLKSKI*GYHQ DWISSRYQDLFHKDMI*FKIMSYWKRRQ VDHWDRIESPETSSQMYEHLIYNKDNIA EW*EKDSFLSKWCWDN
2870	16771	A	2889	1	436	IAILT*YDYTL*RVGPRGQEFGRATV ITNLLSAIPYIGADVVK*GGYSLDSP TLTRFFTFHFILPFIASLATLHLLFLH *TLSNIPLRITSHSHQITFHPYTDQYS LRLLPFLSFTTLLILPNFLFYPP*TT LTFPF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2871	16772	A	2890	1	218	RKISPLIKLINHSFIDLPSPNISAA**NFGSLLGACILILQITTTGLFLAMHYSPDASTAFSSIAHITRDVNYG*IIIRYLANGASIFFICLFLHIGRGLYGSFLYSET*NIGIILLLATIATAFIGYVLP*GSLLGACILILQITTTGLFLAMHYSPDASTAFSSIAHITRDVNYG
2872	16773	A	2891	3	368	LSNS*ANNLI*LAYTIAFIVKIPLYGLHL*LPKAVEAPIAGSIVLAAVLLKLGYGIIIRLTLLNLPLTKHIAYPFLVLSL*GIITSSICLRQTDKSLIAYSSISHIALVVTAILIQTP
2873	16774	A	2892	3	342	HENLI*LAYTIAFIVKIPLYGLHL*LPKAVEAPIAGSIVLAAVLLRLRGYGIIRLTLLNLPLTKHIAYPFLVLSL*GIITSSICLRQTDKSLIAYSSISHIALVVTAILI
2874	16775	A	2893	2	361	ARVCLRQTDKSLIAYSSISHIALVVTAILIQTP*SFTGAVILITAHGLTSSLLFC LANSNYERTHSRIIILSQGLQTLPLIAF**LLASLANLALPPTINLLGELSVLVTFS*SNIT
2875	16776	A	2894	229	3	YTFVQSFI FSVVLFICKVCLL*PAHSMV CACECMCVCLCVCLSSLKIIPLLECL IYLLQILVLSSAIYNSRFE
2876	16777	A	2895	3	391	GFLITNNISPASPFQTTIPLYLKL TALA DTFLGLLTALDNLNLTNKLKIKSPLCTF YFSNIGFYPSITHRTIPYLGLLTSQNL PLLLLDLT*LEKLLPKTISQHQISTSIITSTQKGIKLYFLSFFF
2877	16778	A	2896	381	2	GRCRVSGSIIIDHRMAPQKWRYPKGGPHQWHNFCFF*KKGVPYGPVFLFRAPVFSPPGPPKRWEIKV*TPPALFFFFFVEMGSHCVQAAGLKLGSSTPPTSASQGAETAGVSHRAQPHAS
2878	16779	A	2897	324	1	LYTNNTKHINPQONNTK*YQRNTKNRRKKEQQTKNNIKRHITESARKNS**HRNIQKANKSQSNKHYRARSRHNNNNNNNNNNKKKKIENSHAASD*ITSSGGRSRA
2879	16780	A	2898	120	345	PPAPSS*YTTSLIQDRFLMMAVLSSASLMRGNVGSNIMNALSHFLPQGTATLFIPLVDIMEAISLLIQPIALAV
2880	16781	A	2899	381	219	CVSQDGLDLTTS*STRLSLPKSWDYRCEPPRPAGSGHLYSSFKKQGTGDTHNF
2881	16782	A	2900	1	224	LSWCLTLFYAYLLALFYFYFLKILDLAILPRLVPYSWP*ASSPASASQSSGITGMSHYTWPLPQTLNPFLLFFVP
2882	16783	A	2901	1	228	KYLINNRLITTTQ*LIKLTSKQMITIHN T*GY*YNRSGSSFNQVVDYHLLRSESEHPWMIVDNTEYDEIYTRGGIE
2883	16784	A	2902	2	332	LPPSFSLLLAPSPSSSLPSPSSSLPSPSSSLPSPSSSLHTSHSSTLTSPASCTLTITESTQRLAQSYITILP*ASRTMQLLKYRTLQTRNNTHTSMTRPKALTKI
2884	16785	A	2903	3	243	DIGFGTDFSDMTPKAQTKQVDQLDFIKI*NFWPQVAHTCNPSTLGGRGM*ITKLG V*DQPGQGETTQKLAGHGGVDAV
2885	16786	A	2904	179	2	CGYFNAYICYSLLCFLYLSLNCQPFWKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IFLPLFGLVFFFFF*NRV*FCCPGWSA VSQ
2886	16787	A	2905	108	2	GRVDIKLTSKQMITIHNTKGR*SLILV SLIIFIA
2887	16788	A	2906	318	2	YKESNSKNNEKKKITRQRKROKKNRPSM MVHTCNPSPMAGRQGIPIILFNQPHSP RIIRLTILNPLTKHIAYPFLVLSL*GI IITSSIGLRQTDLQSLIAYSS
2888	16789	A	2907	17	308	KLAGYGGMCLWSKLLERPTRMNHLSPRS EGLMEP*SHNCIPDWTP*QNPVSVQITG FCFLTPNLAMPRLNLSPICQQLSLRL LGPRLFASVSGV
2889	16790	A	2908	378	1	RSLHSTETAAKTHGHQTHPGLSTFSK*T PTPIASIPINPHNCLPAFNSTTSASYF SECVLTSSFKETIADFR*KYSSTN*HPY HLFLLKFVFFCSRDSGLTMLPIRPLNS RSQAILPPWPPKVL
2890	16791	A	2909	1	129	HLFGTNHRDIGTLCLLFGA*AGVLGTAL SLLIRAEELGPSTRP
2891	16792	A	2910	1	323	CVCWGYRIPRCNIGHHLKFFFFSLFFFF FGNKVWFCSE*GAGDQLIMEPLASGF KGIFFLNLPQWE*RVSPKLPKFWIF* LKTGFPLVAQVVFELRTSGDQMA
2892	16793	A	2911	367	136	ETPGNHLSPGV*GCSEL*SCLCTPAWAT EQDPIKSKQKRTKSKTLLKNTKADLTRW KHHSKACVCICLCMYMCLRE
2893	16794	A	2912	258	140	FLIFFCLDCFLNIKVLGVGFFFSKKK QT*ROGLALSPRLCGLIIAHCTLEPL GSRNPLTLAQIAGATGMSH*VQGYNEL
2894	16795	A	2913	48	242	YSMIFCVLILPVSFTSSDGIFFLLINLFL FY*STYPLAFFKTESHSVTQAGVRWHHL GSLQPPPPR
2895	16796	A	2914	309	76	GFICVCVCVCVCVCVCVFIFTEYSFH SLFC*IRCCVFYFLALSLIGFYLPWNR YLEVYNISFEVWASLFNRELLL
2896	16797	A	2915	1	122	FSVETGFHHVGQPL*PPTSGDPPSLAS QSAGITGMSHHA
2897	16798	A	2916	167	1	GNMCSKESVSGTNINRKP*YNPRLGT VAHAYNPSTLGGQGRWITGGQEFKTSL
2898	16799	A	2917	2	356	ARGILLRLIMLTTLTRY*RDVTREST YQGHHTPPVQKGLRYGIIILFITSEAFFL PRFLPPFLSSFPPTPSLLKPPFPSSFP SLPSFFPPFLPSSLFL
2899	16800	A	2918	2	351	AREYTSLLQILQMTFIMAFTCTDRTLYE LAFEC*LMRTLDIITR*GNQP*RPNAGS YWLFTLLGTLPLLIALLYTHNTLGSIN ILLTLTAQELSNS*ANNLI*LAYTIAF IVKI
2900	16801	A	2919	32	321	ALMGITFFFLGKGVLPARGGGRGNPG LWGGPPPGLPFG*SLQGGGA*GPPPO AGANFGFLILRKTRGSPGCGGFWIPGP GDRPAGAPQGGG
2901	16802	A	2920	1	361	GTSTRLGVLILLSLHAGSINPLGITLHS DKVTLHPYYTIKDALGLLLFLSLMLTLT LFSPDLLGDPDNYTLANPLNTPPHIKPE *YFLFAYTILRSVPNKLGGVLALLSIL LLAIIPIL
2902	16803	A	2921	3	152	HERLYSVPLRILRRLPDPLSIPQGRHV



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						TRESAYKSHLTLPARRGLQDGIILFITS EVVFFAGFF*AFYHSSLCTPQL*GHW PTGITPLNPPEPLNLTSVLLASGVVIT *AHTKAISHYLREEAFKTG
2903	16804	A	2922	410	1	RAGYRQKNGSLATVIGQLGLPVERGWYG PSGEGGTPQRHCSELVLDLHVITQNR NHRPRCGSLLSELKFAPLALQPGRSK TLSQKKNKQTTTKKNTKKQPGSAHACN PSTLGG*GRQITLPSGVRDQPGQH
2904	16805	A	2923	2	145	ARAARGDVI*SFHVFAQRDLNLLSSRDL PALASQSTGITGMSHCQCPG
2905	16806	A	2924	29	340	EMNEVERRGRK*LFHDSIQSR*EYRCAP QCPANSCVLM*RWGFAMLPKLVSSDLPA LASQSAGITGVSHCAWLVLPLLSSTFI SQRHLYLPRA
2906	16807	A	2925	2	337	ARVLILPGFGIISHIVTYSGKKEPPGY IGMD*AMISIGFLGFIV*AHHIFTVGID VDTRAYFTCATIIAIPGVKVFN*LAR LHGCNMI*SAAVL*SLGFIVFIVSGQA
2907	16808	A	2926	76	388	RYCTPAWATETPSQKKKKKCCQTFEPE SSFVPCLENGGGGNFISLFFLFIILSL FFYFY*FFFIIFVYSYFYFCLFSYFF FYFFINLIIFLLLNYYYYFI
2908	16809	A	2927	48	374	KDQEPDMDGSAHFQVFGWRQVGGANED RINSHGGPVMFSGQYYQLVRFVY*II IFFMLLFSLFYSYFLFISIFFVLVFC LFIFLFYFSFFFIIFVFFYYFIVIF
2909	16810	A	2928	3	294	HEGFHYISQDGLDLTS*SARLGLPKCW DYRREPPRPARFPTLRWLKALYTV LGCYREYAYRPWCWTHRMDGGQVEGR REGTGGGHILGF
2910	16811	A	2929	7	420	IRRRDVLTLTSLSPTAARICYNNGRR GNRLNSLAYLSKELLAWSLRKPSHGLL TPIRCVLVIRGHHF*LLPPSHLLLASA IMGAAGGTG*TV*PTLARNYSQPGVCVN LAMVSLHLSGVSSILGATFITAIMNME APAITQYQTPLFV*YGLITADLLVLSLP DLTAGITILLTDRKLSSTFFDPAGGGDP ILY
2911	16812	A	2930	11	253	GLLHKAPSP*KFFFSKPFNFVWFSPFI FSPPKKKFLSKNPHIVFKFPFPPKGI FPPPLKFGPPRVFFKAPPPPPPPPPPP FFFFF
2912	16813	A	2931	70	341	DSSFFS*LATLHGSNMK*SAAVL*ALGF IFLFTVCGLTDIALPNSSLDIALDTYY VVAHFHYVLSLGAVFALIRGLIH*FPLF SGYTLDQS*AKIHCAIFIGVYITFFPH HSLGL
2913	16814	A	2932	3	340	NYSHPGASVNLIIFTVHLAGVSCILRAI NFITTIINIKPPAITQYQTPLFV*SVLI TGVLLVLSIPVLSAGITILLTDRNLNTT FFDPAGGGDHILYQLLF*LFHGHPEAYIL
2914	16815	A	2933	2	364	RVQKGLRYWILSITSEVLLFAGYF*AL YHSSLAPTQLGGHWPSPGITPLNPLEV PLLYTYVLLASRVST*AHRLIQNNRN HIIQALLITILLGLYCTLLQAS*NFEPP FTISDGIYG
2915	16816	A	2934	2	367	PRVRPRVRYLLFCA*AGVLGTALSLIR

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						AELGQPGNLLGNDHIYNVIGTAHAFVIT FFIVIPITIGGFGN*LGPLIIGAPDMAF PRINNISF*LLPPSLLLLLASAIVEAGA RTG*TVYPPL
2916	16817	A	2935	3	365	YHIV*PNP*PLTWALSALLMTSGLTM*F HFHSITLVILGLLTNTLTIIYQ*WRDVS *STYQGHHTPPVQKGLRYGIMLFIT*DR FFFAGVF*ALYHSSLAPTPHLGGHWPPT GITPLNPLE
2917	16818	A	2936	3	144	DSHGRHIVING*TCVTICFIRQLIGHFTS KHFFGFEEAA*YWHKKKK
2918	16819	A	2937	3	422	QRLLATNHHDIGTLYLSFGA*PGALGTD LSLLIRAELEGQPRDLLGNDHIYNEI*TG HALGILFFIGLPIIIEGFGN*LHALIIG APDMALPRINNISF*LLPPYLLLLLASA IVEAGAGTG*TVYPPLAGNYSHPGASVE
2919	16820	A	2938	3	382	RTRGLFSTNHIDILTLYLLEGA*AGVLG AALSLLIRAELEGQPCNLLGNDHIYNVIV TAHAFVITFFIVIPITII*CFGN*LLPLI IGAPDMAFPRINNISL*LLPTSLLLLLA SAILEA*SGTG*TV
2920	16821	A	2939	225	3	NISWRMKQIVPKGEPYNGVPVFSVLWFH KMFIFETGSHSVYQAGVQ*RHLGSLPH PPGIKQFYLSPSSWDY
2921	16822	A	2940	1	247	PTRPPVIYSTIFAGTLTALSSH*FFT* VGLEINMLAFIPVLTKKINPRSTEAIAIK YFLTQATASILLIAILENNIKKKKK
2922	16823	A	2941	3	369	TRDSTYLGHTTPPVHTGLRYWRLFIT DAFFFAGFF*AFYHSSLAPTPRLGGHWP PTGITPLNPLEVPLLYTSVLLASGVSVT *AHSLSVEDDRYQIIQALLITILLGLYF TLLQASEDFE
2923	16824	A	2942	3	401	LTVCCVIVLRKLTFFFNKPFLLTKQGY FNTPEEGFFKKPNRRVGPSPMTDPTML TNLIKGVKVPKAPPRILMGGGINMTF*GF VTPRAPFPLTLRLNPMLQQGIDLLTLKA SGGSPASGNFLKELGLRSINF
2924	16825	A	2943	189	348	RNARGWVTDKEKRLRLGMVAHACNSSTL GGDGR*IA*GQEFETSLANMVKPCL
2925	16826	A	2944	2	349	ANSNYERTHSRIIILSQGLQTLLPLIAF **LVASLANLALPPTINLLGELSVLVT FS*SNITLLLTGLIILVTALYSLYIFTT SQWGSLSLTHINNIPKSF*TRENTLMFILL SPIL
2926	16827	A	2945	621	929	GCSSGTGCCPILCDLPRPWSCRGVGGSP SSTAHLCPRGWRSGRCFLPPLSAS*VDS AMSLIQAANKLMNAVQTVKASYVASTK YQKSQGMASLNLPAVSWKM
2927	16828	A	2946	379	395	SQHFGRLRREDHEVRSS*PRDPPALTSQ SAGITGMSHCARPLVATSIHKIDNRYID DRS*NINIGTIFINLLIFYLSIYLSIYL SIYLSIMYSFTVAQAGVQWRDYGSLQPE SPGPK*SSCISLSSSRNHSHTPPHGWD PKIP
2928	16829	A	2947	2	357	HTYDIRKPRR*TLACALSALLTTSGLAM TDCFHYITLLILCLLTNTLTIIYQ*WRDE TRESTYQGHHTPPVQKGLRYGIILFITS EAYFFAGFF*AFYHSSLAPTPQLGGHWP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PTGITP
2929	16830	A	2948	2	357	PRVRYSTDHSDIGTLYLLFGA*AGVLGT AISLLIRAE LGHPGNLLGNDHIYNVIGT AHAFVIIFFIVIPIIIGGCGN*LGPLII GAPDMAFPRINNISF*LLPASVLLLLAS AIVEAG
2930	16831	A	2949	2	217	KNLKIVQYGDMLWSQLRELRLWEDRLS SGG*GCSELCSCHCTPAWTTQQDCLKKK KNFWPVGEVKGRHML
2931	16832	A	2950	2	354	ATPMTTARLTIEAYLIILERTTTTTTKD VKNPRRIAAAITASCLGGGLEDAISQY GIATKDRPTGLGTPEVLLGALPGAGGTQ RLPKMVVPAALDMRLTGRSIRAHRAK M*LVD
2932	16833	A	2951	3	150	LFSCSPTFSSDPLTTPLLIIT*LLPLT IMASQRHLSSEPLSRKKKKKK
2933	16834	A	2952	283	344	EKKKKKKKKKKKKKKKKKK*KLRRKKK KKKKKKKKKKKKKKKK
2934	16835	A	2953	3	378	DAWADAWNQTPLFN*SVLITAVLLLLSL RVLAAGITILLTDRNLNTTLFDPAGGGH PILYQHLF*CFGHPEVYILILPGLGIY RIVTDYGYGTKEPFGYIGMV*AMRSIGFL RFIVRAHHIVTVG
2935	16836	A	2954	3	387	ILYQHLY*FFGHLEGYILILPGFGIISH MVTYYSGKEEPFGYIGMG*AMISIGPLG FIGRAHHIFTVGIDVDTRAYFTYATII AIPTGVKVS*LATLHGSNMK*SAAVL* ALGFIFLFTVCGLTGI
2936	16837	A	2955	2	432	PRVRPRVRKHIAYPFLVLSL*GIITSS ICLRQTDLKSIIAYSSISHIALVVTAIL IQTP*SFTGAVILIIAHLTSSLLFCLA NSNYERTHSRIIILSQGLQTLPLKKKK KKKKKKKKKKKKGGGLLKESLGGPNLTG EGK
2937	16838	A	2956	12	391	SYFISSSKPHLSPPWLSSPDEATSKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KGGGFK*KRIGGSFKKGGGEKKIFFPKG GKKKKKTGGFFEKKFFLGGEKY*DNLPKK NKTVGEKKNFLGGG
2938	16839	A	2957	1	352	PTRPYFPVDAGEAQHHPRTCRRPLRALW SSHHERWKVTLCTHCSLGVFFLYCCTYY IFVLFIPI*SSCGLTLIFITCIILFGSIS FFLFFTIVFSIIIVTTFKFRLLYSIIFL SYLLC
2939	16840	A	2958	1	243	NLERLNPKEIEILNRSIICNKIKAIKS LLSKKSSGHNDVTAEFY*TFKEELITIL LKFYLTTPKKKKKKKKKKKKGGPF
2940	16841	A	2959	373	3	FSSLKKRVTPPPPKTGFSLEGLHLKK NFPQKPPPPPKSFSQKNPPPKKPPF* KKKPPPPPI*HPPPKILQPPPPPPFF FFFFFFFFFFFVFDTDMR GFIVRKFRTRG
2941	16842	A	2960	2	136	PRVRSTLPISYKWNRRALMKAHLMK*F TEYFKTTDELYLHDNT
2942	16843	A	2962	1	358	HTPPVRKGL*YGIILFITSKVFFVPRFI *AVYHSSLCP TLQLGGLWPATGMTWLN L*VPLCTTFVLLA**VSIT*AHNHLIDL NRCHVIYALVITILLRLYFTLLPASEYF

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						EAPLTIS
2943	16844	A	2963	2	373	RAYDIVRPRP*PLLGALSALLMTYGLAM *VHWDCITLLILGLLTNTLAIYQ*WRDV SRESTYQGHHTPPVQKGLRYGIILFITS EDVFFAGIV*AFYHYSLAPTPQLGGHWP PTGITPLNPLEV
2944	16845	A	2964	403	61	LFFPLEKNFLPPGFSAFFSPFSP*KFFF SPKALIFWGNFSPFFPPKIRFLPKIPP WVFFSPFWEKLFSSPPPLNFGPPRVLF KGPEPLFFFFFFFFFFFFFRFEGECW RL
2945	16846	A	2965	2	360	LTPNLAMVTR*GNHPQRLNAGTYLLFDT LDGSLALLIGLTYTRNTLGLSNVILLTI TAQELSNS*ANNLV*LAYTLAFIEKIPL YGLHL*LPKAHREAPIAGSIVLAAVLSK LGGSGKN
2946	16847	A	2966	321	2	STGMHFPFHINMAINPPPPRPPPLFPP NPKTKNPTQ*KGGFPLGPF*KKLSPF LTLFFFFFFFFFGHHPGPWQKKKKKVF FFCVCFSFQRVHNIYKNTHQQQ
2947	16848	A	2967	200	1	RRTYTSHLLACLRLQGLAFSPRLCEGKI RAHCSLQLYGSSDPPT*APQTAGTKQHN ORIAQCNADN
2948	16849	A	2968	2	354	LLTASSSEIAPLQSSLDGRARLCLIK*K EGVLNSI*SGNQGKSYANVYRLLYLDP PKIYAEAYTP*NVNSTNLETKSPKTIQK FPEDEFKNDFFEKTKNGDRETGAHFPF LLFLV
2949	16850	A	2969	99	400	ALGIHFIFTVSGLTGIGLANSSLHIVLH DTYYVVAHFHYVLSLGAFAIIGGFH* IPLYSCYTLDQTYAKIHFTIIFIGVNL TFPQHFLGLSGMPRRY
2950	16851	A	2970	2	377	NILLTLTAQELSNS*ANNLV*LAYTIA FIVKIPLYGLHL*LPKAHREAPIAGSIV LAAVLLKLGYGIIIRLTLINPLTKHIA YPFLVLSL*GIIITSSICLKKKKKKK KKKKKKKKRGPF
2951	16852	A	2971	1	407	GTRSYTHLYRVFLELIKMSVYDLNHTVI MVISGHVRLAFYGVHVLTLINLLTDHI LYPFLVLSLGSVIIISSIFLRRTDLESL IAYSSISHIALVVTAILIQTP*SFTGAD ILIIHVGLTSSLLCCLANSNYER
2952	16853	A	2972	10	259	SRSVAIYFKGMASA**RMFSSKKKKKK KKKKKKKKKKKKTAITKTTAKWKN *RTEKIRHTRLPLISSRDAKCVDFLYT
2953	16854	A	2973	12	400	LNCRTPSLYLQRAGELLSVENPHIWCQK CVRKNNFFLFFFFFFKTDLYCPHICAL SITCFLAISISGLFAFFLLNSFNHYFII VP*NFSLIYLCLSLFPVVGFFFSFDM IFSILT*TLFFCLLHL
2954	16855	A	2974	125	3	RPRRPAAQGVQ*KNLSSLQPVPPGFKL FFPLSLLSSWAS
2955	16856	A	2975	2	332	RECTNYPAQPPPPPLEAEEGFQPLPPTD TG*LECLPPLGGGQHRALGLGATWHLEN ACALVLADLGTGPKPSGPFSGQACGASG RLPLLSGPILPPLGQGHLSAWGHHA
2956	16857	A	2976	7	329	SRDILVMTEDGEFF*GHV*P*DRSRAD TPRLGGHWPPTGITPLNPL*VPLNLSV

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						LLASGGSTT*THHRLIEVIRHQITHALLITILLGLYFTLLQASEYFESSFT
2957	16858	A	2977	2	339	AHHIFTARIDVDTRAYFTSATIIIAIPTGDKAFS*LATLHGSNMK*SAAVL*ALGFIFLFTVRGLTGIVLADSSLDIVLHDTYYVGAHFHYGLSIGAVFAIIGGFH*CPLF
2958	16859	A	2978	394	0	QGCSEL*SCHCTPAWVTE*FPVSKKKKQ RK
2959	16860	A	2979	149	383	PLCFPSQHWGKSSNCLSSLYFPSSGLPLRCKAELDDVKQKADKELDVVAHACNPSTLVGQGGRTILRSGV*DQPGQH
2960	16861	A	2980	2	378	ARVSI GFLGLIVGAHDMFTGRMDLYTRTYCTFATILIAHTGVPVFI*LATLHGCN MK*SAAVL*ALRFIFISTVCGLTGIVLP N*SLDIVLHYMYAVAHLYVLSIGAVF AILGRFIHRLPVF
2961	16862	A	2982	2	409	PAVAEAYLKPVVDDSKGSFLWGKPDLDGIRECCQRNFGWNRTRTDESIFPVLKQLDAQQTQLRIDSFFTLAQQEKDDAKRIKSQRLNRAVTCMLRIEIEASSEIEAVSVD*QKELELIDKAVACHLEYMYETDP
2962	16863	A	2983	3	453	HASAHASAHASGQRKGAAPAEKKCGAEA QHEGLELRVENLQAVQTFDSSDPLQKVVCFNHDNTLLATGGTDGYVRVWKVPNLEK VLESKAHGGEIEDLVLPVPEGML*IVCPD HYSVPGINDFMWLL*LNWGNRLYPHIS VYLMFHFRTF
2963	16864	A	2984	3	417	LILPGFGIISHIVTYYSKGKEGFGYICMV*AMISIGFLGLIVRAHHIFTVGIDVYS RAYFTSATIIIAIPTGVKVF*LSLTHG SNMK*SAAVL*ALRFIFLFTVSGLTGIV LANSLLDIALHDTYYV*THFYVLSI
2964	16865	A	2985	273	408	MKIFIF*VSPPLFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFLAVTFI
2965	16866	A	2986	176	335	TFQPSSELWRTALLPRLECSGLIIAHCSL ELLGSSSPLASAS*IAGTTGSILRY
2966	16867	A	2987	65	398	KKEFKIGRKAAEKMTNRINNAFGPGTAN ECTVQWWPKFKCKGNKSLDEECGRPL EDDNDQWRALIEADPLTTREVAEELSV NHSMVQHLK*VGKVKLNKWPHELS
2967	16868	A	2988	2	158	PGWSLTPDLR*STCLSLPKCDYRHKRP SPTSRTFDHAPNKNSSHSPPIYM
2968	16869	A	2989	435	23	GVVPPNPQKSFYFPQRLKIWGGGGRKRP PPKKKGSQKTPEGF*KPPPKRRKKIFH DPGKKGPPKGIFKRGPPLEFFFFYFFFF FFFFFFFIITIECLHSRFPHRHNNKKFP PNPPSPRFWPQHLNLSLPNPKNKEP
2969	16870	A	2990	410	3	GGRGHFFSGAFFIKFPWNKKGISQPLCF PRGGSPPLGPVRRGGPPCWGPLCHKG PVKKTGAPRGKNGISPFPCFPPLGSFNR SGFFWALLGSPPLFFFFFFFF*DRVSLHHP GWNVAQS*LTKTSTSWQVILL
2970	16871	A	2991	371	132	KQSLPFKVGFFFFPPEVENAIYPDSHTA FYSW*KRSTFSKKKKKKKKERKKKEE RKEGRKEGRKERKKEGKKEIENA
2971	16872	A	2992	336	1	CPRWSRTAGLK*STCFGLPKCDNRHES PCPASSVLND*QLSTVQRAT*WQTKSLV LKAPPARGALPVSRVSPPPSSHHFAYF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
2972	16873	A	2993	317	440	LHMT*QVSCFLRLR*SLALVPQAGVQ*RD HLGRLRQEHHLSPG*LRKFFFFFFGRDGV LMLSM LVFNSWTQVMLLPQPQVLGLR
2973	16874	A	2994	2	181	FHHVGLDLLTL*SACGLLPKCWDYRREP LCPALVILLTAKFTNFRYRVKNVCTPHV ESN
2974	16875	A	2995	1	165	GFHCISRDGLDLLTS*YARLGLSNCWDY RHEPPSPAPLFI SYSICLFLSKLIQFL
2975	16876	A	2996	405	2	KKGFP IFSRMFFLYKHTEKPPLASQKFG DPKWSPHPRPIFFFLKKGVLYVWREGF KEHPP*FPPGPPKRW*RVKPPHPPPF FFFFFFLYVMGSHCVAQAGLKLLGSSTP PTSASQGAELAGVSHRAQPHAS
2976	16877	A	2997	2	415	CLFTGGGLTGIGSAGSSLDIVLHDTYYV VAHFHYDLSIGAGFAITGGLIH*FPLFS GYALDQTYARIHFTIIFIGVNLTFLEPQH FLGLSGMPRRCS*PDAYTT*SMLSSVG SVITLTAVIVLIIMIREAFDSKRTVL
2977	16878	A	2998	349	370	HHFY*SITAFRPFQHMELRNFFFFFFLFF FFFFFFFVFLFIFLFLFYFLFYELIYL ILFFL*HHFYSAV
2978	16879	A	2999	36	139	LCHCTPAWETFSKEKKKKKKKKKKKKK KKKKKKKPGGS*KTALSHDCATVLQPG RLFQKKKKKKKKKKKKKKKKKKKKK
2979	16880	A	3000	104	373	SADREXXSKTDNLLGH*TNVNCCKVPRV IQSVFSSHSGLKLEINNRMKMKSLNT* KINNISYWVQC SLYNLKSNSYTKSSDNT TTQYMY
2980	16881	A	3001	1	396	LDCSKISSYLQSSSHVLFSSFSFFFFFF GGGGGFALENYPYPAGLGPQKKKTLSP WLVGGPPFPPEKAPP*GGHFLGKKPKNP GGQNPKRPSGEGNPFPPGGEKKQIGP PTGFGGKPPFSF*PREPPGP
2981	16882	A	3002	412	104	FFFFFFLPVRQTFYPPQPFVSFFPLFPFKF FFFP*AFNFFWGFFPIFSPPKFGFFSKI SRLVFFSLPFWEKFFFLPPFFFAPLRF FFKGPPXFFFFFFFFFXXY
2982	16883	A	3003	400	46	LFFFFFFYKLFPFPAFGGFPPFPL*NFF FPPGPFFFLGGFPFPPPPK*VFFPKIP PGFFFPF*KKFFFSPPFFLPPPGFF FNPPPPFFFFFFFFFFFFFFFFFLCVV VQVEAY
2983	16884	A	3004	411	69	YSPLPPLFFSSPPSKFPWPPFSLFLTR VYKGGFFFPFFPELFGPPGLSLGSKPP PVFLGGDPAFFSIPHRVGS LPPPNWP FIGPSFW*ALFPAPPLFFFFFFFFLSSFFF F
2984	16885	A	3005	3	200	DAWG*LFSTNHKDIGTLYLLFGA*AGVL GTALSLIRAE LGQPGLNDHIY NVI VTAHAFVII
2985	16886	A	3006	259	146	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFGLNDILL
2986	16887	A	3007	118	414	QNQPPQNKATHTVKIEKKEKPKETKTVA EHNKAKTAEKSEE*TKKEVKGKQEKVN HTAAKVKEVQKTPSKPEKEDNKKAAVS KHEQKDQYAFIRYMI
2987	16888	A	3008	427	111	FFFFSPVGNFSPQQFPPPPPPPKIF FFPPPL*FFWGGFPFPPPPKVFPPKS

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						PPGFFFFPPP*GKKFIFPPPP*FCPPPGF FLSPPPPPPPPPPPPPPPPPPP
2988	16889	A	3009	3	302	SLASCLSYLVCVIFLGQPKPTI*LQNST PHKK*NPTEYVKTCTQIFIALLFKKEK QPRCPSAGEWINKMLYACTIEYWLAIKR YEILYATV*MYLEKI
2989	16890	A	3010	1	409	RLHDATFPPIIEELITFDHALVITFLIW LLVLCALFLTLTKLTNTNISHAQELET V*TILAAIILALMVLPSLRILYITDEDN DPSLTIKSIGHQWY*TYEYTDYGLMFN SYILAPLFLBPGDLRLLDVDNRVV
2990	16891	A	3011	157	2	GRVDLKIQLARCAGGACLSQHTQQNHL NPGKEKCSSES*LPPCPPD*VTKQ
2991	16892	A	3012	2	423	ARAARAHIVTYYSKGKEFPYIGMG*AM ISIGFLGFIGRAHHIFT**IDGHTRAYF TSATIIIAIPTGVKVF*I*LATLHGSNMK *SAAVL*ALGFIFLFTCGLTGIVLANS SLYIVLHDTYVVAHFHYVLSIGAVFAI
2992	16893	A	3013	2	140	ARANILLTLTAQELWDEPRANNLI*LAY TLAFIVKKPLYGLHL*LPAHVETPMDG PILLAALKLLKGGSGIIRLTLILNPMTK HIAYPLLGLSL*GIIITRSICLRQTELK WLIAYS*ISHIALVVDILIQTP*SKHF TTNSHCPRMTGPQSQQNLMTSLHTSFYS KETSRLRTPMLTP
2993	16894	A	3014	2	420	PVLAAGISILLTDRDLLTLFDPGGGGD PILYQHLF*FFGHPDDYILILPGFGIIS HIVTDYGRKEPSGYIGMV*AMTPVGFL GFIE*AHHIFTVGIDAHTRAYLTSVSIL IVIPTWRQVFS*LATLHGSNMT*YAALF
2994	16895	A	3015	6	292	AHHIFTV*IDVYTRAYFTSATIVIAIPT GVKVFS*LATLHGSNMK*SAAVL*ALGF I*LFTVGGGLNGIV*SY*LLDIELHDTY* FVMGCPKRVYF
2995	16896	A	3016	3	422	TPIIIGGFGN*LFPLIISAPDMEFPRIS NISL*LLPPSILLLLASAIVEAGT*TD* TVYPPLAGNYSHPGASVDLTIFSLHLTG VSSILGAINFITPIINIRPPAITQYQTP LCA*CDLMTAVLLLSLPDLAAGITILL
2996	16897	A	3017	21	490	TPFPGRHLTMFSLHLAGGCSILGAINYI TTLINIRPPAITQYQTPLEFV*SVLITAV LHLLSLPGLTAGVTILLADQNLNTFFD PAGGGDPILYQHLF*FFGHPEVYILILP GFGIISHIVTYCYGKEPEFPYIGMC*AM ISIGFLGIIV*AHHIF
2997	16898	A	3018	98	402	LRSQHSKSFQISGKPSQEWQISPST DYIINT*HFNAQMLKNY*HQPGLHDF FPKKKKKKKKKKKKKKKKKKKKKKKK KKASSSSKKDPPGGGPT
2998	16899	A	3019	399	229	PPPPGGGGPQGGPPPPRGGFLPKSPGGVF YPPPRGGKIFSPPPGFFGPPRGFF*GAP P
2999	16900	A	3020	2	401	SDAVL*ALGFIYLVLEGGLTGIVLADSF LDLELHDTYVGAHFHYVLSIGAVFAII GGFVD*FPLFSGYTLDTYAENHFTIIL IGANVTFLPQHFLGLSGMPRRYSYPDA YTT*NILSSVGSFITLAAALL
3000	16901	A	3021	413	67	PPPPGKIFFKKTPKKKIFPPPPQF*IFFP

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						PLPPKKFFFSPPNP*FFLGGFSPPFFPPQK KIFFFPKIPNFFFSPPPLKKKIFFFFPP* IFFPPRFFLKPPPPFFFFFFFFFFFFFFFF FFF
3001	16902	A	3022	2	332	LTL SILSIIAGS*GGLNQTQLRKILAYS SITHIG*IIAVLPYNPNTILNLTIIYII LTTTAFLLNLSSTTTLLSRT*NKLT *LTPLIPSTLLSLGGLPPLTGFLPKW
3002	16903	A	3023	1	412	RGPPFFFFFCVFFFFFFFFFFFFNKGCR HSKRFFFFFFKKKKSSRTRDRV*FYPK GWRSPFLFFSPGGRGFFFLSHQVGFNS EVLVVFKKNLELFRGSPARKKKKKKKHL E
3003	16904	A	3024	279	1	LGRNTELWKSCKGMDILKTNCGKLANEP FRQPRVLGIGGEAPRAGSGPPSRAPPA* TPGPSSAGSWP*PPGTGRAPRGPPAPSAP GARSPGRPG
3004	16905	A	3025	151	401	KKPLGGPNLTGEGKKKFFSLKGGKKKPP GKFLKKTFFLGGEEKMGKTPPKLKP*GK KKIFGKRGKKNPKTLAVKKFSKKKKK
3005	16906	A	3026	416	140	YLSPLKKFFTPPPLRMFLPPNPLKNIFF PPQLKIFWGGWAQNSPPPKGFFSKNPK RVFLPPPIRKRYNFPFHGKILAPPKNL* SAPPPPIFF
3006	16907	A	3027	379	31	PPRRAGVFFFKNPKNPKPPPPREGGRF* PFFPLKF*FFPKPQNFLGGGGAITPPP KRLGQIPIPTERFNLSPPTQKRINFPPPG KGGPPPPLLKPPPPPPPPPPPPPPPSL NSFI
3007	16908	A	3028	28	420	MQQTMAHIFLCNKFANCAHVPRT*SET KPMSTPLQFD*TYKGEKSCKYAEHRTW KQ*CVFSLYQIIP*EKTWKNQCGTNF NQFFKQTTHL*NHTRDNQICFSKIGLEY YYRITTRQHLLKLRTVCIL
3008	16909	A	3029	1	401	LGNNGEAVSEKREKSKQEKSHNVVVG FFFFWGGKPPFVPQAEGQGRNFC*PKPWP PGWGEFPGPAPRGNGRQKQPGRGNGF V*REKGGSMGGPRGA*NPGPKNHPWPP QGPEITGGTTRPHPSGIFKKT
3009	16910	A	3030	285	397	MFIKGDGLNKLRLPGAAAYACNPSTLGG* AGRITRSGD
3010	16911	A	3031	265	2	KKESSCIKATNSNSLFFLF*SVFFFFVF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFF*HFKSALLWVTDLGLNSD PRV
3011	16912	A	3032	410	49	GFSPPPP*KFFFSPKPLNFWGGGGPNFP PPKKRFFPKNPPGVFYSPPKKKKKFFSP PP*NLAPPKIFLKSPPPPPPPPPPPPP FFLSNVSNGLTNMYILPCKDPSCPTTFP ILGSLISL
3012	16913	A	3033	177	2	VTPPPPPFFETRSHSVARTGV**SDRCS LQPHPPSIK*SSHFSLPSSWDYRSMPPH AS
3013	16914	A	3034	75	395	MSYKHXKXKKKKKKKKKRGAP*KKPWGG PKLTRDGKKKFFSLKGAKKKPTWKFWKK TLILGGRKMGTTPPKLKLPLRKKKIFKG *RGKKHPKSLPVEKFASRGRIKK
3014	16915	A	3035	400	83	KKEGPARVVSPTVTPPLEGPGVGRSPQTR



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NF*PTPPTHRKSLPS*KSKIDWRGIPLY PPPPRVKPKKSFNPGNRRFC*TKIFPCP SPWAPKTHPPFQKKKKKRVYK
3015	16916	A	3036	3	196	DSMPQT*NKSFARAKKKKKKKKKKKKK KKKKKKKRGPPPLKKTGGPKLPGGKKK NFFFFRGG
3016	16917	A	3037	1	411	FCYDVCVESGCADYSIVIIMKKKKEK*K KKKKKKGGGPKKNPGGAQNYPGVEKKI FSLKGGGLKKTPRGNFEKKPYFGGKNGA PPQKNKPLGEKKKKFKREKGGKKLQFPW GKKISLPGFYLKKIYPPGRGFFNFS
3017	16918	A	3038	3	429	NFFFFKKPRGNNFFPPPKGFFSPPSPLK FFFFFFPFFFGGGPHFPPPPKRRFFQ KPPRGFFFPPL*EKNFFPPPVFFAAPP VFFLTPPPP
3018	16919	A	3040	1	111	IGLSGMPRRFSDYPDAYAT*NILSSVGS FMYLQQDNK
3019	16920	A	3041	76	967	QLLKGGVSGVCPLLMFRVRSFFLLVGS WSSLASGVKQPQTFAVSVTVLKAARLELF IPPRGLVSLASGVKLQTFVSVTAHKS SVDPKNSGAQLASPSGSRTRAAGGAACQ SRCRVALLSPWVVDGTGRRGAGGGARR GSGRTGAHGVGGRLRHGGHLVPSAPW KGS*GLARNRAQRRWAGTAGGPSTPSAA AGPGA KSLTALCEQGWPAAPSAGPTKPT PTRNSSWPASVARSPGSRSLSLHTSLQ AEGVGSSLGQPSKGLPQCSGGAEGLLKC RQSGSPGRGGTESERGL*GLPQCSGGAE GLLKCRQSGSPGRGGTESERGL
3020	16921	A	3042	39	141	LSIRGLNIIIKRQRL*DWIKQDSTLCC P*EIH
3021	16922	A	3043	2	405	LFSTNHIYIGTLYLLFSTRAGVLGTALS LLIPAE LGQPGNLLGNDHIYNAIVTAHA FVIIFFIERPIIIGGYGN*LGPLIIGAP DMAVPRINNITF*LLPSSLLLLASAIE EAGAGTG*TVYPPLAGNYSHPG
3022	16923	A	3044	3	134	HLNPGGRGCSEPRLLHCTPSWATE*DSV SKKKKSRKGWTGLFI
3023	16924	A	3045	44	187	DPRVRQYQTPLFV*SGLIFAGLLLLSLP TLGAGITILLTDRLNLTAVFDPDGGGDP ILYQHLP*FFGHPEVYILILPGFGIICH IVTYYSKGKEPFGYIGMV*AMISIGFLG FIAGAHHIFTGGIDVDTRAYFTSATIII AIPTGVKVS*LRILRPNLCLRTSPISP NPRGRHHYTTNRPPPHRRV
3024	16925	A	3046	434	40	GAPPPPPGRRFFFLNPREDTFPPPPQKG GFSPPPPPKFFFSPPALFFFGGWPNSP PPQKNFFF*KPPEFFFFPFLKKKIFFP PPLFFPPQIFF*TPPPLFFFFFFF FFFFFFFRGCKINFIVRGF
3025	16926	A	3047	1	399	LFTGGGLTGIVLTNSSLDIVLHDTY*VV PHFHYGLSIGAGFAIIGGSIH*FPLFSG YTLDQTYAKIHFTIIFIGVKLTFFPQH LGLSGMPRRYSYDPDAYTT*NILSSVGS LISLTAAIILIFMS*EAFASK
3026	16927	A	3048	116	367	GASMILSSMIFLECTVGGFPVFSVYLFK LQILRQSSTMCFVLFCFFEIRSCSVTQA GV*RRGHGSL*PQPPGLSHPSSRDHGHV

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3027	16928	A	3049	6	345	SQLLRRLRKENCNLNCGGGYSHQR*HQC PLAWATE*DYLKKKKKNSLFLKTGGFY PFLKKAPLGTTLSPKNNLPLSPLYKKRT GPWNWERKNFGKKKGGVIGLQGGKTIPK
3028	16929	A	3050	261	2	NKKSPPVNLWWKMGFFFKAKRVLSWK GGGGFFFFSWRRSFTFVAQAGMQWRNLS SLQPRLPDLR*SACLGPDPD*DYRREPQ YP
3029	16930	A	3051	160	2	ICVDEQAGVQWRYLGLSLQAPPPGLATLS CLSLMSSWECRQPPPLG*FFVCPR
3030	16931	A	3052	89	3	PLTSGLLLLT*QKLAPISIIYQISPSLN
3031	16932	A	3053	344	2	HVEAPIAGSIVLAAVLLKGGYGITRLT LILNPLTKHIAYPFLVLSL*GIIITSSI CLRQTDKLSLIAYSSISHIALVVTAILI QTP*SFTGAVILIIAHGLTSSLLFCLAN SN
3032	16933	A	3054	266	2	FQPPISAYTKISPSLNVSLLLTSLISL IAGS*GGLNQTQLRKILAYSSITHVG*I I AVL PYNPNITILNLTIIYIILTTTAFLL LNLN
3033	16934	A	3055	3	32	KYNSLIMPTMIATITLNLIFYLSPILLY **SSCPP
3034	16935	A	3056	3	33	KNNSLIIPITTIATITLNLIFYLSPILLY **SSSPPS
3035	16936	A	3057	57	445	ANVWAPHGPAKLTNKNYHIWKSRLKI ANMTIKKLENEVIGLTLDPFKTYVELVQ* RQNAID*RKHQPVKQSP*PHSYSQL IFHWGAKANHGKDSLFYK*CW*NTTIS SQKLNLTDLTNFTKIN
3036	16937	A	3058	311	1	RVGLLLKLNKISWPPPPFYGPS*EKEPL CFSQIGLFLTRTMVLNHLSPVKTTRPY NKIAPFRELEFFFKDRVSI CLPGWSAVV *SQLTATSTSQASSDPGRV
3037	16938	A	3059	138	411	WERPWKAQEAFFWI*VSFAWAPPPLMEK QIPPDLEQHYNVPVGNRNQPFVSFFLR WSLTVAQAGVWWRDLGSL*PLLPGFKRF LCLSLLS
3038	16939	A	3060	1	189	FCRVGQAGLKLLTSSDPASAS*SAEIT GVSQRAWSKITILKSSSFSYFPNSCKMC FWLICLN
3039	16940	A	3061	3	406	DAWADANVLILPRFGRTSHIVTYSGKK EPFAYIGMV*AMISMGLGFIV*AHHIF TVGIDVNTRAYFTSATIIAIPGVKGF S*LATLHGSNMK*SAAVL*ALRFIFLLK KKKRGAVLKVPWGGPSLPGCG
3040	16941	A	3062	451	82	PPPTNYFSPPPAFLPGGGPPRPPPPKK WSPPTPPPVVIMPPPKKKKKFFPPRGRW GPPPKIF*KPPPPFFFKKNPPFSPGE NRGVFFSTKPPPPWGGKNFAAPGAPPPP PFFFFPRTGGG
3041	16942	A	3063	430	1	FFPPKQLIFWGGGGPKSPPPKKKFFPKK PPGVFFSPKKKKKKFFPPPLNLAPPKI FFKSPPPLSFLFFPFFFFFFFFFFFFFFF FFFFPLSVQTLKRTAPPQPPPLD*EK APAPRVP*TGEGMPAVNVAFAPPFFYKE RPS
3042	16943	A	3064	1	409	PTRPRESTYQGHHTPPVQKGLRYGIILF ITSEVFFAGFF*AFYHSSLAPTPQLGG

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						HWPPTGITPLNPLEVPLTT
3043	16944	A	3065	1	137	HTFNFSIYQKATVIKTWYWNRRHTVE SPEINPYIYS*LIFFLF
3044	16945	A	3066	4	426	KLEN*KMVLKEIKEDLNKQTDILFS*LQ RLITVRMSILPKLIYKFSAPIQIPA*F L*IKIIKCMRKGK*TRIAETIFFFFFL SQSFILSPKLDHRGGITANCTPPWAIKG KLLKKKKKKPKTKPEKFFIQKATGAEG GVH
3045	16946	A	3067	411	187	RNLPNVPPRPETHFVLLVKTGVSQVGQGG GKLLASKNPPSPAPPKSNDYRGEPPRPA PRKFFF*LNKFKIYGGPKN
3046	16947	A	3068	193	471	QCTCIKVHSGQKTGSTPLVIGELQIKIT LGCYYTPTLMAQIKKTDRTKCW*GYGAI GMLILCWRECKIVQSL*KRVWQFII*LN IYLAIKLNI
3047	16948	A	3069	323	478	FFXFXFLFFFIILXYFYVF*KLFYLYLFX YIFKIYFIYNFYIILFYIIFII
3048	16949	A	3070	1	378	GTRRFFFHSITLLILGLSNTLTIYQ*W RDVTRESTYQGHHTPPCQKGLLNGIILF ITSEVFFFAGFF*AFYHSSLAPTPQLGG HWPPTGITPLNPLEIPLNLCVLLASGV SIT*AHHSLENNR
3049	16950	A	3071	201	2	TTPIQLFLKHYHT*NFNYNFFFEIGSCS IAQAKVQWCDLCLLPQTLGLKHSSHLS LQSSWDYRHA
3050	16951	A	3072	261	1	EKAMGGGPFVKKSPGEGPTTKGWPLKG PLEGGQRLTGPFKSNGLRLLLLFGSNE VSLCCPG*SRTPDFK*SACLSLPKCWDY RHG
3051	16952	A	3073	333	52	EIFKKKKKGGGRFFNKRVPFRVSNR PRAQFFLETFFFFPERGFFFFFETES YSVTQAEV*WNYLGSQQPFRKRFHLS LPSSWNYRCK
3052	16953	A	3074	7	214	SQLQENRLNPGGGCGEPRSCHCTPVWA TE*DSVSKKKKKKKRGWVPPSLGGGP KKKNPFFNQEGGL
3053	16954	A	3075	180	419	QKHLSTLHYLFKRDVFFFLKGSFVVSQ VGGQGHNLG*LKAPPPRLTHFSCLTRE TWKNRPYFFCFFIKTGPHVTR
3054	16955	A	3076	371	208	QKLSGHGGSRL*S*PF*EAKAG*QLVSG GRGCSQL*SHQCTPAWVTE*RLVCKR
3055	16956	A	3077	349	3	TFCWQKYMCRSLCHPFPRTWSTKKKR PFFQKGQGDAPPYKKVQRGNPPPLKGR PSRGPPKKCKVFKAPVFLFRFSPPPFF PPPLFFFFF*DRVLFCCPGWSAVAQLT ATS
3056	16957	A	3078	124	1	ISSETPAVKSSFPGVGVVHACNPSTLGR *GKEITRSRDRDH
3057	16958	A	3079	205	1	CLVQNIWACVSHWRYTMSCKGC*RLGLM CVCVCVCVCVCVCVYFCCCCCCCCYC*DE LSLCHSDCSAVA
3058	16959	A	3080	3	413	GHHTQPVQKGLLYGIILFIT*EGFFFSG FF*AFYHSSLAPTPQLGGHWPPTGITPL NPL*VPLNLSVLLASVSIT*AHRLI *NNRNQIIQALLITILLGLYFTLLQASE YFETPFTISDGIYGSTFFVATGFHR
3059	16960	A	3081	1	321	NSLNPGDGGCS*PRLHYCTPAWGTELD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ISKEKKYPYHVYHPSMKMTIYNRQQNV NHIYIMLVEHSQTQENTCFMISGNFFFN LPVLGEGEKNQHSISFKLFFNF
3060	16961	A	3082	117	484	VLKYFIDSEVNAVLFSSCSFVTDVFVL FFFFGKGVSFPCPPAGIKGGGFGFLEPLA SGFKRIFFPNPLEKWE*RAPPPRGKFW NFFFFFFLRELFFAPRWEGRGKILVYL KGPPWGYPHF
3061	16962	A	3083	381	227	CISRDGFYHLGQAGLELLTSSDPPALDS *SVGITGVSHRTRPLLRNVQF
3062	16963	A	3084	2	391	SHAYHTG*PSR*PVTGALSDLLMTSCLA M*IDFHSITLLILCLLNTLSIYQ*WRD VTRESTYHGHTTPVPKGLRYGIILFIT SEVFFFARFF*AFYHSSLAPTLPQLRGHW PTCITPRNTLDVPLNT
3063	16964	A	3085	2	248	IMRSGDRDHPG*HGETPSLLKYKRLAGH GGMRLWSQLLGKGGTADSHHVVLLILET FYSRLRERRHLTSVPTLGMNYWAQDIR
3064	16965	A	3086	276	243	EKWPD*SRACPVLCRNGQYSKGRCLC FSGWKGTEDVPTTQCIDPQCGRGIC MGSCACNSGYKGESCEAPRYIPEKE
3065	16966	A	3087	3	130	GFYHVGQAGLELLTL*SACLSLPKCWDY RREPPRPAHTPPHS
3066	16967	A	3088	277	2	SSSSVFCLLVWTSSSSSSAARLPPLTG FLPKWAIIEFTKNNSLIPTIIATITL LNLYFYLRLLIYSTSITLLPISNNVKIK* QFEHTKP
3067	16968	A	3089	404	60	FSHGKMRFFSPSPKIFFSPQSFYFLG GGGAKMPPPKRFFFKTPRGFYFPP*K KKNFFFPDPVKFGPPRGFLKSPDPFFF FFFFFFFFFFFFSPTFTTVFHLMLKSD ND
3068	16969	A	3090	405	186	INKKPEAFTNTVDQMVLTNSHRTFYPTA TACSLSGAHRFTFSRMDHV*DHKTSLNKF KTEITLSTLSNHKLEP
3069	16970	A	3091	371	1	SPFLVQKGLRYGIILFITSEVFFFAGFF *AFYHSSLAPTLPQLGHWPTGITPINP LEVPLNTSVLLASGVST*AHHS LIEN
3070	16971	A	3092	263	3	NKRSPPVNLWWKMGSFKFKA RVKISWK GGGGFFFFSWRRSFTFVAQAGMQWRNLS SLQPRLPDLR*SACLGPPDC*DYRREPQ YP
3071	16972	A	3093	1	392	FFFADFKKMFILINHFKMELTTYFELKR NEATASENC*DAVKAVLGKFIIVLSTYI RKEERPRINNISFQIKHWTKKN*T*GKQ KKKKKKKVTGPEIPKFLIVKSGKPPKV ILTGAWGPIKFLSFITRL
3072	16973	A	3094	3	367	EM*IEITMRHYNTARRLKF*KTDNIKC **GHGTSGLTIYHWQE*KMVQLWKIV* QLL
3073	16974	A	3095	3	257	HEVSQDGLNLLTS*SARLGLPKCWDYRR EPPCLAWLILPDDCVIFQKLKLLHHNLL NLSCIDVLMGIYSLNFSQSNFPFFFFFF
3074	16975	A	3096	189	414	KGLVMVTS*CKMFFCLSIFFFFFBERGFC FFAQAGVQGHNLSSLEPLPPQLKQFFCL TLPRS*KYRPAPPCPANFY
3075	16976	A	3097	1	299	ENYRPISFMNTDAKILNKILANQIQQCS KRITHRDQVGFLPGMQGFYI*KSIXSI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NAITHHISRLKKRNHMIPSI EAKKAFNTHS *FMKKNKKLAFQET
3076	16977	A	3098	362	126	FIHTHTHTHTHTHTHIYIYIYIIASFQW NAIRGRMKCINKP*KDMEEKLCILPSE SQSAKATYLLYDSNYITTEKAKL
3077	16978	A	3099	3	423	RHEHAYHIVKPTP*PLTGALSALLMTSG LAM*FHFHSITLLILGLLTNTLTIYQ*W RDVTRESTYQGRHTPPVQKGLRYGIILF ITSKVFFFAAGFF*DFYHSSLAPTPQLRG HWAPTGITPLNPLEVPLLYTCVLLASGV
3078	16979	A	3100	392	83	LRNTNCGHGAPFKNSPFFFPQFLVKNSPA YFQNKEKDVGKPPFFFRAPDGAPFFKKK KK*GLALSSRLEYGGMISLELLGSSDTF ASASRVARTTQGCHAGPT
3079	16980	A	3101	81	247	GGWGGPPLKPPLF*KKTGNFNWPPFFKG KEKPPPNNPRGGGKKGGPKPPPVIFFFF
3080	16981	A	3102	3	388	HEKEPF*YIGMG*AMISTGFLGFIV*A HHIFTVGIYVDTRAYFTSASIIIAIPTG GKVFS*LATLHGNNMK*SAAVL*ALGFI FITTESGLTGIVLSNSSLDIVLHDTCYL VAHLHYVLSIGAVFAI
3081	16982	A	3103	3	387	HERHEELSNS*ANNLI*LAYTIAFIVKI PLYGLHL*LPKAHVEAPIAGSIVLA AVL LKLGGYGIIIRLTILNLPLTKHIAYPFLV LSL*GIITTSICLRQTDLKSLIAYSSI SHIALVVTTAILIQTP
3082	16983	A	3104	3	381	HEQSHAYHIVKPS*PLTGALLALLMTS GLAMGYFHFTITLLILGLLTYTLTIYQ* WRDVSRESTDYQGOHTPPVQKGLRYGIIL FIT*EAFFFFARYF*AFYDFRLGPTPQLR GHWPTGITPLNSL
3083	16984	A	3105	412	111	FLGHPLFKKKMGKKRGLPKMGV*HPPA PKGPPPLKKKKKKPGGGAPLYSPFG GEGKKNPLTPEGGGPKPNPSPPPPPPGG KKKNPPPLSPKKKKKK
3084	16985	A	3106	298	98	FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF F*L*IYY*AI CAINNIRGAGAELYSRSD FVCY
3085	16986	A	3107	2	417	ATHVGLQDVTSPIEQILTTFHDHALMNI LIICFLDLGALFLTATLTKTNM*YAQ EI*TD*TILPAIILNLMALPSLRMLYIT DEGDDPSLTIKSIGHQWY*TYEYTDYGG LIFNSYIRPPPLEPELGELRLLDVDNR
3086	16987	A	3108	8	430	VGLVLFLSELPLNGILTFHQGIYSFF PGGRTVALMVGSWGLVMASD DLGLCH AFTPATQLLLNLAVASPL*PAALRIGCH SKTINALTHFLPRGTPTPPRPILVTIET MSLLIPPIADQR LAAGFTARHLLLHLS V
3087	16988	A	3109	3	453	PRAIKFYRDWPGERHKRIAWKGDPC HMV LIKDEKGLMCQKKKKKTFFFWAPKIPLV FPPAQKNQGS*PNPPGGGGNPPLRPGF* RKKPPALMGPPSPSGGINPKSF FYLNP GPAH*PRGEN*LGPVFENLFLPLLKKIF LWGELRCSQT
3088	16989	A	3110	398	2	S LFQKNPNPLVG*KKKGKALPQGGPPPLF PPLGGAGPGGSQGRGWGPPRPPWGNPFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						F*NPKIWPAKGGAPFSPSEKG*AGGFF LPRGGGFLTLQIPPPPHLGGKSKPPFQ KKKKKNRQGTSMWQGWGPQ
3089	16990	A	3111	3	371	SSDPPTSAFQSGTTDMCHHHHAQLIFN FFVETGSCYVAQAGVQWHDHGSLLSQTP GLR*SSGATVLNWPALGPRRPDPTRME SLVLMKPRGSLIRSACPDCLVFWFSFF HEAEGCASEC
3090	16991	A	3112	233	449	FALFS*LATLHGSNMK*SAAGL*ALGFI FLFTAGGLTGIVLANSSLDIGLHDTYYV EAHFHYGLSIGAEFAIIGGFIH*FALFS GYTLDQTYPKIHFTIIFIGGNITFLPQH FLGLSGMPRRYSDDYPDAYTT*NILSSGG SFNALNAGSIT
3091	16992	A	3113	458	2	RGPPPPPPPKFFFF*TPGKNSPPPPPEG VFFPPSPPNFFFSPPPLFFFGVPPIS PPPKSFSPQTPPRFFFFPPPLKKNFFS PPPLFLPPPPFFFPFPFFFPFFFPFF FFFFFPFFFCGDLEGLPGTGMLACVI LLRANRKARTRG
3092	16993	A	3114	1	418	LNTTFFYPDGGGDPNLYQHLY*F*GHPD PDIHILPRPGIRSHIDTDYSGKKEPYAY VGMGWAMTSIGFLWLMVRARPLFTVGVG VDAQAYSSFASITIALPTGAEVFS*LCP LPLSGMK*TGAAVWALGLRFIFTCGR
3093	16994	A	3115	1	425	PRINNISF*LLPPSLLLLLAYAIVEAGA GTG*TAYPPLAGNYSHPGASGNLTIFSL HLAGGSSILGAINFITTIINIKPPAITQ DQTPFLV*SVLITEDLLFLSLPGLAAGI TILLTDLNLSTTFDPAGGGDPILYQHL F*FFDPAGGGDPILYQHLF
3094	16995	A	3116	2	383	GLSCTNHKDMGALYLLGARAGVLSTAL SLIRAEGLQPGYLLGNDHIYNDIVTAH AFVIIFFIVIPTVLGGFGN*LGPLIIGA PDTAVPRINNISI*LLPPCLLLRLACAI EEAGAGTG*TVYPPL
3095	16996	A	3117	1	259	PTRPALVVTAILIQT*PFTGAVILITA HGLTSSLLFCLANSNYERTHSRIIILSQ GLQTLLPLIAF**LLASLANLPAPTPTP HQ
3096	16997	A	3118	3	174	LIRGGRGCHELRSRHCTPAWATRARTLS OKK*KTTNPKKKLCLIFFGGKKKKLKKG
3097	16998	A	3119	155	1	PDFFNKSMDDKKKTARGWEDSSSSFCFFK RDRVLLCCPGWSAVAQS*LTAAS
3098	16999	A	3120	420	2	PPPKFFFPPTPPFLGEGGAKTPPKKIF FLKKPPGVFFFPPLKKKKFFFSPP*FLA PPKIFFKRPPPPPPPPPPPPPPPPPP FFFFFFFFFLVFIVLQVQKVHFLKKCFN IQFPLASDNS*PSMIHEKFYCESNIEF
3099	17000	A	3121	48	387	RDPVLQKKEKKKKKKPKNQKKKKKGGP F*KIP*GAKIKPGKEKNFSPKRGAKKK NPGNFEKKTNFGGKKWKGKPPKN*RFK GKKKFLKGKGGKKTQIPWGLKIFNGFD
3100	17001	A	3122	237	2	PPFVVLPPFPLKASSP*SL*FLGGWP NLPSSPNKGSFPKFPWFLLFRPP*GKNF YLALPR*DWPPQGFL*TAPP
3101	17002	A	3123	448	130	PPRFFFEFFYSGPPKPPFFKTPVFLGVK PGVFFFSPLYQKKPTNFGPKMGAL*RIPL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FETPIWVFPKIGFPHKKKPPVLN*PPTRK PPDKILKKKKDDCISLARN
3102	17003	A	3124	453	3	SSAREGGGVPPPPPKIIFPPPIFSWG GGGTSKPPPEREVFPKNHGGCFFSPP*K RGKYFSPPPRMGPPPGVFFKGPPPNFFF FFFFFFFFFFFFFFFFFFFFFFFFTKKNWF FFKAFRMSPKVPVPPFFFCNYRVVFRPR VRPRVRPRV
3103	17004	A	3125	443	2	YFPPFGRVIWGDLSLGGVNLNPPRPHKGT PFPPKKIIFSIRPGWGGPPLPPPQRMW GGPPPLFGLFRPQKIPFPKKKKIKPP GGVCVGVGVCV*KKKKNPFPFLWAGLK EPCFFFFFFFFMEFECSCCPGWSAMARSQ LNCNLHL
3104	17005	A	3126	3	186	PVIYSTIFAGTLITALSSH*FFT*VGLE INMLKKKKKKKKKKKKKKKKKKKKR GGGL
3105	17006	A	3127	171	38	KKKKLFFPPPREKWGPPKNFLKRAPPFFF FFFFFFFFFFFFFFFFWSERS*VA
3106	17007	A	3128	16	189	ILGEVIWV**FF*FIKKKKKKKKKKKK KKKKKRGAPFKKTPGGPQITPGEKKKIF SL
3107	17008	A	3129	401	85	LVNFFSPQEKRGFFPPPPPKNFFFSRPG FFFLGGGGPIFPPPKKSFFSKNPPGVFF SPP*KKKIFFPPLFWADPRFFFKGPP PFFFFFFFFFFFFFFFFFSQF
3108	17009	A	3130	2	312	ANLI*LAYTIAFIVKIPLYGLHL*LPK AHVEAPIAGSIVLAAVLLKGGYGIIRL TLILNPLTKHIAYPFLVLSL*GGGVF
3109	17010	A	3131	449	3	FFFFFFFFLGGPPEIFFFFFCPPKKPKPP LGCGKKKPPFF*NFPQKPLQVLGAPPPP LCFFIKKKKGGGKKFFSPPLF*KGGPFK KFFFPKPPKPPFLKNLRGWVFFKPP PKKKALSFFKKKKKKKKKKKRAAAR DLELADAW
3110	17011	A	3132	95	448	VINRE*KVCV*MKKKKKKKKKKKKKKK KKKERAGKGGG
3111	17012	A	3133	60	442	LGGFFFFGKKGFCWLCPRWGAKAGIPV NGTPPRGV*RNFLAQP*EGGITGPPL PQ*FGFLRENGVPLRPGGFEPPILGEP PPLPPQKGGKNGRNPPPLKGFVLFPK EFSSLVPSWKARGDP
3112	17013	A	3134	236	45	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFGAAD*VILFRYFQ FEATIMGV
3113	17014	A	3135	441	88	KQQTTPGLIFF*KAPRREIFLPPPIMV FSPSPFKFFFLSPFIFFGGVLPFFPP PKKGGFFKNPRRVFFCPPLKKKNFFLP PFFFGPPRVFFYPPPIFFFFFFFFFFF FFFFFFF
3114	17015	A	3136	2	328	TMLSPKPQQLNQONCSPEHYEPOLKTQR TWR*KKKKKKKKKKKKKKKKKKKKK KKKKRGGGQKKKMVGEEKKPG*KIFF FFIKKVKKKTALGDKKTQFWGGS
3115	17016	A	3137	281	2	KATKSGTPIPSQGQSLAWSWAGIGSAQ PPALLHS*PIGKIFKNCMPVGRKSPQLP RNTSWQLGAVAHPSNSSTLGGRGGRITR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SGVRDRTRG
3116	17017	A	3138	448	3	FFFLPPSPFFPY*KRGSLEGRVVFNFPPVFPWPSPQIFGFQALIFLPPPPPLFESFPVGFFQTALFPNGFFPGFFHGLFPLLRFPCPRK*VFVGWGGFFFFFLLRDKVSLCHPGWNAVAQSEFTTALTSKAQAPTRPTRPPTRP
3117	17018	A	3139	2	436	DR*LFSTNHKEIGTLYLLFGA*AGVLSTALSLLILAEALGQPGNLLGNDHIYVNVITAHALGKIFFIAIPIIIGGFGN*LAPLIIGAPEMAIPIRINNIS*GLLPPSILLLLASAIIEAGAGTG*TDYPLAGNYCHPGASGLLIIF
3118	17019	A	3140	362	2	KPRRGKFFPPREGGGGFPFPPPKNFFFPKGGKFLGGGGGKNSPPQKGGFFQKNPGGVFFPPPKKKKNIFFPPGKMGAPPGFF*RGGPPPPPPPPPPPPPPPPPPPPGQSGQVKLKSPKCKL
3119	17020	A	3141	440	102	PTPPPCCKFSFKRPPKTLFFPTTNLVFESPIPP*NFFFSPPQALIFVGFLAPIFPPQKKFFFSKFPPLFFITPLIKKFFVPPPPIILSPLKIFYKPPPIIFFFFFFFFSF
3120	17021	A	3142	1	79	FKLDYFSIIFIPVALFVTWSIIEFSL*YINSDPNINQF*KLDYFSIIFIPVALFVTWSIIEFSL
3121	17022	A	3143	3	441	FFFFPPPLKKKKFFPPPPNIGPPPKSL*KPPPPPPFFFF
3122	17023	A	3144	223	3	LPYWKLPYLKH**LQDNTQESRG*HFLRPRPFKNQMKSGTVAHACNPSTLGGRGGRITRSGV*DHPGQHGEI
3123	17024	A	3145	65	414	KKKKKKKKKKKKKKKKKKKKKKRGGPKKKTRGGPQNPPPKKKKFPQKGGKKKPPLG*KKTPPLGGEKIPPPPKKNTPPKKKKK*GGGGQTPPPPPGKKFSPPRNKKKK
3124	17025	A	3146	410	31	RANQKAFRGKPLCDLAVGKNLSSRTQIALTI*KWINWTILKLRTSGH*KTPIKTIKRYPIEGEKISDEELYLY*QVL*IGKKKPDNPVEKWANDLKRSFMKGNILTVFKGMQR*LGSMAHICSL
3125	17026	A	3147	182	241	SHPSHHSTINITNKGGL*TPLPINPLVNLNLGLLFIATSSSLAVYSIL*SGGASN SNYALIGALRAVAQTISYEVTLAIILLS TLLIRGSFNL
3126	17027	A	3148	254	1	KTKKGLKTKDPLTRF*ISVC*ITKSI*FKLLPFFPPLKEHIPKYLFFFFFFLLET EFRSCCPGWSTMV*SLLTATSTSQIQAI
3127	17028	A	3149	499	2	NTPPAAGGGCFFFFFFGKFNFPHPPTP RFFPPPLKNFFFFSRVFFFWGGGAQKAPPKKVFF*KIPRGFFPPPKKKKIFFFSPGFFGAPPGFLLSGPPSFFFFFFF FFFFFFFFLLINFLSLQGFFLVSKELFLFGLTVKFTRGFRGFCGQ
3128	17029	A	3150	256	146	KNAKVTQVCPEFNKGPG*HTHTHTSHHTHTHTLQ
3129	17030	A	3151	333	1	TISCLCTRGEHPLSPRRAGPYTGSPLHC CVDVVDKVFSSWKDLTDWPLGLDIEYF TDGSSFILRGVCRAGYAAVTLDSAVEVL



SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3130	17031	A	3152	43	379	SVSAETSA*KAEIALTRALWLGKEQK NKTSLFGWDYIWEWGAPEPETPPKRAAG ALHSLAQPFSSVALPPCFDPCAPSLSPG *HALRPLDPLGLASEIQTAPSWHVPPKS LSPAPQPCPIPTLVPVGYKTPP
3131	17032	A	3153	398	12	NTTPGGGKFFLKKTREEKFFPPKKRGRF FPPPPPKNFFFPQGGNFFGGGGGQISPP QKKGFFQKNPRGVFFTPPKKKKIFFSPP GKMGAFFGF*RGPPFFFFFFFFFFFFFF FFFFFFFFLKKSWRLAI
3132	17033	A	3154	371	105	SPSPQVNFILKGPKPFPK*IL*RAPNPP LPKKKFSNPPTWGPQPFPSPKSKFAR FFFLPPPPFFPKKEPPKKKIFFPTKEGTV I*KNPPFSGFQSPDSIK
3133	17034	A	3155	3	371	DVGADPILHTSTGL*LAMQY*PEA*TAF SSIAHIT*DVYVG*VIRYLHANGA*IFF ICLLHLHIGRGLYYRPFYLYSKT*KIGLIL LLATITTAFIGYVLP*GPI*F*GATVMT NLLSAIPYIGT
3134	17035	A	3156	1	398	IAIPTGVKVS*LATLHGSNMK*SAAVL *ALRYIFLFTGGGLTGIVLPNSSLNIVL HDPYVVAHFHYVLSIGAGFAIIGGFH *FPLFSGYTLDTYAIHFTIFIGVNL FFPQHFLGLSGMPRRYSYDYP
3135	17036	A	3157	401	46	PPGGRNFFKKTGPKKIFSTKKKKGFPP LPPKNFFSPGGFFFGGGGPNFPKPK GFFSKNPRGVFFSPP*KKKIFFFPPG*I WAPPRVFLKGPPPPFFFFFFFFFFFFFG KKSVA
3136	17037	A	3158	404	18	FFSPPPPPPGGGVFPNPNKNFPPPPP PFFLGGGPPPPPPPP*FPPPTPPNVF FFSPPKKKNFFPPPPGPPPPPKPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP MEKGRPRGDIGSNPPS
3137	17038	A	3159	3	192	SLVIAGCPR*NLSSLNLPTSPKSPCK FNC*KKKKKKKKKKKKKKRGALKKN PWGKK
3138	17039	A	3160	205	80	VQRDNFGFLQSPSGVKLFCLSLPNKW DFRCGPPNPG*FFS
3139	17040	A	3161	3	384	LIVPTIILLPLT*LSKKHII*INTTTHS LIISIIPLLEFFNQINNLFSCPTFSSD HLSPILKKKKKKKKKKKKKKGGGA FKRTPGGAHWWGGGRETFPPKGGEKKN RPGVFWKQTFWGGK
3140	17041	A	3162	348	70	GPPPKRVFSKTPKVVNLNKPQKKKKFI FPPPVNLGPPKNFLKGPPPPPPPPPP FFFFFYFFWMGCDR*CSWRHSSPRLSG TPKCSPSVT
3141	17042	A	3163	2	353	LKTIPLTSTCLTIGSLALAGIPFLTGFY SEDHII*TANVLYTNA*ALSITLIATSL TSAYSTRIILLTLTGQPRFPTLTNIETK KKKGGPFNRYPLGAQVGGGQNEKFFLI GREII
3142	17043	A	3164	1	221	PTRPRDCSELRSCHCTPAWATEGDSISR KKKKLSTRTAF*YTEAINSLIYSLNIGT FKTYFPKIKTYDRHDF
3143	17044	A	3165	26	383	IPFYQ*SLI*YTRKKKKKKKKKKKKKK KKKKRG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3144	17045	A	3166	251	381	GNLGAGWARWLTTPVVPALWEAEAD*SRGQEIGAILANTVTKPHL
3145	17046	A	3167	391	115	LEKKISPHAGIWGFFSPLTP*NIFFSLEPFIFGRGLAPIFPPPK*RFLSKNPPVVFIPPPLMGKPPPPPPVRLGPPPIYSFKGAPPPPPPP
3146	17047	A	3168	94	389	SPGILGQKGQIGPIGNHVPGLAAPVTP*FRFKPRLP*GFGPKASPPLALKPERAQVGGTPPPGPRGPNGQPPPFKENQPGLGFRFRGKLAELKRGFHL
3147	17048	A	3169	3	363	WATALQPGQQSETQSQKKKKKKKKKRGPPPPPPFKKKIFFSPGAKNKRKGF*KPPKKKKKIFFPPPPPLKKKKKKKKKKKKKKKKKKMGGAFLKKPRGAPPPPGKRKLIFFLKGV
3148	17049	A	3170	2	171	KEPLGYIRMV*AMISIGFLGGIV*AHHIFTVGIDVDTRAYFTSATIIIVIPTGVKVF*S*LATLHGSNMK*SAAVL*ALGFIFLFTVGGLTGIVLTNSSLDIVLHDTYYVVAHFHYVLLIGG*FYLRYNHNCYPHRRQSI
3149	17050	A	3171	390	27	QSLTVKSPYPVVILIKTKGHH*VMNAGLTRYQSLLCENPHIRSEVCITLNPPLLPVSESPVKHSCVQLDSVSSGPNL*DHP*TSVDWELVVDGISFANPCKVSLKMTSPAPVTPRS
3150	17051	A	3172	127	310	KNPGGAKILRGGGERKNFFLKRGGKKKHLGIFGKKTFFWGGKKWAKPPK*WRFSPFSP*KFFFSLKALIFFGGFCPPFSPPKSFSSKNSQVFFSPPFKEKIFPPPPP*NGPPRVFLKGPFPFFFLGVFFFFFFF
3151	17052	A	3173	376	3	FFFFFFLRRQSLAVTLAGV*RCNLSSIQSPPPGIK
3152	17053	A	3174	365	14	RENFFSPEGGAPKNKPPPPPPPGGKKKIFFQKKKKKIFYPWKNFPPPKKKKKNP*KPGPLKSQGFFFFKKNQNLWPWGPPQISFPKKKKKKKAKTVQERKYNSTQLVSAETQLL
3153	17054	A	3175	1	377	VPLHSSLGGKARLHLRKKKKKNPGFLKNFGPLALLGMGVGNIKGLKGQKGNPAFGAHTGGGCFSLRGRNTPFPKRAEGIIICYNSPH*KET*KALEPRGYKGL*QALALENLKSGKMEHILRGAP
3154	17055	A	3176	352	125	GHEVLDSSDLPASASQASAGITGVSHHAL*EILLSMFETTWACDLLFQNISFIKSSIPCFIGLDFIMPHRYCRFF
3155	17056	A	3177	139	366	TAHTS*GY*VKNYINLSFCFFFFFFLERNHSAIQPGQGHNRSLSQWPFPLKQFSCLSLPRSWDNGLVPQHLVNF
3156	17057	A	3178	206	1	KGTLFKKDFFKFNFPKKVFLGVPKNSLF*KILTLPVLNPPYPPFFFFFFFETVSLCHPGWNAVVRLEP
3157	17058	A	3179	330	1	IVSTLETICYIAYNEEEKDTFITLRIYVIGGNGKFLGI*IKQHIKKIHHQVGFIPGMQGWFNICRSINVIHHISRIKGSRAQWLTPVIPALWEGDAGGSPEVRSSRPA
3158	17059	A	3180	3	399	HASAPLQSSLYRARPCKKKKKKKKGGGGGGFFFPKGGFGPLPKKGFSGKGGGKWLGLGAGKTPGIKKPLGKPPKRGCK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KGQKGPHF*KKKKKKGGKKLKKGPF*KP FKKPLLGRGVQP*NPHLLGG
3159	17060	A	3181	2	204	CPTACPFW*NKELLMPKKKKKKKKKKKK KKKKKKKKKKRGAPFKNSLGGPHFPAG KKNFFFFWGGY
3160	17061	A	3182	71	377	PKRGGQPKQKKIWGPPPPGAPPQKGMGF FNERGFKKQITFFPPPPPEKKKPPFF* KKKKKKKKKSNCS
3161	17062	A	3183	151	2	FFFLEELVPLLLKLFQKIEEGCSPNSF NEAFILILIPKPR*TTKKENF
3162	17063	A	3184	152	387	YFQGFYVACICTSFLFFFLKREFC FVTQVEVQGNFT*LNPLFLGLKKFFCL TLQIGWNNRPLPPPQVIFCFFK
3163	17064	A	3185	22	336	YEKCTALLQMVSSFIWMEREGTHQYSFY RKDFSLASKVNIVSYLSPIVE*FFFFL RGSPFAPQAGGQGNLGSWKPLPPGLMP FSCLTLPGGWNCRPPPGPVN
3164	17065	A	3186	344	1	WVLKKIFFYPGRGGPPFIPPLGGQGGP IPWARGF*PPRGPPPKNGF*KKKKKRG GGPPPGFPPPGPRGGVPFFLGGGGPRK PKKITKKKNPGEKKKTSFKNQKRKTKIK TT
3165	17066	A	3187	296	1	NPKKILTLPKTKVYKCEGENQVPIIFQ GIKNIFWKGIF*PKKEREVCV*SMRHVI PVFPKKRGSKRNSKCCYKDTCTRMFIV ALFTIGKTWKQPKY
3166	17067	A	3188	2134	1	GVAAHACNASILGGQGGRII*GWEFETS LANMVKPC
3167	17068	A	3189	1	159	LQDHPG*HGEPPSIVKIQKLARHGSRL *S*LLGRLRQMRQETCLNPGAR
3168	17069	A	3190	119	340	QIKKNRLVSARGKNNKR*IKP*VDIF FKEDIQAGKQMKRDLISLIIRIQT TITCYLIHARMGTITRD
3169	17070	A	3191	75	1	LSVNNFWPGTVAHACNPSTLGG*GG
3170	17071	A	3192	343	1	IFILGGGPCSPVFFQFEGGGGGFFLP QNFFPPRGKIFRPFFF*KKKLKRPNWGF F*NFFNPPLGFFNLFFFFPKKKPNFFF LGGFFFFFFFFFFFFLAGCDLALSPRL EC
3171	17072	A	3193	105	368	KFKDPPFPFPFPFPKQLPPPPGKIGA PHF*TPKGPPPPKKKKC*KKKILKGGRG KKKKKTPPKRPQKIWGPSKKKNPWGGGK TPPL
3172	17073	A	3194	1	365	FCRDEVLLFCPDWSPTPLKQFSLCLP KCWSYRC*PPYPAQGVFLK*HLTKSLSC LKLFMASLCLQDKVPAPQPCVKGLSKFF LCHLLSTLIPFTHSLFFFLGWFLRQHR SVTQAGVQWR
3173	17074	A	3195	1	362	GNQPKRLNAGTYLLFYTLGSSVPLIAL MYTHKTLWSLNILLTLTGQELSN*AN NLI*LAYTRALIVMIPLYGLHL*LPKAH VEAPIAGSI*LAAVLLKGGYGIIRLTL ILNPLTNT
3174	17075	A	3196	137	3	KGQPRFPFISLKKGSQKKGFFFFF*Y RIPLCHPGWCPVVQSW
3175	17076	A	3197	1	266	EGRGCSEL*SCHCTPA*VTVRYPVSKKK KKKKKKGGGKGGKGGKNTLFGPKKGG LRGPQKRGGKIGPEKKVGNLKKGIFFR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EKTF
3176	17077	A	3198	217	446	YWSEHYAMTQVLEGFSYSLODHFYFCFR SIRRIIFYSLIKPSIND*GERELEPITT SQALQIAGRGRFSSRFKEG
3177	17078	A	3199	345	314	QPGPEGKIRFFLKIPLNLTSPSGGKSLKFP LFKRVKPENCLSLRG*GCN*PI
3178	17079	A	3200	2	330	SRHYTPAW*QSKTLSPKKKKKKKKKKKK PPFPKNTQKKPKKKKRGGLNWGVKTPPP LKTQKMGISPGKKLKKNLFPKKKKKPEG NPLF*FRGF*KKKKAPFKKKKNPPK
3179	17080	A	3201	2	385	FFPFLGGPQIPKFLKFFLRAN*NLFGFL FLGGVLKKIPLRKPFSLWIKPFPTFPKG KKIFFKTFQKPLFFF*KKKFFFCFPFF FFLSRGFFVFFSPKKPFFFFFFFFFLL
3180	17081	A	3202	355	2	FFFFFSETESCSVAQAGVQWHYLGSG*A LPPRFTP
3181	17082	A	3203	156	1	LKSLLEAKVGGLLLEVRSRPA*ATWRD FISTKN*KISQVWYILVVVTTWE
3182	17083	A	3204	352	175	QPRGRPAPAHPP*CPLRLALPC*CPCPA CCPPWAEASPSGVQASPARAPACPARAL LNE
3183	17084	A	3205	280	373	QRGTRIFSDLQT*KKKNKSPFKILLID NALGHSRVLTERYKDIRPANTTSFLRP MVQELIPTFQS
3184	17085	A	3206	1	367	EIESIQIDGHTKNKFLGIHLTYLTKEVK DLCKKNYKTLLEKIIDTEKYDMLMD*N NIVKMAILPKAIYRFDTISTKLLMSFFM ELEKIF*NL*KA*MAETTISKKNKAGG ITLLDFKLYY
3185	17086	A	3207	368	12	FAQKKKKKKKKKKKKKKKKRAPPQN* RAPQKPLKPPPRVFLIPPLGSPPPPAF FWRGGGPPPGFFSKKKKKMRLTGGGRLF LLA
3186	17087	A	3208	2	356	KYLFSSIPEGKEKMGIANLFNEIISEN CPSLARDLDIQKTRHANPYNLKSSPQH IIVKLSKVKDKERILKTARKECFITYKR TPIRPGMVAYACNPSTLGG*GGWIMRSG DQDHPG
3187	17088	A	3209	359	170	INIKQLPRCGGTCLWSQLSRRLRRQDCY SLGGQGCSSEL*SSQCSPAWATERDSVSK YKINNFL
3188	17089	A	3210	295	122	VIKTV*NNWKDRHIDQCSRIESPKIHLH IDDQLIFDKDVKTPE*RNGLFNKWCWE N
3189	17090	A	3211	218	466	ATFDTTLPSCYQNA PNRRFDDLSD*EQE IDTMTVNIILPLRSLNIVITNPYNI*HH QHDLDTYPTDTTGQLVNCAYFINLLQP
3190	17091	A	3212	340	355	LGLQG*REGNFGSLQTSPPGFKRFSGLS LLSSWDYRV
3191	17092	A	3213	254	40	WPGTMAHACNLSTLGG*GGCITRPGDRD HPG*HNNNN
3192	17093	A	3214	198	25	YNEKEKPVKMLKIANS LGAVAHAYNPS TLGGQGGRIMKSGDRDHPG*HADAVET VL
3193	17094	A	3215	376	3	PPGVF*RGPPGFRTLPPKSSSSSPPKI LGGPPFLAFGGAPPQKPPSSSSSASS PPSSSSRAPLKGGFPNPAGGFPLFGGP PRGGPPFSSSSSSSSSSSSSSSGRRSR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SRTSRTTRGTRG
3194	17095	A	3216	393	260	VSQDGLDLLTS*STRGLGPKCWDYRREP PRPACTLCISSTYNDP
3195	17096	A	3217	3	387	HASASSGSRAPPFFFFFFNKKTKGSKELET TRGTVLKTCLFFKKKKKVLGGPKPPLGN PKGVGKPLKGFPGPNWPPP*KGPGCHF *KNGF*DPGPKKSHIPSWVGKGSSLLP GPLGGPSEVYFSPRLA
3196	17097	A	3218	77	406	RMARPELGLPGNLLSNDHIYNGIVTAHA FVIFLIVIPITINGGFGN*LIPLIIGAP DMAFPRINNISF*LLPSSLLLLLASAIV EAGAGTG*TVYPPLAGNYSHPGASVK
3197	17098	A	3219	394	2	KRRYFPDGLNFFWGGPGLKIFVKKKVSS LKKKKKKNFPPVFLQWGGNKNFKGGGL KFSKPNLI*FFFPQKEAR*KVFFFFRS PQKDPLREFFFFFLRQVSLCHPDWSAVA RSQLTSAISRAQGAGRV
3198	17099	A	3220	376	157	KFFFSP*KFFSPKPLKFGGGVGPIIPP PKKRFFFKNPQGVFKKPPQKKKKIPFQP PVNFGPPRDFLKGPPPPFFFFFFF
3199	17100	A	3221	394	1	VPPPQKFKTPGPPPPPREFFFF*KKKGF PPLGGFLNPAPKNPPPGPPKKVGFPGGP PPPPGGFFFSPLSF*NPGERVFFGPKI PKRKFLWKWGGGKFFPKKPIFPFPPKK KKKKKKRAAARDLELADAW
3200	17101	A	3222	207	402	SILM*LCCLFPLPGVTPIDGAPHRYSRE CYPVLLDGVVMGVVDKDLAPGIADSLRH FKVMREKRI
3201	17102	A	3223	309	3	YPPFHLIDLAIHPCVCFTKPYKATVTQT AWSWYQIRYIDQ*NGTEISEIPPHIYNH VICDKHDKNKQWGKDSLFNKWCWEN*LA ICRKLKLDFFPTPYAKI
3202	17103	A	3224	3	382	LDRERPPFFFWGARHMDIPQLVNLISINK GHWANFNFLGYKKKGWEKKKKKKKKK RGGPP*KKPPGGPK*PPGGKR*IFPYMG GKKKPPGGFLEKPPPLGGAHLGNPPQK YTPPGKKKLNKRET
3203	17104	A	3225	133	2	FFFETESHVTRLECSGTISAYCNLCPL GSSDSPASAS*AAGI
3204	17105	A	3226	349	2	AGVPPGNPPLWGGEGGSPRGGGLKPGF PQRGNPFFFKKSQPTPPGGGPPLIPPPW GGGAGGSPLPQGQRFQ*TKIGFPSPRG KKKKPPFPKKKKKKKKRKEKSEMPGFMV LNA
3205	17106	A	3227	3	239	LNKVGRCSEPRSRHCTPAWATE*DSIS EKKKKKPESRGILKVGLTQALFYLAALW LYYLHPTAKQIIGFFIYFSKP
3206	17107	A	3228	205	1	IGLKIQNSCPLKDSLKKIKRQATDWRKY LQNTSDKASVFIIYKEHLQLSNYKAVDP IK*WAKEMNKLH
3207	17108	A	3229	174	1	VQMLEDKSFEETP*FSSETLVLKIPIHVQ PGAVAHTCNPSTLGGRGGRITRSGDRDH PG
3208	17109	A	3230	2	340	KNHSVYLLCVFSIPFPTFCFF*F*VFNT F*FKLN*IN*FTYIDRVLLCHPGWSAVA *S*LTAALNSWAQAVPCLSLLLAHHHAW LIIFKKTAYIIHIWVWYDTTYPFKVYN S

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3209	17110	A	3231	1	313	KKSTPYQRGFDPISPARVPFSIKFFLEA ITFLLEDLEDAALLPLP*ALRFIFLFTV GGLTGVVLANSLLDIVLHDTYYVAPHFH YVLSIGAVLAIIGGFH*FP
3210	17111	A	3232	207	355	ELSPFRLKKTLY*LGMVAHACNPSTLGA RGGQIA*AQEFKTSLGNMAKP
3211	17112	A	3233	3	355	TTQQ*LIKLTCKQTIATHNTKGR*ALI LISLIIFIATTNLLGLLPYSLTPTTQLC INLAMAIP*ADAEVIGFRSKIKNALAH LLPQGTPTPLIPILVIMETINLLIEPIA LARRL
3212	17113	A	3234	2	355	KYLINNRLITNQQ*LIKLTSKQMITIHN TKGR*SLILISLIIFIATTNHLGLLPY SFTPTTQLSINLAMDIP*SGAMVIGFR SKIKNALAHFLPQGTPTPLIPILAIET ISLLI
3213	17114	A	3235	43	370	QGCVGWVLEEQVRRGWILDSSEKTDL KQRGSPGWSPEHVGWGSVGM*SEAWTG QARWLTPITALWEAEVGSRLRPGVQWH NLGSLQPLPPRFKRFYSFLPSSWD
3214	17115	A	3236	15	356	LIQPSLKLMISIHNTKGR*SVILLSLI IFIATTNLLGLRPYLFPTTQLSINLSM VIHL*AGAMVIGFRSNIKNALAHLLPQG TPTPLMPILVIETIRPLILPIALAVRL TA
3215	17116	A	3237	1	376	GTRNTLTIIYQ*WGDGTRESTYQGHHTP PVQKGLRYGIILFITSEVFFAGFF*AF YHSSLAPTPQL*GHWPPGTITPLNPLEV PLLNTCVLLASGVSI*AHHS LIENNRD QIIQALLTIVLG
3216	17117	A	3238	1	358	GTRNG*YTNA*ALSITVIGASLTSAGGS RIILLTLTGQPRFPPTLNINENNPTLLN PIKRLAAGSRFAGFLITNNISPGCPFQT TIPLYLKITDLGVTFGLLTGLDLNXYLT NKLIKA
3217	17118	A	3239	258	390	RQGLLMLAGLVLSNWPLQSSHLGFPCW DYGREPPCLGN*LIL
3218	17119	A	3240	2	372	ARARFHHVSRDGLDLT*NTHLRLPKC WDYRREPLRPGKTFFLKKKKNSIFLFF REGFKEKSILGIKFFRPTGGVLITGNH GWGCKTGTELLVPSRFPGLAFKICGLWA HDTPHRVNRWL
3219	17120	A	3241	3	283	HERLWGGWKTGAAGLGRSTSRPTASLTQ T*TTMT*SRRTGCGSTGSGRTWTRSRHS CAWGMAGLYRVAVASRGPRGMM*PTPPH WLCWAWKVP
3220	17121	A	3242	170	3	IKSQAGLVGFLGPFSFQDSLNLVVFVGF FCF*DRVSFCSPGWSAVVQSEFTAALV
3221	17122	A	3243	2	385	ARADVTPSYLTSDTIMRDIPTGGQVFS *LSTLHGSNMK*TAAPLLTLGFI FLFTA GGLTGLELTNSWLDIVLHDTYYVGPDPFH YVLSIGAVFAIIGGLH*YPLFSGYTLY RTYAQIHFAIFIGEN
3222	17123	A	3244	1	106	GTRYVGQAHLKCLTSSDSPASTSQSAGI TGVSHSA*PASTSQSAGITGVSHSA
3223	17124	A	3245	2	360	ARANTLTIIYQ*WSDVSLentyQGHHTPP VQKGLRYRIILFITSEDYFFSGFL*AF* HSSLSPTPQL*GHWPPGTITPLNPLKMP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLNTSVLLASGVSI*AHHSLENNRNQIIQALLI
3224	17125	A	3246	17	160	GG*GCSCSEL*SCHCSPAWVTEQDFDSK KKPAILASCLKHLNPLSSH
3225	17126	A	3247	236	2	WAHIYMTPLSPPSFLKPQ*KNFYIYST YSLDN*NPSSPKAKRAPKSYTLPLYHL CVCVCECV*VCVCVCVCVCVWV
3226	17127	A	3248	2	2220	FFGGGRPSPPQGYFLLNNHSSPSPVKL NPGPA*FYPTKGNFPPQR*PSPPKN IKTPPSFFFS
3227	17128	A	3249	2	372	AYTISFIGRISFYGLH**LPKAVEAPI VGSIVLAEELLKLGFGIHLTLIFNPL TKHIAYPFLGLSL*GISITSSMWLRQTD LKSLIAYSSISHIALVVTAILIQTP*SF TGAFLLIIDHG
3228	17129	A	3250	293	56	EGSPKVIENKSPPHHFLFLFFFFIFFF *FFFFFFFFFFFFFFFFFFFFFLYL LAMFYLSEFFKQDNQRRQYSIK
3229	17130	A	3251	169	370	LKMTLRLGAPASKPRGQEPHPHYCHHH HHHHHFL*VTKGQGPWWPSPTRDPGW L*SPS*EDQRR
3230	17131	A	3252	22	156	GERIGLGLGGQGCSEP*LCHCTLAUVGD TVRPCLKKKKKKGGPF
3231	17132	A	3253	3	400	QNQTPLLD*GGLITAVLLLLYLAVLTGG ITILLADRLDSTLFYPAGGGDPILYQH LF*FFGHPEVYILILPGFIVSHIETNY WGGKEPFGFVGMV*AMIAMGLGFIG*A HHIFTVGVDVHTRA*FTSAT
3232	17133	A	3254	373	31	REVGPPTP*KIFFFPKGLNFWGGGPKF PPPKKKGFKKSPVGVPPPPGG*KSGPG PGFKKPPQKGNISFPAGGKIGPPRGT LKRAPPFFFFFFFFFLLWVVVQVERP TL
3233	17134	A	3255	1	379	LNLIQRQ*R*V*KFL*LPPQT*KKKKK KKKKKGGGAFKKNLGGAKFNGGRKKKIF FLKGGVKKKAGGGFKRKGKKCYLGI FEKKPFFGGKKNWENPPKKIKGLREKKK F*GEKGEKKPEKAG
3234	17135	A	3256	42	376	FCYISLVHHCITYNDLSFERKKNI FVPGQ INSISSIA*EAHCNKNSLLHAVKKKKK KKKKKKKKKKKKKKKKRGEKKKKKK KEGRSSLKKEK
3235	17136	A	3257	353	67	CYPLSPLKFFFSPRSLKFWKGVGPIISP PKKKVPSQNSQEAGFPSPNVLKRRPGPN FKTTP*KEKNFPFPVPKFGPPKESLKR PPLFFFCGLQ
3236	17137	A	3258	2	129	PHRISQDGLDLLSS*SARLGLPKCWDR CEPPRPAKNKILLS
3237	17138	A	3259	205	415	QOKNRRLHFKGARTHNSYNRGQPTPS ITAHMPRLRQSHTIIVLRVHHP*VPSA IEGPVSV*ALLHSSTIVVAGNLLLIRFH PLAEKSPLIQTVTLCLGANTTLVAGGWA LTQNDSKRIAAFSTSRGLGLIIVTIGVN QPHLALLHICTHAFVKAILFMCSSGSIH NLSKEQDIRKIGGLLITIP
3238	17139	A	3260	3	393	SFNLSTLITTOEHL*LLPS*PLAII*F ISTLAETNRTPFDLARGEAEVSGFNIE YAAGPFALFLIAEYTNIIINTLTITIL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LGTYYDALSPELYTTYFVTKTLLTSLLL*IRTAYPRFRYDQLIHL
3239	17140	A	3261	2	400	ISDLSEK*FKRLVVKLIMEAPEKGAQC KEIQKMTQEVKGEIFKE*IA*KKKSKF QETLDTLIEMQSALESFSNRKQVEERN SELKDKIFELTQSNKDKGKRIRKYEQSL *VAWDYIQ*PNLGIIGIPEEE
3240	17141	A	3262	450	129	NNLAFN*V*EFCVLAIKLLKVKRYPIEW EKMFAHNSIDKGLVSGYKELFRLSNKQ AIDLTF*KWAAGHGGSP
3241	17142	A	3263	238	3	KEKKIGLKKCLQGSHFSIHTAWSIIYM FSPLTIISRKRMGQPGIVAHTCNPST*G G*GRWITRSGVRDQTGQHGKTP
3242	17143	A	3264	350	3	SPTLLGSKDPNLLGFRFPLWKKGKIIRA PLSLGLN*RFSEVVLIP*KPPKNWPGG TFLVVCFLKRGFPFLSQKKKKKNPGAVA HACNPSTLGGRGGRSQQELETSLANTV KTR
3243	17144	A	3265	69	200	RLECSGVISAHCNLLNPGSGDSPASAS* LAGITVMVKLPVIAK
3244	17145	A	3266	223	408	GGFPPFPFGGEGGNFGELEPLPPGLRK FFCLGPPRRGD*GPRSSSPGSFVVFKN GVSP
3245	17146	A	3267	185	420	DQGLWGFIIYFYRQSLA*VHWNPNSSL* PRTFGLKHTFVPSLLISWDYGRTPPHLT NFCIFFDRGSFFF*DRVSATHA
3246	17147	A	3268	3	392	TGCHSIPQAGVQWHNGLLQPPGLR* SSCLSLPSSWHY
3247	17148	A	3269	1	398	KFSCISSKHQKLKLTPKPPKPPKKSPL VLPIGKKIRETFWGAFKSPPPNQPKGAQ TLPLKIWDKMGGGGGLALVV*KAPPGNF KGPPGKPMQEP*LGPGPPLKWKGLPH QKGGFSKAPGEKKKGEGRL
3248	17149	A	3270	422	183	ETEVVSLFKVIITEKSPNLEKDTNIQVQ ESYRTPSRFILMKTTSRHLIIILPKVNN TERIL*MQQDRGNNIQWSSGCSA
3249	17150	A	3271	3	35	KNNSLIIPITIIATITLLNLYFYLSPLLY **SSSPPS
3250	17151	A	3272	155	1	KDFFFFFFLQSFLLVAQAAAEWCDLCSL QPKPPGFK*FSYNSLSSSWDYIG
3251	17152	A	3273	413	71	PPSTGLFLTEEYEVSFPPFPL*KFFFPF SGLFFGGVPPFPFPKKGFFPKYPRLV FKGPLLGGGGLPPPPP*ILPPLGSFLPA PPLFFFFLFFL
3252	17153	A	3274	336	45	DRVLSCSPAWRAMARSHDFG*IQLPFPPR VKVFSCLSNPSSWDPRHVPKGNFVFL VKTGNPNWNLGGQGCRRRLCPICPAWGT DKDSVSKKKKKS
3253	17154	A	3275	206	366	SVFFFVLFGGFFYGALLCFPNPWLECSGT ILVHCNLFPGSKDSSASPS*VAGT
3254	17155	A	3276	334	75	ENTRRVERRRRTHIIYNNFF*EFMNRFF FFIFFDGRFSCVFFFFFLFYFFFFFFFFFF FFFFFFFFFFFFFFFFFWSARSIYFLFPRH VT
3255	17156	A	3277	144	17	KAPPLFFFFFFFFFFFFFFFFF*FRG*T HWNGDACMCNLTKS
3256	17157	A	3278	2	109	YHIVKPS*PLTGALSALLMTSGLAM*F HFHSITL